Human SCC Amino aci Protein d Protein d Protein d Human str Ovarian c Chuman hea Chuman hea Chuman hea Antipsori Human HSC Ruman HSC Rat SCCE Ruman Str Human HSC Rat SCCE Human Str

Abb84406
Abu07440
Abu07440
Abu07471
Abr58471
Adb80484
Adj6883
Adm39180
Adm04182
Adm72880
Adm72880
Adm72880
Adm66515
Adm76881
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Adm66882
Adm68828
Adm68828
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Adm68828
Adm68883

Human str Human str Bovine SC Streptoco

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ALIGNMENTS
                                         AAU82740
ABU07440
ABU07440
ABRS8471
ADB80484
ADJ66883
ADJ06515
ADN04182
ADN04182
ADR7286
AABR4422
AAE08298
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                                                                                                                                                        July 13, 2005, 16:12:23; Search time 76.6667 Seconds (without alignments) 45.402 Million cell updates/sec
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                            2105692 seqs, 386760381 residues
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Listing first 45 summaries
                                                                                                                   - protein search, using sw model
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AAE08236
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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A X X X	
	AAEU8294 Btandard; peptide; y AA.
	AAE08294;
	01-NOV-2001 (first entry)
	Human stratum corneum chymotrypsin enzyme peptide #59 (residues 72-80).
o XX XX	Stratum corneum chymotrypsin enzyme: SCCE: cytostatic: vaccine: tumour:
_	cancer; ovarian; breast; lung; colon; prostate; carcinoma; human;
es XX	antisense therapy; malignant hyperplasia.
	Homo sapiens.
X X N N	WO200159158-A1.
	16-2417-2001
	07-FEB-2001; 2001WO-US003977.
	11-FEB-2000; 2000US-00502600.
	(UYAR-) UNIV ARKANSAS.
MX PI	O'brien IJ;
	WPI; 2001-514676/56.
PT	Diagnosing cancer comprises detecting stratum corneum chymotrypsin
	פוודאַוויפי
D SA	Disclosure; Page 115; 127pp; English.
	The invention relates to diagnosing cancer especially ovarian cancer. by
	screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are
-	considered to be an integral part of tumour growth and metastasis, and
	therefore, markers indicative of their presence or absence are useful
_	ancer,
0.5	carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used
	and other cancers in which SCCE is overexpressed. The present sequence
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× S	Sequence 9 AA;
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ADR68792;
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                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleoride may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other_cancers in which SCCE is overexpressed. The present sequence is
                                                                                                                                                                        Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:89.
                                                                                                                                                       Human stratum corneum chymotrypsin enzyme peptide #1 (residues 72-80).
             Gaps
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              0; Indels
   Pred. No. 1.8e+06;
100.0%; Preα. .....
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          Claim 25; Page 102; 127pp; English.
                                                                                                 AAE08236 standard; peptide; 9 AA.
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            9; Conservative
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  Best Local Similarity
Matches 9; Conserv
                                KWNEYTVHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human SCCE peptide
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Best Local Similarity
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The invention relates to a novel method for vaccinating an individual against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating an individual with a SCCE peptide, which elicits an immune response in the individual with a SCCE peptide, which elicits an immune response in the individual. A peptide of the invention acts as a stratum corneum chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating an individual against SCCE, particularly an individual having, suspected or at risk of getting ovarian, lung, prostate, pancreatic or colon cancer. The oligonucleotide is useful for treating a neoplastic state in an individual, such as ovarian, breast, lung, colon, prostate, or peptides are also useful in the monitoring and development of immunotherapies for ovarian and other malignancies. The present sequence represents a peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of stratum corneum chymotrytic enzyme (SCCB) peptides, for vaccinating an individual against SCCB, and in monitoring and developing immunotherapies for ovarian and other malignancies.
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serine protease; stratum corneum chymotrytic enzyme; SCCE; immune response; ovarian cancer; lung cancer; prostate cancer; pancreatic cancer; colon cancer.
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100.0%; Pred. No. 1.8e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Santin A;
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Best Local Similarity
'.^a 9; Conserv
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                                                                                                                              Homo sapiens
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01-NOV-2001;
17-APR-2002;
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                                                                                                                                                                   The invention relates to a novel method for vaccinating an individual against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating an individual with a SCCE peptide, which elicits an immune response in the individual. A peptide of the invention acts as a stratum corneum chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating an individual against SCCE, particularly an individual having, suspected or at risk of getting ovarian, lung, prostate, pancreatic or colon cancer. The oligomucleotide is useful for treating a neoplastic state in an individual, such as ovarian, breast, lung, colon, prostate, or peptides are also useful in the monitoring and development of immunocherapies for ovarian and other malignancies. The present sequence represents a peptide fragment of serine protease SCCE (stratum corneum
                                                                                                      Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for vaccinating an individual against SCCE, and in monitoring and developing immunotherapies for ovarian and other malignancies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:109.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             serine protease; stratum corneum chymotrytic enzyme; SCCE; immune response; ovarian cancer; lung cancer; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 49; DB 8; Length 9; 100.0%; Pred. No. 1.88+06; ive 0; Mismatches 0; Indels
                                                                                                                                                5; SEQ ID NO 31; 117pp; English
                                                                Santin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Santin A;
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20-FEB-2004; 2004WO-US005134
                     21-FEB-2003; 2003US-00372521
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Matches 9; Conservative
                                                                Cannon MJ,
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                                         (UYAR-) UNIV ARKANSAS
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                                                               O'brien TJ,
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                                                                                                                                                            against stratum corneum chymotrytic enzyme (SCCE), comprising incentating an individual with a SCCE peptide, which elicits an immune response in the individual with a SCCE peptide, which elicits an immune response in chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating an individual against SCCE, particularly an individual having, suspected or at risk of getting ovarian, lung, prostate, pancreatic or colon cancer. The oligonucleotide is useful for treating a neoplastic state in an individual, such as ovarian, breast, lung, colon, prostate, or pancreatic cancer, and other cancers in which SCCE is overexpressed. The peptides are also useful in the monitoring and development of immunotherapies for ovarian and other malignancies. The present sequence
vaccinating an individual against SCCE, and in monitoring and developing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represents a peptide fragment of serine protease SCCE (stratum corneum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
ineurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                                                       The invention relates to a novel method for vaccinating an individual
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                             immunotherapies for ovarian and other malignancies
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                                                                               Disclosure; SEQ ID NO 109; 117pp; English.
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2001US-0327449P.
2001US-0327917P.
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2001US-0328056P.
2001US-0328849P.
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2001US-0330142P.
2001US-0330309P.
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2001US-0349575P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001US-0346357P.
2002US-0373260P.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KMNEYTVHL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chymotrytic enzyme).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KMNEYTVHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003029424-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-OCT-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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Query Match
Best Local Similarity
                                                         Sequence 97 AA;
             Smithson G,
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1 KMNEYTVHL
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(MILL/)
(PEYM/)
(KEKU/)
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(GUOX/)
                                                                                                                                                                                                                                           ADN62904
                                                                                                                                                                                            RESULT
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à
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(e.g. NOVI). Also described: (1) a composition comprising a polypeptide

coefficial above and a carrier; (2) a kit comprising, in one or more

containers, the composition described above; (3) an isolated nucleic acid

comprising the nucleic acid molecule described above; (5) a cell

comprising the nucleic acid molecule described above; (5) a cell

comprising the nucleic acid molecule described above; (7) methods for determining the

presence or amount of the above polypeptide or nucleic acid molecule in a

sample; (8) methods for determining the presence of or predisposition to

a disease associated with altered lavels of expression of the above

co a disease associated with altered lavels of expression of the above

polypeptide or nucleic acid molecule in a first mammalian subject; (9) a

method of identifying an agent that binds to the polypeptide described

above; (10) a method for identifying a potential therapeutic agent for

use in treating a pathology that is related to an aberrant expression or

aberrant physiological interactions of the polypeptide (11) a method of

screening for a modulator of activity or of latency or predisposition to

c a pathology associated with the polypeptide; (11) a method of

cor preventing a pathology associated above; (13) methods of treating

cor preventing a pathology associated with the above polypeptide. NoVX

sequences have antidiabetic, anorectic, antibacterial, virucide,

immunomodulator, cytostatic, noorpoic, neuroprotective, antiparkinsonian

c mammal; and (14) a method for producing the above polypeptide in an aderiance or preventing a method for producing the above polypeptide or the nucleic

and antilipaemic activities, and can be used in gene therapy. The

polypeptide is useful in manufacturing a medicament for treating and antilipaemic activities, and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       on G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; ajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; ts RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, hacematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 171; 586pp; English.
                                                                           2002US-0373884P.
2002US-0374977P.
2002US-0381037P.
2002US-0381038P.
                                                                                                                                                                                                                                      2002US-0381042P.
2002US-0381642P.
2002US-0383656P.
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2002US-0391335P.
                                         2002US-0373826P
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N-PSDB; ADA05739.
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                                                                                                                     22-APR-2002;
16-MAY-2002;
16-MAY-2002;
                                                                                                                                                                                                                                           16-MAY-2002;
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                                                                               19-APR-2002;
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Eisen AJ, G
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Gaps ô

100.0%; Score 49; DB 6; Length 97; 100.0%; Pred. No. 0.11; ive 0; Mismatches 0; Indels

9; Conservative

Matches

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anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder;
                                                                                                                                  human; NOVX; metabolic disorder; diabetes; obesity; infectious disease.
                                                                                                                                                                haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
                                                  ADN62904 standard; protein; 97 AA.
                                                                                                                                                                                                                                                                                                                                                                       17-0CT-2001; 20010S-0330142P-
18-0CT-2001; 20010S-0330309P-
24-0CT-2001; 20010S-0339266P-
24-0CT-2001; 20010S-0343829P-
29-0CT-2001; 20010S-0343829P-
01-NOV-2001; 20010S-034535P-
17-AFR-2002; 20020S-0373815P-
19-AFR-2002; 2002US-0373815P-
                                                                                                                                                                                                                                                                                                                                09-0CT-2001; 2001US-0328044P.
09-0CT-2001; 2001US-0328056P.
12-0CT-2001; 2001US-0328849P.
15-0CT-2001; 2001US-0339414P.
17-0CT-2001; 2001US-0330442P.
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2002US-0373884P.
2002US-0374977P.
2002US-0381037P.
2002US-0381038P.
2002US-0381042P.
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09-0CT-2001; 2001US-0327917P.
09-0CT-2001; 2001US-0328029P.
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                                                                                           01-JUL-2004 (first entry)
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ORT T.
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EDINGER S R.
ELLERMAN K.
53 KMNEYTVHL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MILLET I.
PEYMAN J A.
KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMITHSON G.
                                                                                                                                                                           wasting disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-APR-2002;
16-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAY-2002;
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                                                                                                                                                                                                 Homo sapiens.
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                                                                                                               Human NOV18e
                                                                                                                                                                                                                                                                               02-OCT-2001;
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(ELLE/)
(MALY/)
(ORTI/)
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ABG23378 standard; protein; 136 AA.

RESULT 8 ABG23378

53 KMINEYTVHL 61

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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                    Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease
                                                                                                                                                                     Millet I,
GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
                                                           STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
                                                                                                                                       GANGOLLI E A.
                                                                                                                                                RIEGER D K.
SPADERNA S K.
                                                                                                                          DIPIPPO V A.
                                                                                                                                                                                                                             WPI; 2004-213931/20.
                              CATTERTON E.
                                            MILLER C E.
RASTELLI L.
                                                                                                          AGEE M L.
BERGHS C.
                                                                                                                                                                                                                                     N-PSDB; ADN62903.
                                                                                                                                  EISEN A.
                       ZHONG M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 97 AA;
                                                                                                                                        (GANG/)
(RIEG/)
(SPAD/)
GORM/)
                                                                                   (SHIM/)
(ROTH/)
(LEAC/)
                                                    (RAST/)
(STON/)
                                             (MILL/
                                                                                                                   BERG/
                                                                           SHEN/
                                                                                                                                  EISE/
                      ZHON/
                               CATT/
                                      (JIWM/
                                                                     PENA/
                                                                                                          (AGEE/
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The invention relates to isolated NoVX polypeptides and polynucleotides.

NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the abstrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and cartivity of NOVX by supplementing the patient our expression or activity of NOVX by supplementing the patient our production or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polynucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX.

Caponists and antagonists) of the expression and activity of NOVX polypeptides and antibodies, agonists and antagonists may also be used as diagnostic agents for detecting the presence of NOVX polypeptides and polynucleotide expression and activity of novX polypeptides and polynucleotides may be used all in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, haematopoietic disorders, and the various dyslipidaemias, metabolic disturbances associated with obseity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        They may also be used as antibacterial agents. The present represents the amino acid sequence of a human NOVX protein.
Claim 1; SEQ ID NO 100; 395pp; English.
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain caction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of [II]. The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed consists of [I] is useful in gene therapy techniques to restore normal activity of [II] or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a cuplypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders cupylypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations collypeptide and polymucleotide sequences have applications in diagnostics, forgensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in celectronic format directly from Wipp at the printed specification, but was obtained in celectronic format directly from Wipp or contacts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID NO 53737; 103pp; English
                                                                            Novel human diagnostic protein #23369.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT;
                                                                                                                                                                                                                                                                                                    30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                       18-FEB-2002 (first entry)
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAS87565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 136 AA;
                                                                                                                                                                                                                       WO200175067-A2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biodiversity.
                                                                                                                                                                                Homo sapiens.
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  ABG23378;
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9; Conservative

Matches

Query Match Best Local Similarity

0; Indels

0; Mismatches

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chymotryptic enzyme; scce; enzyme.
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05-OCT-2001; 2001US-0327435P.
                                                                               JS2003199010-A1
                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                O'brien TJ,
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                                                                                                                        23-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA05738
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Production of activated immune cells or dendritic cells by exposing immune cells to tumor antigen derived gene protein fragment consisting of amino acid sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dendritic cells directed toward extracellular serine protease termed tumour antigen derived gene-14 (TADG-14). The method of the invention involves exposing the immune cells to a TADG-14 protein fragment, where exposure to the TADG-14 protein fragment activates the immune cells. The invention is used for the production of activated immune T cells or invention is used for the production of activated immune T cells or dendritic cells. The invention allows screening to identify proteases overexpressed in carcinoma. The present sequence is stratum corneum chymotryptic enzyme (scce) catalytic domain. This sequence is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to novel activated immune T cells or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine protease; tumour antigen derived gene-14; TADG-14; neoplastic state; cancer; ovary; breast; lung; colon; prostate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                          Immune T cell; dendritic cell; extracellular serine protease; tumour antigen derived gene-14; TADG-14; carcinoma; stratum corneum chymotryptic enzyme; scce.
                                                                                                                                                                                                        Stratum corneum chymotryptic enzyme (scce) catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 49; DB 8; Length 144; 100.0%; Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stratum corneum chymotryptic enzyme (scce) catalytic domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; SEQ ID NO 4; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADI37151 standard; protein; 144 AA.
                                                                           ADI39727 standard; protein; 144 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYAR-) UNIV ARKANSAS MEDICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUL-2000; 2000US-00618259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-00915659.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Underwood LJ;
                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KMNEYTVHL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Local 9; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-118109/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                         JS6642013-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O'brien TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAY-2004
                                                                                                                                                               15-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                  04-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
                                                                                                                    ADI39727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADI37151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                   ADI 39727

XX ADI 15 - ADI 15 - ADI 15 - ADI 17 
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The invention relates to extracellular serine protease termed tumour antigen derived gene-14 (TADG-14) and its nuclaic acid. Composition composition an entity of derived gene-14 peptide is useful for treating a neoplastic state in an individual. The neoplastic state is chosen from ovarian cancer, breast cancer, injung cancer, colon cancer, prostate cancer in which TADG-14 is overexpressed. The present sequence is Stratum corneum chymotryptic enzyme (scce) catalytic domain. This sequence is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated DNA encoding tumor antigen derived gene-14 protein, useful for treating neoplastic state (such as ovarian cancer, breast cancer, lung cancer, colon cancer, prostate cancer) in an individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 49; DB 8; Length 144; larity 100.0%; Pred. No. 0.17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID NO 4; 46pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human NOV18d protein SEQ ID NO:98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exemplification of the invention.
                                                                  21-AUG-1997; 97US-00915659.
21-AUG-1998; 98US-00137944.
18-JUL-2000; 2000US-00618259.
13-JUN-2003; 2003US-00461787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-OCT-2002; 2002WO-US031373.
                                                                                                                                                                                                                                                                                                 Underwood LJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                      (UYAR-) UNIV ARKANSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 KMNEYTVHL 17
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9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KMNEYTVHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 144 AA;
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The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOV1). Also described: (1) a composition comprising a polypeptide
described above and a carrier; (2) a kit comprising, in one or more
containers, the composition described above; (3) an isolated nucleic acid
molecule which encodes a NOVX protein of the invention; (4) a vector
comprising the nucleic acid molecule described above; (5) a call
comprising the above vector; (6) an antibody that immunospecifically
binds to the polypeptide described above; (7) methods for determining the
presence or amount of the above polypeptide or nucleic acid molecule in a
sample; (8) methods for determining the presence of or predisposition to
a disease associated with altered levels of expression of the above
polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
method of identifying an agent that binds to the polypeptide described
above; (10) a method for identifying a potential therapeutic agent for
use in treating a pathology that is related to an aberrant expression or
aborrant physiological interactions of the polypeptide; (11) a method of
correct a madulator of activity or of latency or predisposition to
a pathology associated with the polypeptide; (12) a method for modulating
cor preventing a pathology sesociated with the above polypeptide. Novx
mammal; and (14) a method for producing the above polypeptide in a
mammal; and (14) a method for producing the above polypeptide in a
mammal; and antiliabentic, anorectic, anorectic, antibacterial, virucide,
immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian
correct and antiliabent and an be used in gene therapy. The
polypeptide is useful in manufacturing a medicament for treating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, Paturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 171; 586pp; English
                                                                        2001US-0328056P.
2001US-0328849P.
2001US-0329414P.
2001US-0330142P.
2001US-0330309P.
                                                                                                                                                                                           2001US-0339266P.
2001US-0343629P.
2001US-0349575P.
2001US-0346357P.
2002US-0373260P.
2002US-0373815P.
2002US-0373817P.
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2002US-0381642P.
2002US-0383656P.
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2002US-0381037P.
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                                                       2001US-0328044P
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                                                                      09-0CT-2001;
15-0CT-2001;
15-0CT-2001;
18-0CT-2001;
22-0CT-2001;
24-0CT-2001;
24-0CT-2001;
29-0CT-2001;
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human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dystlipidaemias. The nucleic acids can also be used as Mybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                   ö
                                                                                                                                                                    100.0%; Score 49; DB 6; Length 181; 100.0%; Pred. No. 0.22;
                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                             ADN62902 standard; protein; 181 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-2001; 2001US-0326483P.

05-OCT-2001; 2001US-0327435P.

05-OCT-2001; 2001US-0327449P.

09-OCT-2001; 2001US-0328029P.

09-OCT-2001; 2001US-0328049P.

12-OCT-2001; 2001US-0328044P.

12-OCT-2001; 2001US-0328044P.

15-OCT-2001; 2001US-0329414P.

17-OCT-2001; 2001US-0339140P.

18-OCT-2001; 2001US-0339169P.

22-OCT-2001; 2001US-0339169P.

22-OCT-2001; 2001US-0339266P.

24-OCT-2001; 2001US-0339266P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001US-033039P.
2001US-034105BP.
2001US-034956P.
2001US-0349575P.
2001US-0349575P.
2002US-0373260P.
2002US-0373260P.
2002US-0373815P.
2002US-0373817P.
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2002US-0383656P.
2002US-0383831P.
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                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                             σ
                                                                                                                                                    Query Match
Best Local Similarity
9; Conserv
                                                                                                                                                                                                                           1 KMNEYTVHL
                                                                                                                                                                                                                                                       53 KMNEYTVHL
                                                                                                                 present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                wasting disorder.
                                                                                                                                          Sequence 181 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS2004038223-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-OCT-2001;
01-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                              Human NOV18d.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-APR-2002;
19-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-APR-2002;
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29-MAY-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                         ADN62902;
                                                                                                                                                                                                                                                                                                 RESULT 12
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digease, anorexia, cancer, cancer-associated cachexia, neurodegenerative

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The invention relates to isolated NOVX polypeptides and polynucleotides.

NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the abserrant expression and activity of NOVX by supplementing the patient our polynucleotides may be used to treat disorders associated with decreased polynucleotides may be used to treat disorders associated with decreased conduction or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NoVX polypeptides by binding with the cells own genes and preventing their expression. NoVX polynucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NoVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators anti-NoVX polypeptide antibodies, agonists and antagonists may also be used to modulate NoVX polypundleotide expression and activity of NoVX. Dolypeptides and polynucleotide expression and activity of NoVX polypeptides. The anti-NoVX polypeptide antibodies, agonists may also be used as diagnostic agents for detecting the presence of NoVX in samples. NoVX polypeptides and polynucleotides may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smithson G, Millet I, Peyman on, Shithson G, Millet I, Bengar SR, Ellerman n, Catterto Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterto Ort T, Gorman L, Zerhusen BD, Anderson DW, Pena CEA, Shenoy SG, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG, Ji W, Miller CE, Rastelli L, Leach MD, Agee ML, Berghs C, Dij Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dij Shimkets RA, Rothenberg ME, Leach MD, Agee ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 98; 395pp; English.
 25-JUN-2002; 2002US-0391335P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
                                                                                                                                                                                                                                GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                          MILLER C E.
RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
                                                                                                                                                  SPYTEK K A.
EDINGER S R.
ELLERMAN K.
                                                                                                                                                                                                    MALYANKAR U M
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGEE M L.
BERGHS C.
DIPIPPO V A.
                                                                                                                                       PATTURAJAN M.
                                             MILLET I.
PEYMAN J A.
KEKUDA R.
                                                                                                                                                                                                                                                                                               CATTERTON E.
                                SMITHSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                      LEACH M D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ADN62901.
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                                                                                                                                                                                                                                                                                  ZHONG M.
                                                                                                          LI L.
GUO X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EISE/)
(GANG/)
(RIEG/)
(SPAD/)
                                SMIT/)
                                                           (PEYM/)
(KEKU/)
(JUJJ/)
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(GORM/)
(ZERH/)
                                                                                                                                                                                                                                                                                                                            (MILL/)
(RAST/)
(STON/)
                                                                                                                                                                                                                                                                                                                                                                                                       (SHIM/)
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                                                                                                                                                                                                                                                                                             (CATT/)
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                                                                                                        (LILL/
(GUOX/
(PATT/
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(MALY/
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                                              (MILL)
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disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, haematopoietic disorders, and the various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obseity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
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                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 49; DB 8; Length 181; Best Local Similarity 100.0%; Pred. No. 0.22; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADA05736 standard; protein; 198 AA.
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2001US-0328056P.
2001US-0328849P.
2001US-0329414P.
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2001US-0349575P.
2001US-0346357P.
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2001US-0327917P.
2001US-0328029P.
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2002US-0373815P.
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2002US-0391335P.
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                                                                                                                                                                                                                                                                                                                                                                                   1 KMNEYTVHL
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                                                                                                                                                                                                                         Sequence 181 AA;
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09-0CT-2001; 2
12-0CT-2001; 2
15-0CT-2001; 2
14-0CT-2001; 2
18-0CT-2001; 2
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24-OCT-2001;
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09-0CT-2001;
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01-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kekuda R, Ju J, Li L, Guo X;
SR, Ellerman K, Malyankar UM;
Parson DW, Zhong M, Catterton E;
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25-JUN-2002;

(first entry)

01-JUL-2004

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The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; in one or more molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a call comprising the nucleic acid molecule described above; (5) a call comprising the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for a boyreptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aborrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating or preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide in a mammal; and (14) a method for producing the above polypeptide in a mammal; and (14) a method for producing the above polypeptide in a mammal; and antilipaemic activities, and can be used in gene therapy. The immunomodulator, cytostatic, noctopic, neuroprotective, antiparkinsonian and matilipaemic activities, and can be used in gene therapy. The colypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation
                                                                                                          Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T. Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton B, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 170; 586pp; English.
01-OCT-2002; 2002US-00262511.
                                                        (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                              WPI; 2003-381626/36.
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human, NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer, cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder;
                                                                    disorder; dyslipidaemia; metabolic syndrome X;
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09-OCT-2001; 20010S-03279435P.
09-OCT-2001; 20010S-0327917P.
09-OCT-2001; 2001US-0328054P.
09-OCT-2001; 2001US-0328056P.
12-OCT-2001; 2001US-0328044P.
15-OCT-2001; 2001US-0328149P.
15-OCT-2001; 2001US-0339142P.
18-OCT-2001; 2001US-0339168P.
22-OCT-2001; 2001US-0339266P.
24-OCT-2001; 2001US-0341628P.
24-OCT-2001; 2001US-0341628P.
24-OCT-2001; 2001US-0341628P.
24-OCT-2001; 2001US-0341628P.
25-OCT-2001; 2001US-0341628P.
26-OCT-2001; 2001US-0341628P.
27-OCT-2001; 2001US-0341628P.
27-OCT-2001; 2001US-0341628P.
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2002US-0373815P.
2002US-0373817P.
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22-APR-2002; 2002US-0374977P.
16-MAY-2002; 2002US-0381037P.
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2002US-0381042P.
2002US-0381642P.
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SPYTEK K A.
EDINGER S R.
ELLERMAN K.
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PEYMAN J A.
KEKUDA R.
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RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
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                                                                              wasting disorder
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                                                                                                                      US2004038223-A1
                                                                     haematopoietic
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                    Human NOV18c.
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19-APR-2002;
                                                                                                   Homo sapiens.
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(ELLE/)
(MALY/)
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(ANDE/)
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(RAST/)
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(PEYM/)
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(GORM/)
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                                                                              Dipippo VA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
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(SHEN/)

ADN62900;

RESULT 14
ADN62900
ID ADN62
XX
AC ADN62

Local Similarity

Matches

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Human NOV18g protein SEQ ID NO:104.

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The invention relates to isolated NoVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or creat a medical condition in human related to the abbrrant expression and activity of NoVX polypeptides are example, NoVX polypeptides and activity of NoVX polypeptides. For example, NoVX polypeptides and polymucleotides may be used to treat disorders associated with decreased expression or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NoVX polypeptides by binding with the cells own genes and preventing their expression. NoVX binding with the cells own genes and preventing their expression. NoVX polypeptides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of the production of antibodies and in assays to identify modulators capcing and antagonists and antagonists and antagonists and in assays to identify of NoVX. The used to modulate NoVX polypeptide antibodies, agonists and activity of NoVX polypeptides and polymucleotide expression and activity of NoVX polypeptides and polymucleotide may be used in this way to prevent, capcing and the presence of NoVX in samples. NoVX polypeptides and polymucleotides may be used in this way to prevent, diagnose and treat: metabolic disorders, inmune disorders, disorders, and the various dyslipidaemias, metabolic disorders, hammatopoietic disorders, and the various dyslipidaemias, metabolic disorders, and disturbances associated with obesity, the metabolic syndrome X and cappanents and the various dyslipidaemias, metabolic and antibuted and the various displacement and antibuted and antibuted and antibut
                                                                                                                                                                                                                                                     Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Nastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represents the amino acid sequence of a human NOVX protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 96; 395pp; English.
                                                                                                                             EISEN A.
GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
ROTHENBERG M
                                                                                                  DIPIPPO V A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-213931/20.
N-PSDB; ADN62899.
                       LEACH M D.
                                               AGEE M L.
BERGHS C.
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                                                                                                                          (EISE/)
(GANG/)
(RIEG/)
(SPAD/)
ROTH/)
                       (LEAC/)
(AGEE/)
(BERG/)
                                                                                                     (DIPI/
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ö 100.0%; Score 49; DB 8; Length 198; 100.0%; Pred. No. 0.24; cive 0; Mismatches 0; Indels Local Similarity 100 Query Match Matches

KMNEYTVHL 80 KMNEYTVHL 9 Н 72 염 ò

ADA05744 standard; protein; 224 AA. ADA05744; ADA05744 23235X

RESULT 15

06-NOV-2003 (first entry)

human, NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antipaemic; gene therapy; human disease; antipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia 22-OCT-2001; 2001US-0341058P.
24-OCT-2001; 2001US-0343629P.
29-OCT-2001; 2001US-0349562P.
01-NOV-2001; 2001US-0349575P.
01-APR-2002; 2002US-0373260P.
19-APR-2002; 2002US-0373815P. 05-0CT-2001, 20010S-0327449P.
09-0CT-2001, 20010S-0327917P.
09-0CT-2001, 20010S-032805P.
09-0CT-2001, 20010S-0328056P.
12-0CT-2001, 20010S-032849P.
15-0CT-2001, 20010S-032944P.
15-0CT-2001, 20010S-032944P.
17-0CT-2001, 20010S-033944P. 19-APR-2002; 2002US-0373884P. 22-APR-2002; 2002US-0374977P. 16-MAY-2002; 2002US-0381037P. 16-MAY-2002; 2002US-0381038P. 16-MAY-2002; 2002US-0381042P. 17-MAY-2002; 2002US-0381642P. 2002US-0373826P 2002US-0391335P 2002US-00262511 02-OCT-2002; 2002WO-US031373 402003029424-A2. 22-APR-2002; 16-MAY-2002; 32-OCT-2001; 19-APR-2002; Homo sapiens 01-OCT-2002; 10-APR-2003. 29-MAY-2002

Dipippo VA;

Malyankar UM; Shenoy SG; Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyank, Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catlyin W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

(CURA-) CURAGEN CORP.

Dipippo VA;

Catterton E; Guo X;

> WPI; 2003-381626/36. N-PSDB; ADA05743

> > ò

Gaps

The present sequence

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics

Claim 1, Page 172; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell

comprising the above vector; 16) an animosperited for determining the binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above con a disease associated with altered levels of expression of the above con polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential activity or of latency or predisposition to consider a pathology associated with the polypeptide; (11) a method of modulating the activity of the polypeptide described above; (13) methods of treating considers are activity of the polypeptide described above; (13) methods of treating the activity of the polypeptide described above; (13) methods of treating considers have antidiabetic, anorectic, antibacterial, virucide, nown and antilipaemic activities, and can be used in gene therapy. The collypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic configueacy immune disorders such as diabetes or obesity, infections, cancer, neurodegenerative disorders, haematopoletic disorders and various colleease; immune disorders, haematopoletic disorders and various colleease; in chromosome mapping, tissue typing, preventive medicine and proper incompanies. The present sequence represents a human NOVX from the comprising the above vector; (6) an antibody that immunospecifically present invention

Sequence 224 AA;

Gaps ö 100.0%; Score 49; DB 6; Length 224; 100.0%; Pred. No. 0.27; ive 0; Mismatches 0; Indels Query Match 100. Best Local Similarity 100. Matches 9; Conservative

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1 KMNEYTVHL 9

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Search completed: July 13, 2005, 17:19:49 Job time : 78.6667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein July 13, 2005, 16:54:03 ; Search time 13.5556 Seconds Run on:

(without alignments)
63.882 Million cell updates/sec

US-09-905-083A-31 Perfect score:

1 KMNEYTVHL 9 **BLOSUM62** Scoring table: Sequence:

Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

hypothetical prote spermidine/spermin hypothetical prote B. subtilis YwbN p conserved hypothet lysis protein t -lysis protein t -conserved hypothet hypothetical prote conserved hypothet acylase and dieste RING finger protei ring finger protei replication protei replication protei spermidine/spermin serine proteinase Description B98019 D75207 T25395 T34239 AI1406 AI1782 H75431 AD1794 T09013 T09482 AH1120 AC1481 S28682 A53968 DB Query Match Length 421 421 204 Score Result Š

lysis protein t - phage K3
C;Species: phage K3
C;Species: phage K3
A;Note: host Eacherichia coli
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A27083
R;Riede, 1.
J. Bacteriol. 169, 2956-2961, 1987
A;Title: Lysis gene t of T-even bacteriophages: evidence that colicins and bacteriophage A;Reference number: A27083
A;Accession: A27083
A;Accession: A27083
A;Accession: A27083
A;Accession: A27083
A;Accession: A27083
A;Nolecule type: DNA
A;Residues: 1-218 «RIE»
A;Residues: 1-218 «RIE»
A;Residues: 1-218 «RIE»
A;Rosidues: 1-218 «RIE»
A;Genetics: 1-218 «RIE»
A;Genetic

calflagin Tb-1.7 -flagellar calcium-calflagin Tb-44A -

hypothetical prote

two-component

FixJ Transcription

nitrogen fixation

calflagin Tb-24 -

S53354 E83724

853355

preprotein translo oligopeptide ABC t

hypothetical prote

hypothetical prote TonB-dependent rec pyrl-3 protein - s pyrl-3 protein - s pyrl-3 protein - s pyrimidine synthes 50s ribosomal prote hypothetical prote hypothetical prote MdaB protein homol hypothetical prote Mypothetical prote hypothetical prote probable membrane- conserved hypothet citrate/sodium sym	ange 09-Jul-2004 .; Carlstein, A.; Egelrud, T. um corneum chymotryptic enzyme PIDN:AAC37551.1; PID:g532504 253; ls 0; Gaps 0;	
C72379 A87470 A87470 B71623 B71622 QZDOP3 QZDOP3 QZDOP3 C91301 C90033 A89800 P97121 A89800 C9	ptic enzyme 11-1995 #text_cha 12ation of stratu Mallbrandt, P. ization of stratu MID:8034709 MiD:9521214; DB 2; Length ches 0; Indel	
апприничини	cursor corneum nce_rev , M.; B. 19426, on, and ; MUD: 7730 7730 7730 100.0%; ive	
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66 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	ult 1 Jean proteinase SCCE precursor literate names: stratum corneus section corneus section corneus section corneus section corneus section (man) ate: 07-Jul-1995 #sequence_revocession: A53968 ansson, L.; Stroemqvist, M.; B. Biol. Chem: 269, 19420-19426, Biol. Chem: 259, 19420-19426, Biol. Chem: 259, 19420-19426, Biol. Chem: 259, 19420-19426, Biol. Chem: 253, 44NN coss-references: UNIPROT: P4986 ene: GDB:PRSS6; SCCE ross-references: GDB:37730 app position: 7435-7435 houserymatch conservative set Local Similarity 100.0%; atches 9; Conservative limits and recommended to the set Local Similarity 100.0%; atches 9; Conservative limits and limits l	
	proteinase nate names es: Homo es 07-Jul-19; sion: A539 on, L; 531 chem: 26; chem: 26;	
ш ш ш ш ш ш ш ш ф ф ф ф ф ф О H Ω ш ф m о C m	RESULT 1 A53968 serine proteinase SCCE precursor - human NAlternate names: stratum corneum chymotry) C;Species: Homo sapiens (man) C;Date: 07-Jul-1995 #sequence_revision 07-Ju J;Ele: (1001ng, expression, and character. A;Refence number: A53968; MUD:94308225; A;Retus: preliminary A;Rotesion: A53968 A;Rotes	RESULT 2 YVBPK3

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C;Accession: D75207
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
submitted to the EMBL Data Library, July 1999
A;Beference number: A7501
A;Accession: D75207
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-393 <KAM>
                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:09V291; GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB4910:
A;Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:09XU04; EMBL:292813; PIDN:CAB07289.1; GSPDB:GN00021; CESP:T28
A;Experimental source: clone T28A8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F26F12.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Oct.1999 #sequence_revision 29-Oct.1999 #text_change 09-Jul-2004
C;Accession: T34239
R;Wilson, R.; Bentley, D.; Gattung, S.
submitted to the RMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid F26F12.
A;Reference number: Z21493
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CiSpecies: Caenorhabditis elegans
CiSpecies: Caenorhabditis elegans
CiDate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
CiAccession: T25395
Rilloyd, C.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z20027
A;Reference number: Z20027
A;Reference number: L2395
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Residues: 1-627 <WIL->
                                                                                       C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Introns: 51/2; 89/2; 183/2; 221/2; 296/2; 607/3
C;Superfamily: Caenorhabditis elegans hypothetical protein Y57AlOA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: PAB2235
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH0196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.5%; Score 37; DB 2; Length 393; 66.7%; Pred. No. 12; ive 2; Mismatches 1; Indels
                                                           hypothetical protein PAB2235 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T28A8.6 - Caenorhabditis elegans
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66.7%; Pred. No. 31;
tive 2; Mismatches
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129 KLPEYTIHL 137
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62 KMNEYSIEL 70
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A; Reference number: A97872; MuID:21429245; PMID:11544234
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-334 < KUR>
A; Cross-references: UNIPROT:Q8DPG2; GB:AE007317; PIDN:AAK99982.1; PID:g15458811; GSPDB:CC; Genetics:
A; Gene: spr1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Molecule type: DNA
A;Residues: 1-218 <MON>
A;Residues: 1-218 <MON>
A;Cross-references: UNIPROT:P06808; GB:Y00408; NID:g15368; PIDN:CAA68470.1; PID:g15369
A;Cross-references: UNIPROT:p06808 identical with that of the E.coli phage K3
A;Note: the sequence is almost identical with that of the E.coli phage K3
C;Comment: At the end of the growth cycle, phage T4 expresses two genes with lysis funct about the gene product of t, although it has been suggested that it acts as a phospholi
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                                                                                                                                                                                                                                                                                        lysis protein t - phage T4
C;Species: phage T4
A;Note: host Escherichia coli
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: JF0028; S07395
R;Montag, D.; Degen, M.; Henning, U.
Nucleic Acids Res. 15, 6736, 1987
A;Title: Nucleotide sequence of gene t (lysis gene) of the E. coli phage T4.
A;Reference number: S07395; MuID:87316934; PMID:3628006
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  Score 39; DB 1; Length 218;
Pred. No. 2.5;
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Pred. No. 2.5;
1; Mismatches 0; Indels
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A;Gene: t
A;Gene: t
C;Gene: t
C;Superfamily: phage T4 lysis protein t
C;Keywords: host cell lysis; transmembrane protein
F;35-49/Domain: transmembrane #status predicted <TMN>
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Pred. No. 10;
1; Mismatches
                                                        1; Mismatches
79.6%;
87.5%;
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Similarity 87.5%;
7; Conservative
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Conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Decc-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Adcession: H75431
R;White, O.; Risen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Maß Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Accession: H75431
A,Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Robecule type: DNA
A,Robecule type: UNA
A,Robecule type: UNA
A,Robecule type: UNA
A,Forserreferences: UNIPROT:Q9RV79; GB:AE001964; GB:AE000513; NID:g6458881; PIDN:AAF1072; C,Genetics:
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Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
Cipates 27-Nov-2001
Richast, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Ritle: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acylase and diesterase homolog lin2898 [imported] - Listeria innocua (strain Clip11262)
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Pred. No. 39;
1; Mismatches 2; Indels
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A;Map position: 1
C;Superfamily: conserved hypothetical protein b0835
       Pred. No. 12;
2; Mismatches
   ilarity 75.0%;
Conservative
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Best Local Similarity 66.7%;
Matches 6; Conservative
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   Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J. Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma A;Authors: Kreft, J.; Kuhn, M.; Title: Comparative genomics of Listerrae, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: AB1077; MUD:21537279; PMID:11679669
A;Accession: Al1782
A;Access
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CjAccession: Alidos Royal Control C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jonnes, L.M.; Karst, U. Science 294, 849-852, 2001
AjAuthors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma AjAuthors: Schlueter, T.; Simoes, N.; Tierrez, A.; Varquez-Boland, J.A.; Voss, H.; Wehland, AjTitle: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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A,Experimental source: strain Clip11262
                                  A;Cross-references: UNIPROT:Q19815; EMBL:U55373; PIDN:AAC25894.1; GSPDB:GN00023; CESP:P2
A;Experimental source: strain Bristol N2; clone P26F12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-159 <GLA>
A,Fesidues: 1-159 <GLA>
A,Cross-references: UNIPROT: Q8Y419; GB:NC_003210; PIDN:CAD00871.1; PID:g16412158; GSPDB:
A,Experimental source: strain EGD-e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spermidine/spermine N1-acetyl transferase homolog 1mo2658 [imported] - Listeria monocyto
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C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
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C.Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
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Pred. No. 97;
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                                                                                                                                   A;Gene: CESP:FZ6F12.7
A;Map position: 5
A;Introns: 110/3; 441/3; 801/2; 1244/3; 1693/2; 1784/1
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Pred. No. 12;
2; Mismatches
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71.4%; Pred. No. >',
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Best Local Similarity 71.4
Matches 5; Conservative
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LNEYTIH 771
A; Residues: 1-1829 <WIL>
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Matches 6; Conserv
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C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: $28682
B;Nakagawa, M.; Tsukada, S.; Soma, T.; Shimizu, Y.; Miyake, S.; Iwamatsu, A.; Sugiyama, P.
Nucleic Acids Res. 19, 4292, 1991
A;Tills: CNNA cloning of the murine 30-kDa protein homologous to the 32-kDa subunit of hn
A;Reference number: $28682, MUID:91334146; PMID:1908076
A;Residues: 1-270 cNAG>
A;Residues: 1-270 cNAG>
A;Residues: 1-270 cNAG>
A;Coss-references: UNIPROT:Q62193; EMBL:D00812; NID:g220583; PIDN:BAA00693.1; PID:g22058
C;Superfamily: Schizosaccharomyces pombe single-stranded DNA binding protein 30K chain
A;Residues: 1-270 <ERD>
A;Cross-references: UNIPROT:P15927; EMBL:J05249; NID:g337349; PIDN:AAA36560.1; PID:g33735
C;Superfamily: Schizosaccharomyces pombe single-stranded DNA binding protein 30K chain
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                                                                                                                            69.4%; Score 34; DB 2; Length 270; 62.5%; Pred. No. 32; tive 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 replication protein A 32K chain homolog - mouse
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Job time : 15.5556 secs
                                                                                               Query Match
Best Local Similarity 62.5.
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152 MNEFTTHI 159
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152 MNEFTAHI 159
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C;Species: 16-Jul-1999 #text_change 09-Jul-2004
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T09482
R;Perry, J.; Feather, S.; Smith, A.; Palmer, S.; Ashworth, A.
R;Perry, J.; Feather, S.; Smith, A.; Palmer, S.; Ashworth, A.
R;Description: The buman FXY maps to chromosome Xp22.3: Implications for evolution of A;Reference number: 216687
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replication protein repA 32K chain - human

c;Species Homo sapiens (man)

c;Species Homo sapiens (man)

c;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004

c;Accession: A43711

K;Erdly, T.J.

J. Biol. Chem. 265, 3177-3182, 1990

A;Title: The primary structure of the 32-kDa subunit of human replication protein A. A;Reference number: A43711; MUID:90153966; PMID:2406247

A;Accession: A43711

A;Accession: A43711

A;Accession: A43711

A;Accession: A43711

A;Accession: A43711
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-667 <PER>
A;Cross-references: UNIPROT:O15344; EMBL:AF035360; NID:g2827993; PID:g2827994
                   ring finger protein Fxy - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 04-Apr-2004
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llarity 75.0%; Pred. No. 53;
Conservative 0; Mismatches 2; Indels
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                                                                                                                                                R.Palmer, S.; Perry, J.; Kipling, D.; Ashworth, A. Proc. Natl. Acad. Sci. U.S.A. 94, 12030-12035, 1997
Affile: A gene spans the pseudoautosomal boundary in mice. A; Reference number: 216531; MUID:98004518; PMID:9342357
A; Accession: T09013
                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-667 <PAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 71.4%; Score 35; DB 2; Similarity 75.0%; Pred. No. 53; 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Map position: X; Y
C.Superfamily: Fifth transforming protein
C.Keywerdamily: Fifth transforming protein
Fife-65/Domain: RING finger homology «RRN»
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C,Superfamily: rfp transforming protein
F,6-65/Domain: RING finger homology <RRN>
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Gaps

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P49862 homo sapien
Q8n5n9 homo sapien
Q8nfv7 homo sapien
Q9003 bacteriopha
P10393 bacteriopha
P06808 bacteriopha
Q13156 homo sapien
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                                                                                                                                                           July 13, 2005, 16:15:23 ; Search time 62.2222 Seconds (without alignments) 74.069 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               1612378 segs, 512079187 residues
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QBN5N9
QBN5N9
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QBGD83
VLYS_BPK3
VLYS_BPK3
VLYS_BPK4
RPA4_HUMAN
QBDPG2
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Q92621 listeria in Q81bmS plasmodium O81344 homo sapien P82457 mus spretus norv O90wd1 gallus gall Q71r46 gallus gall Q71r46 gallus gall Q6deu6 xenopus tro O70583 mus musculu Q6gx19 actus trivi Q6gx20 cercopithec Q81e27 plasmodium Q9ujv3 homo sapien		orneum chymot sta; Euteleos idae; Homo. andt P., Carl tratum corneu ne proteinase expression o n; H., McCuai ne protease g	intercellular cohesive kin in the continuous
71.4 555 2 0926Z1 71.4 579 2 081BMS 71.4 667 1 MID1 HUMAN 71.4 667 1 MID1_MUSSP 71.4 667 2 090WD1 71.4 667 2 090WD1 71.4 668 2 060BG6 71.4 668 2 060BG6 71.4 688 1 MID2_MOUSE 71.4 688 2 06GX10 71.4 689 2 06GX10 71.4 687 2 081B27 71.4 687 2 081B27 71.4 715 1 MID2_HUMAN	ALIGNMENTS	PRT; 253 AA. ated) t sequence update) t annotation update) (C 3.4.21) (Stratum , SCCE; ata; Craniata; Verteb tes; Catarrhini; Homi EQUENCE OF 23-53. 8034709; L., Baeckman A., Wallb characterization of in-specific human ser 19426(1994). Diamandis E.P.; on, mapping and tissum motryptic enzyme gene motryptic enzyme gene he EMBL/GenBank/DDBJ Argonza-Barrett R., K.; n analysis of the ser some 19q13 region."; y A., Edlund M., Edho; i cf stratum corneum corneum of stratum corneum i of stratum fermatitis."; he EMBL/GenBank/DDBJ 7794273; Egelrud T.; icity of recombinant mmun. 211:586-589(199)	May catalyze the degradation of intercellulars in the cornified layer of the skin in the cor
33333333333333333333333333333333333333		TLT 1 **HUMAN** **KLK7** HUMAN** **KLK7** HUMAN** **FLK7** HUMAN** **D1-OCT-1996** (Rel. 34, Last page (Rel. 34, Last can be an incomply of the	-!- FUNCTION: May structures in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
          residues with aromatic side chains in the PI position. SCCE claves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-Phe-|-Tyr-26, and 26-Tyr-|-Thr-27, Could play a role in the activation of precursors to inflammatory cytokines.

TISSUE SPECIFICITY: Abundantly expressed in the skin and is expressed by keratinocytes in the epidermis. Very low levels are also seen in the brain and kidney.

SIMILARITY: Belongs to the peptidase SI family. Kallikrein
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 shedding of cells from the skin surface. Specific for amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                        PERMIY PRO0089; Trypain; Denominary PRO0089; Trypain; PRO0089; Trypain; SMART; SM00020; Tryp_SPC; 1.
PROSITE; PSS0240; TRYPESIN DOM; 1.
PROSITE; PS00134; TRYPESIN HIS; 1.
PROSITE; PS00135; TRYPESIN JES; 1.
PROSITE; PS00135; TRYPESIN JES; 1.
Signal; Zymogen.
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similarity).
similarity).
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2D68B6B15A76A668 CRC64;
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0
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Kallikrein 7.

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Last sequence update)
Last annotation update)
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EMBL, AF24557; AAG33360.1; --
EMBL, AF33583; AAK69624.1; --
PIR; A53968; A53968.
HSSP; P00760; 1EXX.
MEROPS; SO1.300; --
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(TrEMBLrel. 22, I
(TrEMBLrel. 26, I
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                                                                                                                   subfamily.
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01-OCT-2002
01-MAR-2004
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Q8N5N9;
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Q8N5N9
ID Q8N5I
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Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A pletchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Miting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: Belongs to peptidase family S1.
EMBL; BC032005; AAH32005.1; --
HSSP; P00760; 1EZX.
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SEQUENCE 253 AA; 27608 MW; 2D68B6A41B22A668 CRC64;
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GO; GO:0008233; F:cpptidase activity; IEA.
GO; GO:0008295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001914; Peptidase_S1A.
InterPro; IPR00903; Pept_Ser_Cys.
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Kallikrein 7 short variant protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
Stratum corneum chymotryptic enzyme, preproprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AA.
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SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
PROSITE; PS00135; TRYPSIN HIS; UNKNOWN 1.
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                                                                       Homo sapiens (Human)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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MEDLINE=88011316; PubMed=2958637;
Montag D., Riede I., Eschbach M.-L., Degen M., Henning U.;
"Receptor-recognizing proteins of T-even type bacteriophages. Constant and hypervariable regions and an unusual case of evolution.";
J. Mol. Biol. 196:165-174(1987).
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Monteag D., Degen M., Henning U.;
"Nucleotide sequence of gene t (lysis gene) of the E. coli phage T4.";
Nuclaic Acids Res. 15:6736-6736(1987).
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SEQUENCE FROM N.A.
MEDLINE=22514363; PubMed=12626685; DOI=10.1128/WMBR.67.1.86-156.2003;
Miller E.S., Kutter E., Mosig G., Arisaka F., Kunisawa T., Ruger W.;
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T4-like viruses.
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                                                                                                                                                                                                                                                                      Bacteriophage K3.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
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Pred. No. 13;
1; Mismatches 0; Indels
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SEQUENCE 218 AA; 25222 MW; 21B4DC02ACA0ECF6 CRC64;
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                                                                           01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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Microbiol. Mol. Biol. Rev. 67:86-156(2003).
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05-JUL-2004 (Rel. 44, Last anno
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87.5%;
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PIR; A27083; YVBPK3.
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139 MDEYTVHL 146
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ID VLYS_BPT4
AC P06808;
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DOI=10.1128/JB.12.1.5962-5968.2000;

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"Characterization of the distal tail fiber locus and determination of the receptor for phage ARI, which specifically infects Escherichia coli 0157:H7.";

BACTERION I 182:5962-5968(2000).

EMBL, AF208841; AAG29756.1; -.

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MEDLINE-22623266; PubMed-12738725;
Dong Y., Kaushal A., Brattsand M., Nicklin J., Clements J.A.;
Ulfferential splicing of KLKS and KLK7 in epithelial ovarian cancer produces novel variants with potential as cancer biomarkers.";
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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
T4-like viruses.
MCBI_TaxID=66711;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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PRINTS, PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 181 AA; 19887 MW; 86A2BA03B80C2D78 CRC64;
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GO; GO:0008233; F:chymotrypsin activity; IEA.
GO; GO:0004255; F:trypsin activity; IEA.
GO; GO:000508; P:proteolysis and peptidolysis; IEA.
InterPro; IRR01254; Peptidase SI.
InterPro; IRR001314; Peptidase SIA.
InterPro; IRR001003; Pept Ser_Cys.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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100.0%; Pred. No. 1;
ive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                         Clin. Cancer Res. 9:1710-1720(2003).
-!- SIMILARITY: Belongs to peptidase family Sl
BEBB; AF411215; AAN03663.1; -.
HSSP; P00760; 1EZX.
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J. Bacteriol. 175:85-93(1993).
-!- FUNCTION: At the end of the growth cycle, phage T4 expresses two genes with lysis function, e and t. Nothing is known about the gene product of t, although it has been suggested that it acts as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDILIDE=95280910; PubMed=7760808;
Kebhav K.F., Chen C., Dutta A.;
"Rpa4, a homolog of the 34-kilodalton subunit of the replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Replication protein A 30 kDa subunit (RP-A) (RF-A) (Replication
                                   MEDLINE=93106978; PubMed=8416914;
Orsini G., Ouhammouch M., le Caer J.P., Brody E.N.;
"The asiA gene of bacteriophage T4 codes for the anti-sigma 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.6%; Score 39; DB 1; Length 218; 87.5%; Pred. No. 13; 1:ve 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 49 FOLENCIAL:
218 AA; 25175 MW; 9110BE111D772DF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phage lysis protein; Transmembrane.
TRANSMEM 35 49 Potent
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Y00408; CAA68470.1; -.
EMBL; AF158101; AAD42661.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
SEQUENCE OF 202-218 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X05677; CAA29164.1; -. EMBL; M9941; AAA32481.1; -. PIR; JF0028; YVBPT4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 MDEYTVHL 146
                                                                                                                                                                                                        a phospholipase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 MNEYTVHL 9
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Q13156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=RPA4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=21429245; PubMed=11544234;

DOI=10.1126/JBL.183.195709-5717.2001;

Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C., Edilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz B.J., Lu J., Mateushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Stock C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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SUBUNIT: Heterotrimer of 70, 32/30, and 14 kDa chains. The DNA-binding activity may reside exclusively on the 70 kDa subunit. SUBCELLULAR LOCATION: Nuclear. TISSUE SPECIFICITY: Preferentially expressed in placental and
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"Genome of the bacterium Streptococcus pneumoniae strain R6.";
J. Bacteriol. 183:5709-5717(2001).
EMBL; AE008490; AAK99982.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.6%; Score 38; DB 1; Length 261; 75.0%; Pred. No. 25; tive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSEP, P15927; 1000.
Reactome; 013156; -.
Roo, GO: 0005662; Cinna replication factor A complex; TAS.
GO; GO: 0005629; P: single-stranded DNA binding; TAS.
GO; GO: 0006270; P: DNA replication initiation; TAS.
InterPro; IPR008994; Nucleic acid OB.
InterPro; IPR009059; Wing hix DNA anti;
PF01336; tRNA anti;
PF01336; tRNA anti;
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 AA; 28868 MW; 6A925FAEDBE21718 CRC64;
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/FTId=VAR_
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InterProx, IRR06314; Dyp perox; 1.
Pfam; PF04261; Dyp perox; 1.
TIGRPAMs; TIGR01413; Dyp perox_fam; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U24186; AABO8488.2; -.
EMBL; AF494047; AAM09569.1; -.
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hes 6; Conserv
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                                                                                                                                                 colon mucosa.
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Last sequence update) Last annotation update)

Created)

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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=288681;
                                                                     25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                   Similarity 75.0
6; Conservative
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                              PRELIMINARY;
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                                                                                                                               Bacillus cereus ZK.
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                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                               ORFNames=BTZK4292
                                           Q633P6;
25-OCT-2004
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SEQUENCE
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Best Local S
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067218;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 archaeon Pyrococcus abyssi.";
Mol. Microbiol. 47:1495-1512(2003).
-!- FUNCTION: DNA primase is the polymerase that synthesizes small RNA primers for the Okazaki fragments on both template strands at replication forks during chromosomal DNA synthesis (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           participate in formation of the active center, but the ATP-binding site is exclusively located on the small subunit (By similarity).
-!- SIMILARITY: Belongs to the eukaryotic-type primase large subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Heterodimer of a small subunit and a large subunit. Both
                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                       10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
DNA primase large subunit (EC 2.7.7.-) (DNA primase 46 kDa subunit)
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=GES / Orsay;
MEDLINE=22511545; PubMed=12622808;
Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte (Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C., Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
"An integrated analysis of the genome of the hyperthermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF04104; DNA_primase_lrg; ī. _
Complete proteome; DNA replication; DNA-directed RNA polymerase;
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                                         Length 334;
                                                                                                                                                                                                                                                                                            Name=priB; OrderedLocusNames=PYRAB01830; ORFNames=PAB2235;
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                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
Complete proteome; Hypothetical protein.
SEQUENCE 334 AA; 38137 MW; E207F1EC267334E5 CRC64;
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                                                                                                                                                                                              393 AA.
                                        75.5%; Score 37; DB 66.7%; Pred. No. 51; ive 1; Mismatches
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PIR; D75207; D75207.
HAMAP; MF 00701; -; 1.
Interpro; IPR008918; 5.3 exo C.
Interpro; IPR007238; DNA_Drimase_lrg.
                                                                                                                                                                                             PRT;
                                                                     6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                              STANDARD;
                                                                                                                         302 KANNEYITHI 310
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SEQUENCE 393 AA; 45
                                                                                                1 KMNEYTVHL 9
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                                                     Local Similarity
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Hayabhizaki Y., Shinozaki K.;
"Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAB.";
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richardson P., Rubin E., Tice H.; "Complete genome sequence of Bacillus cereus ZK."; Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                              Gaps
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25-OCT-2004 (TrEMBLE). 28, Last sequence update)
25-OCT-2004 (TrEMBLE). 28, Last annotation update)
25-OCT-204 (TrEMBLE). 28, Last annotation update)
RRNA, partial cds, clone: RAFL23-25-J01 (WRNA, partial cds, clone: RAFL23-09-L14) (Fragment).
Arabidopsis thaliana (Mouse-ear cress).
Spermatophyte; Magnoliophyte; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Totoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,
Narusaka M., Shin-i T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.
Kobayashi M., Toyoda A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,
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                                                                                                                                                                                                                                                                                                      75.5%; Score 37; DB 2; Length 936; 75.0%; Pred. No. 1.5e+02; tive 2; Mismatches 0; Indels
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                                                                                                                                                               EMBL; CP000001; AAU15977.1; -. Hypothetical protein. SEQUENCE 936 AA; 104539 MW; D05C843D8B02DF8A CRC64;
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EMBL; AK176219; BAD43918.1; -.
InterPro; IPR007145; MAP65_ASE1.
Pfam; PF031999; MAP65_ASE1.1.
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RESULT 12

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Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Cheuk R., Shinn P., Brooks S., Buehler E., Chiou J., Choi E., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Chao C., Shinn P., Dunn P., Buehler E., Kahn S., Kim C., Walker M.,
Williams S., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A.,
Hansen N.F., Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S.,
Luros S., Rowley D., Schwartz J., Toriumi M., Vysotekaia V., Yu G.,
subwis R.W., Federspiel N.A., Theologis A., Ecker J.R.;
submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                Score 36, DB 2; Length 627;
Pred. No. 1.6e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.5%; Score 36; DB 2; Length 635;
66.7%; Pred. No. 1.6e+02;
tive 1; Mismatches 2; Indels
       the EMBL/GenBank/DDBJ databases.
Submitted (WAR-1997) to the EMBL/GenBank/DDBJ databases EMBL; Z92813; CAB07289.1; -. PIR; T25395; T25395.

POR PR: T25395; T25395.

WormBase; WBGen012112; T28A8.6.

WormPep; T28A8.6; CE18977.

InterPro; IPR006570; SPK.

Pfam; PR04435; SPK; 2.

Hypotherical protein.

SEQUENCE 627 AA; 71794 MW; 4A56E4D3658ECICC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AC006917; AAF79248.1; -...
InterPro; IPR007145; MAP65 ASE1.
InterPro; IRR008936; MAPG AP.
Pfam; PF0399; MAP65 ASE1, 1.
SEQUENCE 635 AA; 72664 MW; 2871C7DA1E4DA65E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9LQW1;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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QBDVD0;
01-MAR-2003 (TEMBLrel. 23,
01-MAR-2003 (TEMBLrel. 23,
01-MAR-2004 (TEMBLrel. 26,
                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.7°
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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62 KMNEYSIEL 70
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Q8DVD0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P., Dale J.M., Hayashizaki Y., Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lin J., Miranda M., Narusaka M., Narusaka M., Narusaka M., Narusaka M., Daupen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; BNBL, Allosaki K., Davis R.W., Theologis A., Ecker J.R.; EMBL, AY120768; AAM53326.1; -.
EMBL; BT008373; AAP3732.1; -.
EMBL; BT008373; AAP3732.1; -.
InterPro; IPR008956; Rho GĀP.
Pfam; PP03999; WAP65 ASE1.
Hypothetical procein.
                                                                                                                                                                                                                                                                                                                                         Southwick A., Karlin-Neumann G., Nguyen M., Tripp M., Miranda M., Palm C.J., Bowear L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayshizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Saki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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Rhabditidae; Peloderinae; Caenorhabditis.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             603 AA; 69060 MW; 7C2B37A23CBB889D CRC64;
                                                                 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein Atlg14690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                              603 AA
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                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein T28A8.6.
ORFNames=T28A8.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            investigating biology.";
Science 282:2012-2018(1998).
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                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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STRAIN=Bristol N2;
Lloyd C.R.;
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
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                                                   Q81836;
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Search completed: July 13, 2005, 17:29:15 Job time : 64.2222 secs

1 KMNEYTVHL 9 |:|| |:|| 7 KLNEATIHL 15

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RESULT 1
US-09-502-600-31
is Sequence 31, Application US/09502600A
is Sequence 31, Application US/09502600A
is Patent No. 6294344
is GENERAL INFORMATION:
is APPLICANT: O'Brien, Timothy J.
is TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
is TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
is TITLE OF INVENTION: Ovarian Cancer
is TITLE OF INVENTION: Ovarian Cancer
is CURRENT PREFIGURE: D609-02-11
is CURRENT APPLICATION NUMBER: US/09/502,600A
is PRIOR APPLICATION NUMBER: 09/039,211
is PRIOR APPLICATION NUMBER: 03-14-1998
is NUMBER OF SEQ ID NOS: 136
is SEQ ID NOS: 136
is TUBGTH: 9
is TYPE: PRT
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; Sequence 89, Application US/09502600A
; Patent No. 6294344
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Ovarian Cancer
; TITLE OF INVENTION: Ovarian Cancer
; TITLE OF INVENTION: Ovarian Cancer
; TITLE OF INVENTION: 0.02-11
; CURRENT APPLICATION NUMBER: US/09/502,600A
; PRIOR APPLICATION NUMBER: US/09/502,600A
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 89
; LENGTH: 9
                              113, Appl
213, Appl
213, Appl
470, App
5502, Appli
2, Appli
2, Appli
49, Appl
49, Appl
47539, A
26539, A
26639, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
; OTHER INFORMATION: Residues 72-80 of the SCCE protein US-09-502-600-31
US-09-949-016-11065
US-09-323-872A-13
US-09-710-279-2136
US-09-710-279-470
US-09-134-001C-5502
US-08-134-001C-5502
US-08-909-954-4
US-08-9134-001C-5184
US-09-134-001C-5184
US-09-134-01C-5184
US-09-134-01C-5184
US-09-134-01C-5184
US-09-134-01C-5184
US-09-134-01C-5184
US-09-134-01C-5184
US-09-134-01C-10644
US-09-248-796A-26699
US-09-9902-540-110-214
US-09-134-010C-7895
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Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 31, Appl Sequence 109, Appl Sequence 119, Appl Sequence 119, Appl Sequence 109, Appl Sequence 17, Appl Sequence 17, Appl Sequence 12, Appl Sequence 12, Appl Sequence 2, Appl Sequence 3, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 3, Appl Sequence 3
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Sequence 122, App
Sequence 122, App
Sequence 93, Appl
Sequence 93, Appl
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                                                                                                                                                                       July 13, 2005, 16:58:04; Search time 19.4444 Seconds (without alignments) 34.552 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-18-243-109

US-09-261-416-7

US-09-261-416-7

US-09-154-483-33

US-08-557-146-12

US-09-154-344-12

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Maximum Match 100%
Listing first 45 summaries
                                                                                                                            - protein search, using sw model
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                       US-09-905-083A-31
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Match Length
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Result 8

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Sequence 109, Application US/09918243

Patent No. 6627403

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Cannon, Martin J.

APPLICANT: Cannon, Martin J.

APPLICANT: Santin, Alessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

FILE REPERENCE: B6223CH/C/D/CIP

CURRENT FILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-07-33

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 109

LENGTH: 9
                                                                                                               Sequence 89, Application US/09918243

Sequence 89, Application US/09918243

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

APPLICANT: Cannon, Martin J.

APPLICANT: Santin, Alesandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

TITLE OF INVENTION WHEER: US/09/918,243

CURRENT FILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-07-33

PRIOR FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 89

LENGTH: 9
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"NAME/KEY: CHAIN

"OTHER INFORMATION: Residues 72-80 of the SCCE protein US-09-918-243-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Residues 72-80 of the SCCE protein US-09-918-243-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 49; DB 4; L
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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NAME/KEY: CHAIN
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US-09-618-259-4
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| Sequence 31, Application US/09918243
| Patent No. 6627401
| Patent No. 6627401
| APPLICANT: O'Brien, Timothy J.
| APPLICANT: Cannon, Martin J.
| APPLICANT: Santin, Alessandro
| TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer; FILE REPERENCE: D6223CIP/C/D/CIP
| CURRENT APPLICATION NUMBER: US/09/918,243
| CURRENT FILING DATE: 2001-07-30
| PRIOR APPLICATION NUMBER: US
| RIOR APPLICATION NUMBER: US
| RIOR FILING DATE: 2001-07-13
| NUMBER OF SEQ ID NOS: 136
| LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT:
APPLICANT:
O'Brien, Timothy J.
APPLICANT:
O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: Ovarian Cancer
FILE REPERENCE:
D6223CIP-C
CURRENT FILING DATE: 2000-02-11
CURRENT APPLICATION NUMBER: 09/039,211
PRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 109
LENGTH: 9
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                                                                       Length 9;
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                                                                                                                    0; Indels
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; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-502-600-109
; OTHER INFORMATION: Residues 72-80 of the SCCE protein US-09-502-600-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Residues 72-80 of the SCCE protein US-09-918-243-31
                                                                  Query Match
100.0%; Score 49; DB 3; L
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0;
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US-09-502-600-109
S. Sequence 109, Application US/09502600A
; Patent No. 6294344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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NAME/KEY: CHAIN
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COUNTRY: USA
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 61.
TELECOMMUNICATION INFORMATION: 7ELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
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Best Local Similarity 10v...
9; Conservative
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MEDIUM TYPE: Floppy
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STATE: New COUNTRY: U.S.A.
10036-2787
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                                                                                                                                                        CITY:
STATE:
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Sequence 7, Application US/09261416A

Patent No. 6291663

GENERAL INCORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: TADG-12: A No. 6291663el Transmembrane Serine Protease TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma FILE REPERENCE: D6192

CURRENT APPLICATION NUMBER: US/09/261,416A

NUMBER OF SEQ ID NOS: 14

SEQ ID NO 7

LENGTH: 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Serine protease catalytic domain of stratum corneum OTHER INFORMATION: chymotryptic enzyme (Scce) homologous to similar OTHER INFORMATION: domain in TADG-12
                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic OTHER INFORMATION: enzyme (scce) catalytic domain
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            APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease
FILE REFERENCE: D6020CIP2
CURRENT APPLICATION UNMER: US/09/618,259
CURRENT FILING DATE: 2000-07-18
PRIOR PILING DATE: 1998-08-21
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 4
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Patent No. 6232456
GENERAL INFORMATION:
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
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GENERAL INFORMATION:
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ORGANISM: unknown
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                          NAME/KEY: DOMAIN
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US-09-261-416-7
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                                                                                                                                                                                                                                                                          FEATURE:
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STEVEN D.
NOVEL SERINE PROTEASE REAGENTS
AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
OF THE PROSTATE
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| Patent No. 5834290
| GENERAL INFORMATION:
| APPLICANT: Egelrud, Torbjorn
| APPLICANT: Hanson, Lennart
| TITLE OF INVENTION: RECOMBINANT Stratum Corneum Chymotryptic
| TITLE OF INVENTION: RECOMBINANT STRATUM CORNEUM CHYMOTRYPTION: RECOMBINANT STREET: 17
| CORRESPONDENCES: 17
| CORRESPONDENCE ADDRESS: | ADDRESSEE: White & Case, Patent Department |
| STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 49; DB 3; Length 224; 100.0%; Pred. No. 0.029;
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COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                             TITLE OF INVENTION: NOVEL SERINE PRITILE OF INVENTION: AND METHODS USITITLE OF INVENTION: OF THE PROSTATE NUMBER OF SEQUENCES.

ADDRESSER: ADDRESS:
ADDRESSER: ADDRES
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Gaps
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Fatent No. 6451500
GENERAL INFORMATION:
APPLICANT: O'STIEN, TIMOTHY J.
APPLICANT: O'STIEN, TIMOTHY J.
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
TITLE OF INVENTION: O'VERENTESSEE in Carcinomas
FILE REFERENCE: D606411P/D
CURRENT APPLICATION NUMBER: US/09/644,600
CURRENT APPLICATION NUMBER: 09/421,213
PRIOR APPLICATION NUMBER: 09/421,213
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 49; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 9; Conservative 0; Mismatches 0; Indels
             CUUNTRY 10.8.

ZIP: 10036-2787

ZIP: 10036-2787

ZOWDUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
APPLICATION NUMBER: US 08/557,146
FILING DATE: I4-DEC-1995
CLASSIPICATION:
APPLICATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 35,372
REFERENCE/COCKET NUMBER: 35,372
REFERENCE/COCKET NUMBER: 35,372
REFERENCE/COCKET NUMBER: 319-8783
TELEFPHONE: (212) 354-8113
INFORMATION POR SEG ID NO: 12:
SEQUENCE CHARACTERISTICS:
LUNCORMATION POR SEG ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 225 amino acids
TYPE: amino acids
STRANDEDNESS: single
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US-09-644-600-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 KMNEYTVHL 52
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  STATE: New York
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US-09-644-600-4
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"Sequence 4, Application US/09027337B

"Patent No. 5972616

"GENERAL INFORMATION:

"APPLICANT: O'Fien, Timothy J.

"APPLICANT: Tanimoto, Hirotoshi

"ITILE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in TITLE OF INVENTION: Breast and Ovarian Carcinomas

"ITILE OF INVENTION: Breast and Ovarian Carcinomas

"TITLE OF INVENTION: Breast and Ovarian Carcinomas

FILE REFERENCE: D664

CURRENT APPLICATION NUMBER: US/09/027,337B

CURRENT FILING DATE: 1998-02-20

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 4

LENGH: 225
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Patent No. 5981256
GENERAL INFORMATION:
APPLICANT: Egelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Enzyme (SCCE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 49; DB 2; Length 225; Best Local Similarity 100.0%; Pred. No. 0.03; Matches 9; Conservative 0; Mismatches 0; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
             FILING DATE: 14-DEC-1995
CLASSIFICATION: 424
ATTONNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEPHONE: (212) 84-8113
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHRAPATESTICS:
APPLICATION NUMBER: US/08/557,146
                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: polypeptide US-08-557-146-12
                                                                                                                                                                                                                                                                                                    LENGTH: 225 amino acids
TYPE: amino acids
STRANDEDNESS: single
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Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
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ORGANISM: Unknown
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US-09-154-344-12
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i Sequence 2, Application US/08551146

i Sequence 2, Application US/08551146

i Patent No. S834309

i GENERAL INFORMATION:

APPLICANT: Egelrud, Torbjorn

APPLICANT: Hanson, Lennart

TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic

TITLE OF INVENTION: Brzyme (SCCE)

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSER: White & Case, Patent Department

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

STATE: New York

STATE: New York
    Sequence 4. Application US/09654600A

| Patent No. 6649741
| GENERAL INFORMATION:
| APPLICANT: O'Brimen, Timothy J. APPLICANT: Tanimoto, Hirotoshi;
| TITLE OF INVENTION: TANG-15: AN Extracellular Serine Protease;
| TITLE OF INVENTION: Overexpressed in Carcinomas;
| TITLE OF INVENTION: Overexpressed in Carcinomas;
| FILE REPERENCE: 18664CIP/D |
| CURRENT PILING DATE: 2000-09-01 |
| PRIOR APPLICATION NUMBER: 09/421,213 |
| 09/027,337 |
| PRIOR FILING DATE: 1999-10-20 |
| 1998-02-20 |
| NUMBER OF SEQ ID NOS: 98 |
| SEG ID N
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MEDIUM TYPE: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELEDENONE: (212) 819-8783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
COTHER INFORMATION: SCCE
US-09-654-600A-4
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 KMNEYTVHL 52
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US-09-654-600A-4
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LENGTH: 225
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Sequence 109, App Sequence 100, App Sequence 4, Appli Sequence 98, Appli Sequence 38, Appl Sequence 104, Appl Sequence 104, Appl Sequence 102, Appli Sequence 102, Appli Sequence 92, Appli Sequence 92, Appli Sequence 94, Appli

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TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 9; Conserv
US-09-918-243-31
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Sequence 109, Appl
Sequence 31, Appl
Sequence 89, Appl
Sequence 109, Appl
Sequence 31, Appl
Sequence 89, Appl
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                                                                                                      (without alignments)
53.584 Million cell updates/sec
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89,
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                                                                                         July 13, 2005, 17:29:45 ; Search time 64.8889 Seconds
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| cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US10P_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US10P_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US10P_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.ppp:*
| cgn2_6/ptodata/1/pubpaa/USS0_NEW_PUB.ppp:*
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-918-243-89
US-09-918-243-109
US-09-918-243-109
US-09-905-083-89
US-09-905-083-89
US-10-372-521-109
US-10-372-521-89
US-10-372-521-109
US-10-372-521-109
US-10-831-075-31
                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                       1726220 segs, 386332138 residues
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Maximum Match 100%
Listing first 45 summaries
                                                               OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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49
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Sequence 98, Appli
Sequence 3, Appli
Sequence 48, Appl
Sequence 49, Appl
Sequence 49, Appl
Sequence 639, Appl
Sequence 639, Appl
Sequence 95, Appl
Sequence 95, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 122, Appl
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Sequence 93, Appl
Sequence 93, App
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APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
FILE REFERENCE: D6223CIP/C/D/CIP
CURRENT APPLICATION NUMBER: US/09/918,243
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 31
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; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-918-243-31
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llarity 100.0%; Pred. No. 1.6e+06;
Conservative 0; Mismatches 0;
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US-09-905-083-93
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Patent No. US20020142317A1
GENERAL INFORMATION:
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FILE REFERENCE: D6223CIP/C/Div
CURRENT APPLICATION NUMBER: US/09/905,083
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 09/502,600
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Sequence 109, Application US/09918243

Patent No. US20020142317A1

GENERAL INFORMATION:

APPLICANT: O'Brien Timothy J.

APPLICANT: Santin, Alessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

FILE REPERENCE: D62221P/C/D/GIP

CURRENT FILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 109

LENGTH: 9
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APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of IIILE OF INVENTION: Ovarian Cancer
                                                 REALERAL INFORMATION:

APPLICANT: O'BLIEN, Timothy J.

APPLICANT: Cannon, Martin J.

APPLICANT: Cannon, Martin J.

APPLICANT: Santin, Alessandro.

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer FILE REFERENCE: D6223CIP/C/D/CIP

CURRENT APPLICATION NUMBER: US/09/918,243

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US

PRIOR FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 89
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; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-918-243-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-09-918-243-109
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100.0%; Score 49; DB 9; I
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0;
                          Sequence 89, Application US/09918243
Patent No. US20020142317A1
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Patent No. US20020146708A1
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 9; Conserv
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US-09-905-083-31
    US-09-918-243-89
                                                                                                                                                                                                                                                                                                                                LENGTH: 9
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Sequence 109, Application US/09905083

Sequence 109, Application US/09905083

Patent No. US20020146708A1

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer

TITLE OF INVENTION: Ovarian Cancer

FILE REFERENCE: D6223CIP/C)409905,083

CURRENT APPLICATION NUMBER: US/09/905,083

FRICH REPLIAG DATE: 2001-07-13

PRIOR PILIAG DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 109

TYPE: PRI
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Patent No. US20020146708A1

Patent No. US20020146708A1

Patent No. US20020146708A1

APPLICANT: O'BERIENCE:
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer TITLE OF INVENTION: US/09/905,083

CURRENT APPLICATION NUMBER: US/09/905,083

CURRENT FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NOS: 136

SEQ ID NOS: 136
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NAME/KEY: CHAIN
OTHER INFORMATION: Residues 72-80 of the SCCE protein
                                                                                                    100.0%; Score 49; DB 9; I 100.0%; Pred. No. 1.6e+06; tive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.6e+06; Matches 9; Conservative 0; Mismatches 0;
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US-10-831-075-31
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APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
TITE OF INVENTION: Alessandro
TITE OF INVENTION: Methods for the early diagnosis of ovarian cancer
FILE REPERENCE: D623CIP/CP/CD/2D2
CURRENT APPLICATION NUMBER: US/10/372,521
CURRENT FILING DATE: 2003-02-21
PRIOR PILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 89
LENGTH: 9
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Best Local Similarity 100.0%; Score 49; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                       Length 9;
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               FEATURE:

NAME/KBY: CHAIN

OTHER INFORMATION: Residues 72-80 of the SCCE protein US-09-905-083-109
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; OTHER INFORMATION: Residues 72-80 of the SCCE protein
US-10-372-521-31
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                                                                                       100.0%; Score 49; DB 9; I
100.0%; Pred. No. 1.6e+06;
                                                                                                                    0; Mismatches
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                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
 ORGANISM: Homo sapiens
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NAME/KEY: CHAIN
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100.0%; Score 49; DB 15; Length 9;

Query Match

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Fublication No. US20040224891A1
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Cantin, Alesandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;
FILE REFERENCE: D6223CIPF(C/D/CIP3)
CURRENT APPLICATION NUMBER: US/10/831,075
CURRENT FILING DATE: 2004-04-23
PRIOR FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 140
SEQ ID NO 31
LENGTH: 9
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APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro.
TITLE CANT: Santin, Alessandro.
TITLE CANT: Santin, Alessandro.
TITLE CANT: Santin, Methods for the early diagnosis of ovarian cancer FILE REFERENCE: D6223CIP/C/D/CIP2
CURRENT APPLICATION NUMBER: US/10/372,521
CURRENT FILING DATE: 2003-02-21
PRIOR FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 109
LENGTH: 9
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OTHER INFORMATION: Residues 72-80 of the SCCE protein US-10-372-521-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Residues 72-80 of the SCCE protein US-10-831-075-31
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                                                                                                US-10-372-521-109
.; Sequence 109, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
1 KWNEYTVHL 9
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Millet, Isabelle
                   Peyman, John A.
Kekuda, Ramesh
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                                                         Ju, Jingfang
Li, Li
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US-10-262-511-100
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US-09-796-294-4
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                                                  Sequence 89, Application US/10831075
; Publication No. US20040224891A1
; GENERAL INPORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
ITLLE REFERENCE: D6223GIP/C/D/CIP3
CURRENT APPLICATION NUMBER: US/10/831,075
CURRENT APPLICATION NUMBER: US/10/831,075
FRIOR APPLICATION NUMBER: US/10/831,075
FRIOR APPLICATION NUMBER: US/10/831,075
NUMBER OF SEQ ID NOS: 140
SEQ ID NO 89
LENGTH: 9
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APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
FILE REFERENCE: D6223CIP/C/D/CIP3
CURRENT APPLICATION NUMBER: US/10/831,075
CURRENT FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 10/372,521
PRIOR FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 140
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Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CHAIN
OTHER INFORMATION: Residues 72-80 of the SCCE protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY; CHAIN; OTHER INFORMATION: Residues 72-80 of the SCCE protein US-10-831-075-109
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US-10-262-511-100
S-10-262-511-100
Sequence 100, Application US/10262511
PUBLICATION NO. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glennda
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Publication No. US20040224891A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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               RESULT 11
US-10-831-075-89
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APPLICANT: Machada Ramesh
APPLICANT: Machada Ramesh
APPLICANT: Ju. Jingfang
APPLICANT: Ju. Jingfang
APPLICANT: Ju. Jingfang
APPLICANT: Malayerak Kinderity
APPLICANT: Rinnen, Azera
APPLICANT: Rinnen, Azera
APPLICANT: Rinnen, Balanting
APPLICANT: General Linda
APPLICANT: Rateful Linda
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TITLE OF INVENTION: No. US20030199010A1el Extracellular Serine Protease
FILE REFERENCE: D6020C1P2
CURRENT APPLICATION NUMBER: US/10/461,787
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US 09/127,444
PRIOR APPLICATION NUMBER: US 09/127,444
PRIOR PILING DATE: 1998-08-21
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 4
LENGTH: 144
                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: DOMAIN
; OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
; OTHER INFORMATION: enzyme (scce) catalytic domain
US-09-796-294-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic; OTHER INFORMATION: enzyme (scce) catalytic domain US-10-461-787-4
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100.0%; Score 49; DB 14; Length 144;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels
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                 GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Extracellular Serine Protease;
FILE REFERENCE: D6020CIP3
CURRENT APPLICATION UNMBER: US/09/796,294
CURRENT APPLICATION NUMBER: US 09/618,259
PRIOR APPLICATION NUMBER: US 09/618,259
PRIOR PILING DATE: 2000-07-18
SEQ ID NO 4
SEQ ID NO 4
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US20020037581A1
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KONNEYTVHL 17
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Best Local Similarity
Matches 9; Conserv
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ORGANISM: unknown
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ORGANISM: unknown
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NAME/KEY: DOMAIN
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The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human stratum corneum chymotrypsin enzyme peptide #2 (residues 123-131).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stratum corneum chymotrypsin enzymė; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosing cancer comprises detecting stratum corneum chymotrypsin
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ABB84420
AAG19495
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ADR68848
ABG23378
AAG19496
AAG52872
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ABR84477
ADD15250
                                                                                                                         ABU48685
AAE08292
AAE08284
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AAE08314
ADR68871
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                                                                                                                                                                                                                                                                                                                                                                                                                               AAE08237 standard; peptide; 9 AA.
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   AAE08237;
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ABB84421
ABB84406
AAU82740
ABU07440
ABU07471
ABR58471
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ADL06515
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geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
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geneseqp1990s:*
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                      1 RLSSMVKKV 9
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Match
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                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                           Perfect score:
                                                                           OM protein
                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                   Searched:
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                                                                                                          Run on:
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invention.
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                                            ADI39727;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel method for vaccinating an individual against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating an individual with a SCCE peptide, which elicits an immune response in the individual. A peptide of the invention acts as a stratum corneum chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating an individual against SCCE, particularly an individual having, suspected or at risk of getting ovarian, lung, prostate, pancreatic or colon cancer. The oligonucleotide is useful for treating a neoplastic state in an individual, such as ovarian, breast, lung, colon, prostate, or peptides are also useful in the monitoring and development of the peptides are also useful in the monitoring and development of immunocherapies for ovarian and other malignancies. The present sequence represents a peptide fragment of serine protease SCCE (stratum corneum corneum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for vaccinating an individual against SCCE, and in monitoring and developing immunotherapies for ovarian and other malignancies.
                                                                                                                                                                                                                                                                                                                                                                  Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:32.
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                            ;
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0
                                                                                                                                                                                                                                                                                                                                                                                                         serine protease; stratum corneum chymotrytic enzyme; SCCE; immune response; ovarian cancer; lung cancer; prostate cancer; pancreatic cancer; colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 40; DB 8; Length 9; 100.0%; Pred. No. 1.8e+06; Live 0; Mismatches 0; Indels
                                            Indels
                                            ö
                   Pred. No. 1.8e+06;
                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; SEQ ID NO 32; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADI39727 standard; protein; 144 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Santin A;
100.0%; FIE
                                                                                                                                                                                                                                   ADR68793 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-FEB-2004; 2004WO-US005134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-2003; 2003US-00372521
                                                                                                                                                                                                                                                                                                                        02-DEC-2004 (first entry)
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Best Local Similarity 100.
Matches 9; Conservative
                                          9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O'brien TJ, Cannon MJ,
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                                                                                                              RLSSMVKKV
                                                                                    1 RLSSMVKKV
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                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004075723-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-SEP-2004.
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ADI39727
LD ADI39
                                       Matches
                                                                                                                                                                                         RESULT 2
ADR68793
ID ADR6
XX
AC ADR6
XX
ADR BE HUMB
XX
BE HUMB
XX
BE HUMB
XX
BE HOMO
XX
CC ADR
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The present invention relates to novel activated immune T cells or dendritic cells directed toward extracellular serine protease termed tumour antigen derived gene-14 (TADG-14). The method of the invention involves exposing the immune cells to a TADG-14 protein fragment, where exposure to the TADG-14 protein fragment activates the immune cells. The invention is used for the production of activated immune T cells or dendritic cells. The invention allows screening to identify proteases overexpressed in carcinoma. The present sequence is stratum corneum chymotryptic enzyme (scce) catalytic domain. This sequence is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Production of activated immune cells or dendritic cells by exposing immune cells to tumor antigen derived gene protein fragment consisting of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                Immune T cell; dendritic cell; extracellular serine protease;
tumour antigen derived gene-14; TADG-14; carcinoma;
stratum corneum chymotryptic enzyme; scce.
                                                         Stratum corneum chymotryptic enzyme (scce) catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stratum corneum chymotryptic enzyme (scce) catalytic domain.
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98US-00137944.
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Best Local Similarity 100.00
Post Ocuservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Underwood LJ;
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 RLSSMVKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2003199010-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-AUG-1998;
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                                                                                                                                                                                                                                       Unidentified
15-APR-2004
                                                                                                                                                                                                                                                                                                 US6642013-B1
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The invention relates to extracellular serine protease termed tumour antigen derived gene-14 (TADG-14) and its nucleic acid. Composition comprising TADG-14 peptide is useful for treating a neoplastic state in an individual. The neoplastic state is chosen from ovarian cancer, breast cancer, lung cancer, colon cancer, prostate cancer in which TADG-14 is overexpressed. The present sequence is Stratum corneum chymotryptic enzyme (scce) catalytic domain. This sequence is used in the
                                                                                                                                                                                                                                                                            Novel isolated DNA encoding tumor antigen derived gene-14 protein, useful
                                                                                                                                                                                                                                                                                               for treating neoplastic state (such as ovarian cancer, breast cancer, lung cancer, colon cancer, prostate cancer) in an individual.
                                                                                                                                                                                                                                                                                                                                                   Example 1; SEQ ID NO 4; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exemplification of the invention.
                                                     13-JUN-2003; 2003US-00461787.
                                                                                      21-AUG-1997; 97US-00915659.
21-AUG-1998; 98US-00137944.
18-JUL-2000; 2000US-00618259.
                                                                                                                                                                                                   O'brien TJ, Underwood LJ;
                                                                                                                                                               (UYAR-) UNIV ARKANSAS.
                     23-OCT-2003
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ö Gaps ö 100.0%; Score 40; DB 8; Length 144; 100.0%; Pred. No. 1.6; 0; Indels Mismatches ö 9; Conservative Best Local Similarity Sequence 144 AA; Matches

60 RLSSMVKKV 68 1 RLSSMVKKV 9 ò

ADA05744 standard; protein; 224 AA 06-NOV-2003 (first entry) ADA05744; THE SECOND SECON

Human NOV18g protein SEQ ID NO:104.

immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzaheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia human; NOVX; antidiabetic; anorectic; antibacterial; virucide;

Homo sapiens

WO2003029424-A2

10-APR-2003

02-OCT-2002; 2002WO-US031373

2001US-0327917P. 2001US-0328029P. 2001US-0328044P. 2001US-0328056P. 2001US-0326483P. 2001US-0327435P. 2001US-0327449P. 09-OCT-2001; 09-OCT-2001; 09-OCT-2001; 09-OCT-2001; 05-OCT-2001; 05-OCT-2001; 02-OCT-2001;

2001US-0346357P 2002US-0373260P 2002US-0373815P 2002US-0373817P 2002US-0373826P 2002US-0381037P. 2002US-0381038P. 2002US-0383656P. 2002US-0383831P. 2002US-0391335P. 2002US-0373884P 2002US-0381042P. 24-OCT-2001; 24-OCT-2001; 29-OCT-2001; 18-OCT-2001; 22-OCT-2001; 01-NOV-2001; 19-APR-2002; 19-APR-2002; 17-APR-2002; 19-APR-2002; 16-MAY-2002; 16-MAY-2002; 16-MAY-2002; 17-MAY-2002; 29-MAY-2002;

(CURA-) CURAGEN CORP.

2002US-00262511

Dipippo VA; Catterton E; Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipik Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

WPI; 2003-381626/36. N-PSDB; ADA05743. New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.

Claim 1; Page 172; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOV1). Also described: (1) a composition comprising a polypeptide
described above and a carrier; (2) a kit comprising, in one or more
containers, the composition described above; (3) an isolated nucleic acid
molecule which encodes a NOVX protein of the invention; (4) a vector
comprising the mucleic acid molecule described above; (5) a cell
comprising the mucleic acid molecule described above; (5) a cell
comprising the above vector; (6) an antibody that immunospecifically
binds to the polypeptide described above; (7) methods for determining the
presence or amount of the above polypeptide or nucleic acid molecule in a
sample; (8) methods for determining the presence of or predisposition to
a disease associated with altered levels of expression of the above
cc dientifying an agent that binds to the polypeptide described
above; (10) a method for identifying a potential therapeutic agent for
use in treating a pathology that is related to an aberrant expression or
aberrant physiological interactions of the polypeptide; (11) a method of
creening for a modulator of activity or of latency or predisposition to
capathology associated with the polypeptide; (12) a method for modulating
the activity of the polypeptide described above; (13) methods of modulating
the activity of the polypeptide described above; (13) methods of method for producing the above polypeptide; NOVX
cc a pathology associated with the polypeptide; (12) a method for modulating
the activity of the polypeptide associated with the above polypeptide in a
mammania and (14) a method for producing the above polypeptide is useful in manufacturing a medicament for treating a
continue second as diabetes or obesity, infections; cachexia, cancer,
cache manner associated with a human disease. The polypeptide or the nucleic
cache manner and all aborders such as diabetes or obesity, infections; cachexia, cancer;
controlegenerative disorders such as Alzhaimer of alsease or Parkinson's
controle

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                        probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the present invention.
                                                                                                                                                                                                                                 Gaps
dyslipidaemias. The nucleic acids can also be used as hybridisation
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                                                                                                                                                                           100.0%; Score 40; DB 6; Length 224; 100.0%; Pred. No. 2.7; o; Indels ive 0; Mismatches 0; Indels
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2001US-0328029P.
2001US-0328044P.
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2001US-0327449P.
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2002US-0373260P.
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                                                                                                                                                                                                                                 9; Conservative
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                                                                                                                                                                                                                                                                                  1 RLSSMVKKV 9
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(MILL/) MILLET I.
(PEYM/) PEYMAN J A.
                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   wasting disorder
                                                                                                                              Sequence 224 AA;
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29-OCT-2001;
01-NOV-2001;
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15-OCT-2001;
17-OCT-2001;
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                                                                                                                                                                              Query Match
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ADN622008
ADN622008
ADN622008
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The invention relates to isolated NOVX polypeptides and polynucleotides.

NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and colynucleotides may be used to treat disorders associated with decreased polynucleotides may be used to treat disorders associated with decreased conduction or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polynucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators can in entionists and antagonists of the expression and activity of NOVX. The anti-NOVX polypeptide expression and activity of NOVX cused to modulate NOVX polypuble expression and activity of NOVX colypeptides. The anti-NOVX polypeptide expression and activity of NOVX colypeptides. The anti-NOVX polypeptide expression and activity of NOVX colypeptides. The anti-NOVX polypeptide expression and activity of NOVX colypeptides and polynucleotide expression and activity of NOVX colypeptides and polynucleotides may be used in this way to prevent, all agences and treat: metabolic disorders, diabetes, observer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Oxt T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 104; 395pp; English.
                                                                                                                                                                                                                                                               MILLER C E.
RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIKKETS R A.
ROTHENBERG M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                             BISEN A.
GANGOLLI E A.
                                                                                                              ELLERMAN K.
MALYANKAR U M.
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                                                               PATTURAJAN M.
                                                                                SPYTEK K A.
EDINGER S R.
                                                                                                                                                                                ZERHUSEN B D.
ANDERSON D W.
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BERGHS C.
DIPIPPO V A.
                                                                                                                                                                                                                ZHONG M.
CATTERTON E.
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                                                                                                                                                                  GORMAN L.
                                               GUO X
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(SPAD/)
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(RAST/)
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(GANG/)
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(EDIN/)
(ELLE/)
(MALY/)
(ORTT/)
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disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, disease, and the various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers.

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us-09-905-083a-32.rag

(first entry)

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human, NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antibatkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                         Human NOV18f protein SEQ ID NO:102.
ADA05742 standard; protein; 247 AA
                                                                                                                                                                                                             WO2003029424-A2
                                                                                                                                                                                                                                                                                                                                   09-0CT-2001; 2
09-0CT-2001; 2
12-0CT-2001; 2
15-0CT-2001; 2
17-0CT-2001; 2
18-0CT-2001; 2
22-0CT-2001; 2
24-0CT-2001; 2
24-0CT-2001; 2
24-0CT-2001; 2
24-0CT-2001; 2
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16-MAY-2002;
                                                                                                                                                                                     Homo sapiens
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                                                 06-NOV-2003
                                                                                                                                                                                                                                     10-APR-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         une present invention relates to human tumour antigen-derived gene 15 (TADG-15) protein and coding sequence (see AAH23601 and AAB98500). TADG-15 is an extracellular serine protease. It was found that TADG-15 is overexpressed in ovarian tumours. TADG-15 protein or its fragments of 9-20 residues that lack TADG-15 protease activity are useful for vaccinating an individual against TADG-15, having, suspected of having or at risk of getting cancer. Furthermore, the TADG-15 gene can be used as a diagnostic or therapeutic target in cancer. The present sequence was used in a sequence homology alignment with the catalytic domain of TADG-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel extracellular serine protease, termed tumor antigen-derived gene 15 protein overexpressed in carcinomas and DNA encoding it, for diagnosis, treatment, prevention of cancer, particularly breast, ovarian cancer.
                                                                                   Gaps
They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
                                                                                                                                                                                                                                                                         Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain.
                                                                                     ;
                                                                                                                                                                                                                                                                                               Human; TADG-15; cytostatic; vaccine; ovarian tumour; cancer; tumour antigen-derived gene 15; serine protease; Stratum Corneum Chymotryptic Enzyme; SCCE.
                                                          100.0%; Score 40; DB 8; Length 224; 100.0%; Pred. No. 2.7; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 40; DB 4; Length 225; 100.0%; Pred. No. 2.7; tive 0; Mismatches 0; Indel8
                                                                                                                                                                                              AAB98502 standard; protein; 225 AA
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                                                                                   9; Conservative
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                                                                     Local Similarity
                                                                                                            RLSSMVKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 225 AA;
                                    Sequence 224 AA
                                                                                                                                                                                                                                                                                                                                                                          WO200129056-A1
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                        AAB98502;
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2001US-0327449P. 2001US-0327917P. 2001US-0328029P.

2001US-0328056P. 2001US-0328849P. 2001US-0329414P. 2001US-0330142P.

2001US-0343629P. 2001US-0349575P. 2001US-0346357P. 2002US-0373260P.

2002US-0373815P. 2002US-0373817P. 2002US-0373826P.

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VA;
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J. Berghs C, Dipippo
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                                                                                                                                                                                                                                                                                                                  Peyman JA, Kekuda R, Ju J, Li L, Guo >
A, Edinger SR, Ellerman K, Malyankar UM;
Isen BD, Anderson DW, Zhong M, Cattertor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, cancer or dyslipidemia, and in chromosome mapping, tissue typing
                                                                                                                                                                                                                                                                                                                                                                    Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhor
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CE,
Shimkets RA, Rothenberg ME, Leach MD, Agee ML,
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
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                                                                                             2002US-0381042P
2002US-0381642P
2002US-0383656P
2002US-0383831P
2002US-0391335P.
2002US-0373884P.
2002US-0374977P.
2002US-0381037P.
2002US-0381038P.
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, Spytek KA,
                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
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N-PSDB; ADA05741.
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Patturajan M,
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RLSSMVKKV 103

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RESULT 8 ADA05742

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(e.g. NOV1). Also described to a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule described above; (5) an isolated nucleic acid molecule described above; (5) an isolated nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence. of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or above; (10) a method for identifying a potential therapeutic agent for capthology associated with the polypeptide; (11) a method of screening or a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating cor preventing a pathology associated with the above polypeptide. Novx sequences have antidiabetic, anorectic, antibacterial, virucide, and antilipaemic activities, and correction of the above polypeptide or the nucleic and antilipaemic activities, and energial a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule many be used in mean account many many heaven.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dynslipidaemia; metabolic syndrome X;
                                                                                                                                                                                                                                                                                                                                                                                                         acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslighdaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
 present invention describes NOVX proteins, where X can be 1 to 55
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nes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention.
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wasting disorder.
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Shenoy SG;
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                                                    2001US-0341058P.
2001US-034362P.
2001US-0343629P.
2001US-0346357P.
2001US-0373860P.
2002US-0373815P.
2002US-0373815P.
 2001US-0328849P.
2001US-0329414P.
2001US-0330142P.
2001US-0330309P.
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2002US-0373884P.
2002US-0374977P.
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2002US-0381038P.
2002US-0381042P.
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2002US-0383831P.
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RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E.
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BDINGER S R.
ELLERMAN K.
MALYANKAR U M.
ORT T.
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GANGOLLI E A.
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SPADERNA S K.
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N-PSDB; ADN62905.
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MILLET I.
PEYMAN J A.
KEKUDA R.
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17-APR-2002;
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Isolated NOVX polypeptides and nucleic acids, useful for preventing,

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The Invertion Figlaces to isolated wovx polypeptides and polymucleotides are used to the aberrant expression and activity of NoVX polypeptides. For example, NoVX polypeptides and polymucleotides rectivity of NoVX polypeptides and activity of NoVX polypeptides and activity of NoVX polypeptides and polymucleotides may be used to treat disorders associated with decreased expression or activity of NoVX by supplementing the patient our confliction or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NoVX polypeptides by chinding with the cells own genes and preventing their expression. NoVX polymucleotides and complementary sequences may also be used as DNA probables, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of captorative therapy. NoVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NoVX. The cant.-NoVX polypeptide antibodies, agonists and antagonists may also be used as diagnostic agents for detecting the presence of NoVX in samples. NoVX polypeptides and polymucleotide say be used in this way to prevent, cancer agents for detecting the presence of NoVX in samples. NoVX chiefectious disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, haematopoietic disorders and the various dyslipidaemias, metabolic disorders associated with obesity, the metabolic channers associated with obesity. The metabolic capeners and the various dyslipidaemias, metabolic capeners the amino acid sequence of a human NoVX protein.
                                                                                                                         invention relates to isolated NOVX polypeptides and polynucleotides.
   diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease
                                                           Claim 1; SEQ ID NO 102; 395pp; English
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Gaps ; 0 100.0%; Score 40; DB 8; Length 247; 100.0%; Pred. No. 3; 0; Indels tive 0; Mismatches 0; Indels 9; Conservative Local Similarity Query Match Matches

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ADA05732 standard; protein; 250 AA ADA05732; RESULT 10 ADA05732

06-NOV-2003 (first entry)

Human NOV18a protein SEQ ID NO:92.

human, NOVX, antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia

Homo sapiens

WO2003029424-A2.

10-APR-2003.

02-OCT-2001; 2001US-0326483P. 05-OCT-2001; 2001US-0327435P. 05-OCT-2001; 2001US-0327449P. 09-OCT-2001; 2001US-0327917P. 02-OCT-2002; 2002WO-US031373 THE STATE OF THE S

2001US-0343629P. 2001US-0349575P. 2001US-0346357P. 2002US-0373884P. 2002US-0374977P. 2002US-0373826P. 2002US-0381037P. 2002US-0381038P. 2002US-0381042P. 2002US-0381642P. 2002US-0383656P. 2002US-0383831P. 17-0CT-2001; 2 18-0CT-2001; 2 22-0CT-2001; 2 24-0CT-2001; 2 29-OCT-2001; 01-NOV-2001; 16-MAY-2002; 16-MAY-2002; 17-MAY-2002; 28-MAY-2002; 19-APR-2002; 19-APR-2002; 19-APR-2002; 19-APR-2002; 16-MAY-2002;

(CURA-) CURAGEN CORP.

2002US-00262511

01-OCT-2002;

Dipippo VA; Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Aniler CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

WPI; 2003-381626/36. N-PSDB; ADA05731.

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New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.

Claim 1; Page 169-170; 586pp; English.

The present introducing described boves, [0] a kit composition comprising a polypeptide described above and a carrier; (2) a kit composition comprising a polypeptide described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above copypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for a bove; (10) a method for identifying a potential therapeutic agent for a bove; (10) a method for identifying a potential therapeutic agent for a bathology that is related to an aberrant expression or above; (10) a method for identifying a potential or polypeptide; (11) a method of activity or of attenty or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating cor producing the above polypeptide; NOVX sequences have antidiabetic, anorectic, antibacterial, virucide, immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian cor modulation and neuroprotective, antiparkinsonian and antilipaemic activities, and can be used in gene therapy. The cyntypeptide is useful in manufacturing a medicament for treating a cyndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic The present invention describes NOVX proteins, where X can be 1 to

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The invention relates to isolated NOVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or novX polypeptides and polymucleotides are used to treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and conditions associated with decreased polymucleotides may be used to treat disorders associated with decreased conduction or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX binding with the cells own genes and preventing their expression. NOVX polymeticotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of crestorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators anti-NOVX polypeptide antibodies, agonists and antagonists of the expression and activity of NOVX.

Copypeptides. The anti-NOVX polypeptide antibodies may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polymucleotides may be used in this way to prevent, clagnose and treat: metabolic disoders, obesity, infectious disease, anorexia, cancer. cancer-associated cachexia, neurodegenerative disease, parkinson's bisorder, immune disorders, immune disorders, immune disorders, immune disorders, immune disorders, immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer: associated cachaxia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NoVX from the present invention.
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2002US-0383831P.
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09-06T-2001;
12-06T-2001;
11-06T-2001;
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24-06T-2001;
24-06T-2001;
29-06T-2001;
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Pott T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
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RASTELLI L.
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(CURA-) CURAGEN CORP.
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haematopoietic disorders, and the various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
                                                                                                                                                                                                                                       immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilpemic; gene therapy; human disease;
metabolic disorder; diabetes; obesity; infection; cachaxia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
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                                                                                                                                                                                                                               human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
                                                                    8; Length 250;
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                                                                   100.0%; Score 40; DB 100.0%; Pred. No. 3;
                                                                                    Mismatches
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                                                                 Query Match
Best Local Similarity
                                                   Sequence 250 AA;
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                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                              ADA05734;
                                                                                    Matches
                                                                                                                                             RESULT 12
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The present invertion describes Nova proteins, where A can be 1 to 3 by containing a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a Novy protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically brinds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a disease associated with altered levels of expression of the above; (10) a method for identifying a potential theraspettic agent for above; (10) a method for identifying a potential theraspettic agent for above; (10) a method for identifying a related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of activity of the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating cor preventing a pathology that is each above polypeptide. Novx sequences have antidiabetic, anorectic, antibacterial, virucide, and antilipaemic activities, and antidiabetic and endel in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a colypeptide is useful in manufacturing a medicament for treating a colypeptide is useful in manufacturing a resource of the polypeptide is useful in manufacturing a resource of the polypeptide is useful in manufacturing a resource of the polypeptide is useful in manufacturing a resource of the polypeptide is useful in manufacturing a resource of the polypeptide.
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                                                                                                               Shenoy SG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 obesity,
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                                                                                     Catterton E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes NOVX proteins, where X can be 1 to 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine an pharmacogenomics. The present sequence represents a human NOVX from
                                            Malyankar UM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid molecule may be used to diagnose, treat or prevent metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, cancer or dyslipidemia, and in chromosome mapping, tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune disorders, haematopoietic disorders and various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                         Zhong M,
Ju J,
Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shinkets RA, Rothenberg ME, Leach MD, Agee ML, BEisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
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9; Conser
                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ADA05733.
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26-FEB-2004

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The invention relates to isolated NOVX polypeptides and polynucleotides.

NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and carpivates of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polypeptides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators. The production of antibodies and in assays to identify of NOVX. The anti-NOVX polypeptide expression and activity of NOVX. Colypeptides and antagonists may also be used as antigens in the anti-NOVX polypeptide expression and activity of NOVX colypeptides. The anti-NOVX polypeptide expression and activity of NOVX colypeptides. The anti-NOVX polypeptide expression and activity of NOVX polypeptides and polynucleotide expression this way to prevent, adaptones and treat: metabolic disorders, diabetes, obesity, infectious
                                                                                                                                                                                                                                           Dipippo VA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, disease, and the various dyslipidaemias, metabolic disturbances associated with obssity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers.
                                                                                                                                                     Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerbhusen BD, Anderson DW, Zhong M, Catterron E, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                 Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 40; DB 8; Length 252; 100.0%; Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    They may also be used as antibacterial agents. The present represents the amino acid sequence of a human NOVX protein.
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR67888 standard; protein; 253 AA.
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(first entry)
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Best Local Similarity 100.
Matches 9; Conservative
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                  BERGHS C.
DIPIPPO V A.
EISEN A.
GANGOLLI E A.
RIEGER D K.
                                                                                                                        SPADERNA S K.
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  AGEE M L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 252 AA;
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09-AUG-1995
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                                     (DIPI/)
(EISE/)
(GANG/)
(RIEG/)
(SPAD/)
  AGEE/)
                       BERG/)
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    BX444X
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                                     human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; morexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
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2001US-0330309P.
2001US-0341058P.
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2002US-0373815P.
2002US-0373817P.
2002US-0373826P.
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2002US-0381037P.
2002US-0381038P.
2002US-0381042P.
2002US-0381642P.
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2001US-0328044P.
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2001US-0328849P.
2001US-0329414P.
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2001US-0349575P.
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EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
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STORE D J.
STONE D J.
PENA C B A.
SHENOY S G.
SHENOY S G.
SHENOY S G.
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ZERHUSEN B D.
ANDERSON D W.
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PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MILLET I.
PEYMAN J A.
KEKUDA R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMITHSON G.
                                                                                                                        wasting disorder
                                                                                                                                                                                                   US2004038223-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-OCT-2001;
22-OCT-2001;
24-OCT-2001;
24-OCT-2001;
                                                                                                                                                                Homo sapiens.
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17-MAY-2002;
Human NOV18b
                                                                                                                                                                                                                                                                                                                                                                                                         09-OCT-2001;
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01-NOV-2001;
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19-APR-2002;
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22-APR-2002 16-MAY-2002

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(/IIWS)

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PENA/ SHEN/ SHIM/

(ANDE/) (ZHON/)

CATT/

(GORM/ (ZERH/

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Human amyloid precursor protein protease (AAW05383) is involved in the processing or clearance of amyloid precursor protein to form beta-amyloid peptide. Its amino acid sequence was deduced from a cDNA clone (AAT39783) obtd. from a human lung library. Recombinant protease can be produced in transformed or transfected prokaryotic (partic. E. coli) or eukaryotic and testing of codes useful for treating or develop produces for the design associated with beta-amyloid peptide, esp. Alzheimer's disease
                                                         New isolated human amyloid precursor protein protease - used to develop prods. for the treatment or diagnosis of associated conditions, esp.
                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 40; DB 2; Best Local Similarity 100.0%; Pred. No. 3; Matches 9; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: July 13, 2005, 17:19:50 Job time : 77.6667 secs
                                                                                                                 Claim 1; Page 44-45; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                              123 RLSSMVKKV 131
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               WPI; 1996-464694/46.
                                                                                    Alzheimer's disease.
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                            N-PSDB; AAT39783.
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                                                                                                                                                                                                                                                                                                      Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and related vectors, transformed cells and polypeptides, useful for treating sherification of specific inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                        The enzyme encoded by this sequence is used in pharmaceutical, cosmetic and skin care products, especially to treat and prevent acne, xeroderma, or other hyperkeratotic conditions (e.g. callosities or keratosis pilaris), ichthyoses, psoriasis, eczema, etc. It is produced recombinantly following mammal, insect, plant, or microorganism transformation with plasmid pS507. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
               Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis; callosities; keratosis pilaris; ichthyoses; eczema.
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                                                                                                                                                             July 13, 2005, 16:54:03; Search time 13.5556 Seconds (without alignments) 63.882 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283416 segs, 96216763 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                 OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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1: pir1:*
2: pir2:*
4: pir3:*
1: pir4:*
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Score 33; DB 2; Length 282; Pred. No. 14;

82.5%;

Query Match Best Local Similarity

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Cispeciaes: Bacillus subtilis
Cipates: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
Cipates: 10-Sep-1999
Cipate
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D90268: Sulfolobus solfataricus

C;Species: Sulfolobus solfataricus

C;Species: Sulfolobus solfataricus

C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C;Accession: D90264

R;She, Q; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-V.Jong, I.; Jeffries, A.C.; Kozera, C.J.; Mediaa, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

A;Description: Sulfolobus solfataricus complete genome.

A;Reference number: A99139

A;Accession: D90264
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A;Molecule type: DNA
A;Rosidues: 1-351 <KUR>
A;Cross-references: UNIPROT:Q97226; GB:AE006641; NID:g13814305; PIDN:AAK41371.1; GSPDB:Gr
C;Genetics:
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Pred. No. 29;
2; Mismatches
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C,Superfamily: ABC transporter yufN
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tes 7; Conserv
   1 RLSSMVKKV
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C;Date: 23-Apr-1993 #sequence revision 23-Apr-1993 #text_change 09-Jul-2004
C;Accession: S20056; 563131; JC2317
C;Accession: S20056; 563131; JS2
J. Biol. Chem. 267, 4128-4136; JS92
A;Title: COQ2 is a candidate for the structural gene encoding para-hydroxybenzoate:polyganance number: S20056; MUID:92156158; PMID:1740455
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F. Pohl, T.M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63346
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                                                                                                                                                                                                                                                                                                      para-hydroxybenzoate polyprenyltransferase (EC 2.5.1.-) precursor - yeast (Saccharomyces
N.Alternate names: 4-hydroxybenzoate hexaprenyltransferase; protein N3419; protein YNR05
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A,Readdudes: 1-372 <PODA
A,Readdudes: 1-372 <PODA
A,CTOSS-references: EMBL:271656; NID:g1302546; PID:e239832; PID:g1302547; MIPS:YNR041c
A,Experimental source: strain S288C
C,Genetics:
C,Genetics: SCD:COQ2
A,Gene: SCD:COQ2
A,CTOSS-references: SCD:S0005324; MIPS:YNR041c
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C;Keywords: isoprenoid biosynthesis; mitochondrion; transferase; transmembrane protein
F;1.2.2/Domain: transit peptide (mitochondrion) #status predicted <TRP>
F;117-133/Domain: transmembrane #status predicted <TMI>
F;117-188/Domain: transmembrane #status predicted <TMI>
F;203-225/Region: polyprenyl diphosphate binding #status predicted
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Date: 13-Jan-1995 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33, DB 2; Length 372;
Pred. No. 18;
1; Mismatches 1; Indels
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   Indels
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R;Baddock, K.; Churcher, C.
submitted to the EMBL Data Library, December 1994
A;Reference number: S50388
A;Accession: S50401
A;Mclecule type: DNA
A;Residues: 1-560 <BAD>
   Mismatches
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A,Cross-references: SGD:S0004753
A,Map position: 13R
C,Superfamily: NADH dehydrogenase
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Best Local Similarity 77.8
Matches 7; Conservative
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7; Conservative
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                                                                                                                                265 RLSSMLKK 272
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Best Local Similarity
Matches 7; Conserv
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A;Residues: 1-372 <ASH>
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A;Accession: T50316
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Ratus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-64 <MCD>
A;Ross-references: UNIPROT:Q9P7W7; EMBL:AL136536; PIDN:CAB66447.1; GSPDB:GN00067; SPDB:6
C;Genetics: A;Experimental source: strain 972h(-); cosmid c1703
C;Genetics: A;Gene: SPDB:SPBC1703.03c
A;Hap position: 2
A;Hap position: 2
A;Introns: 43/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein AT4939750 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accesion: H88470
R;anonymous, The Buropean Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: H85470
A;Status: preliminary
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C;Species: Arabidopsis thaliana (Mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05012
R;Bevan, M.; Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Hoheisel, J.; Mewes, H.W.; N submitted to the Protein Sequence Database, April 1998
A;Reference number: 215394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: UNIPROT:Q9LDK6; GB:NC_001268; NID:g7270959; PIDN:CABB0618.1; GSPDB:G1
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                             80.0%; Score 32; DB 2; Length 664; 66.7%; Pred. No. 53; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.5%; Score 31; DB 2; Length 912;
55.6%; Pred. No. 1.2e+02;
iive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 925;
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55.6%; Pred. No. 1.2e+02;
tive 3; Mismatches 1; Indels
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A;Experimental source: cultivar Columbia; BAC clone T19P19
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Beet Local Similarity 55.00,
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A;Introns: 142/3; 193/1; 551/1
A;Note: T19P19.140
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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A; Residues: 1-912 <STO>
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A; Residues: 1-925 <BEV>
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A;Gene: AT4g39750
A;Map position: 4
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A;Molecule type: DNA
A;Mosicuse: 1-358 -PERA.
A;Residues: 1-358 -PERA.
A;Cross-references: UNIPROT:Q10252; EMBL:Z69728; PIDN:CAA93575.1; GSPDB:GN00066; SPDB:SF
A;Experimental source: strain 972h-; cosmid c56F8
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Science 281, 375-388, 1998
A.Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-589 <COL>
A;Residues: 1-589 <COL>
A;Cross-references: UNIPROT:083803; GB:AE001253; GB:AE000520; NID:g3323133; PIDN:AAC6579
A;Experimental source: strain Nichols
                                                                    hypothetical Armadillo/beta-catenin domain protein [imported] - fission yeast (Schizosad C;Species: Schizosaccharomyces pombe
C;Species: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
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R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Cadieu, E.; Lelaure, V.; Galibert, submitted to the EMBL Data Library, January 2000
A;Reference number: Z25061
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                                                                                                                                                         Species: Schizosaccharomyces pombe
Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                             C;Accession: T38914
R;Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, February 1996
A;Reference number: Z21817
A;Accession: T38914
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C;Superfamily: Bacillus arginine-tRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Genome: nuclear
C,Keywords: mitochondrion; transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     311 RESSMIYKV 319
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NiAlternate names: ERC.55 protein
C;Species: Mus musculus (house mouse)
C;Daccies: Mus musculus (house mouse)
C;Daccies: O-Jull-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C;Daccies: O-Jul-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
R;Imai, T.; Matsuda, K.; Shimojima, T.; Hashimoto, T.; Masuhiro, Y.; Kitamoto, T.; Sugite Biochem: Biophys. Res. Commun. 233, 765-769, 1997
A;Title: ERC-55, a binding protein for the papilloma virus E6 oncoprotein, specifically in A;Reference number: JC5402; MUID:97312489; PMID:9168930
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A;Residues: 1-319 <IMA>
A;Cross-references: UNIPROT:070341
C;Coment: This protein acts as a vitamin D receptor-specific cofactor modulating its fur
C;Superfamily: reticulocalbin; calmodulin repeat homology
C;Keywords: EF hand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q62703; EMBL:U15734; NID:g606967; PIDN:AAA80197.1; PID:g60696; Suberfainly: rettculocablain; calmodulin repeat homology C;Keywords: calcium binding; EF hand F;62-94/Domain: calmodulin repeat homology <EF1>
                                                                                                                        taipoxin-associated calcium binding protein-49 precursor - rat C.Species: Rattus norvegicus (Norway rat) C.Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004 C.Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004 R.Podds, D.; Schlingen, A.K.; Lu, S.Y.; Perin, M.S. J. Neurochem. 64, 2339-2344, 1995 A.Title: Novel reticular calcium binding protein is purified on taipoxin columns. A.Reference number: IS6519; MUID:95239201; PMID:7722520
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Pred. No. 73;
3; Mismatches
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Fi188-220/Domain: calmodulin repeat homology «EF4»
Fi229-261/Domain: calmodulin repeat homology «EF5»
Fi225-257/Domain: calmodulin repeat homology «EF5»
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Job time : 15.5556 secs
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55.6%;
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Best Local Similarity 55.6
Matches 5; Conservative
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67 RLQSIIKKI
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A;Molecule type: DNA
A;Cross-references: UNIPROT: O80845; EMBL: AC004665; NID: g3386593; PID: g3386621
A;Experimental source: cultivar Columbia
A;Experimental S
                                                                                                                                                                                                                                                                                                                                                                                            R.C.; Sykes, S.M.; Kaul
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A;Cross-references: UNIPROT:O17203; EMBL:AF025457; PIDN:AAB70970.1; GSPDB:GN00020; CESP:
A;Experimental source: strain Bristol N2; clone C08E3
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A;Molecule type: DNA
A;Residues: 1-219 <STO>
A;Cross-references: GB:AE002093; NID:g3386621; PIDN:AAC28551.1; GSPDB:GN00139
                                                                                                                                                                                    hypothetical protein At2g45740 [imported] - Arabidopsis thaliana
NyAlternate names: hypothetical protein F4118_28
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02473; C84894
E;Rounaley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, August 1998
A;Bescription: Arabidopsis thaliana chromosome II BAC F4118 genomic sequence.
A;Reference number: 214674
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
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R; Miller, N.; Kramer, J.; Keppler, D.
submitted to the EMBL Data Library, September 1997
A; Description: The sequence of C. elegans cosmid C08E3.
A; Reference number: Z21155
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Pred. No. 56;
2; Mismatches
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148 RLSSSMKKI 156
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                                                                                                                                                              PRELIMINARY;
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74.069 Million cell updates/sec
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                                                    July 13, 2005, 16:15:23 ; Search time 62.222 Seconds
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       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Q6AIB5
Q7NVJ5
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WEDLINE=2263266; PubMed=173872;

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Оврр92 и
О70341 и
                                   Q73ijl v
Q93w83 g
Q8bb39 g
Q85lx1
Q6av20
Q73ell
Q017203
Q75kll
Q62703 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0LT-2004 (TrEMBLrel. 26, Last annotation update)
Kallikrein 7 short variant protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                            093W83
08BP39
08BP39
06AV20
073E11
080845
017203
075K11
RCN2 RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Biochem. Biophys. Res. Commun. 211:586-589 (1995).

-!-FUNCTION! May catalyze the degradation of intercellular cohesive structures in the cornified layer of the skin in the continuous shedding of cells from the skin surface. Specific for amino acid residues with aromatic side chains in the PI position. SCCE cleaves insulin B chain at 6-Leu-| -| Cys-7, 16-Tyr-| -Leu-17, 25-Phe-|-Tyr-26, and 26-Tyr-|-Thr-27. Could play a role in the activation of precursors to inflammatory cytokines.

-!- TISSUE SPECIFICITY: Abundantly expressed in the skin and is expressed by keratinocytes in the epidermis. Very low levels are also seen in the brain and kidney.

-!- SIMILARITY: Belongs to the peptidase SI family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hansson L., Backman A., Ny A., Edlund M., Edholm B., Tornell J., Wallbrandt P., Egelrud T.;
"Epidermal overexpression of stratum corneum chymotryptic enzyme in mice; a model for chronic ithchy dermatitis.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=95314630; PubMed=7794273;
Skytt A., Stroemqvist M., Egelrud T.;
"Primary substrate specificity of recombinant human stratum corneum
Kallikrein 7 precursor (EC 3.4.21.-) (Stratum corneum chymotryptic enzyme) (hSCCE).
Name=KLK7; Synonyms=PRSS6, SCCE;
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase."; J. Biol. Chem. 269:19420-19426(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yousef G.M., Scorilas A., Diamandis E.P.;
"Molecular characterization, mapping and tissue expression of
human stratum corneum chymotryptic enzyme gene.";
Submitted (DEC-1999) to the EWBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 23-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94308225; PubMed=8034709;
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EMBL; AF243527; AAG33360.1; --
EMBL; AF323283; AAK69624.1; --
PIR; AS3968; A53968.
HSSP; P00760; 1EZX.
MEROPS; S01.300; --
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bahat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Heich F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakesley R.W., Touchman I.W., Green E.D., Dickson M.C.,
Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                              Direct protein sequencing; Glycoprotein; Hydrolase; Serine protease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (By similarity).
(By similarity).
(By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 40; DB 1; Length 253; Best Local Similarity 100.0%; Pred. No. 2.3; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                           GO, GO:0008256; F:serine-type peptidase activity; TAS.
GO; GO:000844; P:sepidermal differentiation; TAS.
InterPro; IPR009003; Pept Ser_Cys.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
PERM; PR00089; TYP981n; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; TYP9 SPC; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-linked (GlcNAc. . .) (Po
2D68B6B15A76A668 CRC64;
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Last annotation update)
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
11-OCT-2002 (TrEMBLrel. 26, Last annotation update)
Stratum corneum chymotryptic enzyme, preproprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Activation peptide.
Kallikrein 7.
Charge relay system (I charge relay system (I charge relay system (I By similarity.
By similarity.
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By similarity.
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                                H-InvDB; HIX0015373; -.
Genew; HGNC:6368; KLK7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 RLSSMVKKV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RLSSMVKKV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 2
176 1
201 2
246 253 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal; Zymogen.
                                                          MIM; 604438; -.
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ACT SITE
ACT SITE
ACT SITE
DISULFID
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SEQUENCE FROM N.A.
STRAINS-A3(2) / M145.
MEDLINE-21996410. PubMed=12000953; DOI=10.1038/417141a;
MEDLINE-21996410. PubMed=12000953; DOI=10.1038/417141a;
MEDLINE-21996410. PubMed=12000953; DOI=10.1038/417141a;
MEDLINE-21996410. PubMed R.P., Cardeno-Tarraga A.-M., Challis G.L.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Gable A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
Marren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                           Anopheles gambiae str. PEST.
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.5%; Score 33; DB 2; Length 273; 66.7%; Pred. No. 85; 1. Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 AA; 30363 MW; 413191DECB25D4C6 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
101-MAX-2004 (TrEMBLrel. 26, Last annotation update)
Putative endo alpha-1,4 polygalactosaminidase.
ORFNames=SC5F7.23c;
                                                                                                                                               01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                     AgCP3543 (Fragment).
Name=agCG53292; ORFNames=ENSANGG0000008607;
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                                                                                               273 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preliminary data.
EMBL; AAAB01008807; EAA04012.1; -.
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InterPro; IPR001611; LRR.
Pfam; PF00560; LRR 1; 5.
PRINTS; PR00019; LEURICHRPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 417:141-147(2002).
EMBL, AL939111, CAB51262.1,
PIR, T35294; T35294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces coelicolor.
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84 RVASMVKKI 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RLSSMVKKV 9
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coelicolor A3(2)."
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SEQUENCE 282 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=PEST
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                                      RESULT 5
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Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anopheles gambiae (African malaria mosquito).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=7165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Morlais I., Foncon N., Simard F., Cohuet A., Fontenille D., Morlais I., Poncon N., Simard F., Cohuet A., Fontenille D., Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases. EMBL; AX334006; AAR00113.1.; -... EMBL; AX334005; AAR01132.1.; -... EMBL; AX334005; AAR01130.1.; -... EMBL; AX334005; ARR01130.1.; -... EMBL; AX334005; AX34005; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 40; DB 2; Length 253; 100.0%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro: IRROUGUSA; Peptidase S1.
InterPro: IRROUGUS4; Peptidase S1.
IRROUGUS4; PROMOS2; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS00134; TRYPSIN DOW; 1.
PROSITE; PS00134; TRYPSIN DOW; 1.
PROSITE; PS00134; TRYPSIN SER; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 253 AA; 27608 MW; 2D68B6A41B22A668 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.5%; Score 33; DB 2; Length 202; 77.8%; Pred. No. 64; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                 Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to peptidase family S1.
EMBL; BC032005; AAH32005.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 AA; 23639 MW; E4F6334A7FC8EEA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:000833; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:trypsis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 AA
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Best Local Similarity
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                                                                                                                       [2]
SEQUENCE FROM N.A.
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                                                                                                                                                                               rissue-skin;
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NON TER
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Q6VPM5

RESULT 4

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RESULT 8
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Antonio R.V., Almeida F.C., de Almeida D.F., de Araujo M.F. F.,
Antonio R.V., Almeida F.C., de Almeida L.G.P., de Araujo M.F. F.,
Antos-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F. F.,
Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
Bardignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,
Camargo A.A., Cascadoso D.D.P., Carneiro N.P., Carraro D.M.,
Carczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
Fantinatti F., Franco G.R., Frelipe M.S.A., Ferrani L.P., Ferro J.A.,
Rerro M.I.T., Franco G.R., Frelipe M.S.A., Ferrani L.P., Ferro J.A.,
Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
Grattappaglia D., Grisard B.C., Hanna E.S., Jardim S.N., Laurino J.,
Agazinelli R.T., Manfio G.P., Maranhao A.Q., Martins W.S.,
Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,
Ai Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira S.C.,
Anschaento F.F., Nicolas M.F., Oliveira J.G., Perrai J. B.,
Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
Santos B.B.P., Santeos F.R., Sohneider M.P.C., Seuanez H.N.,
Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Souza E.N.,
Santos C.M.A., Soares R.B.A., Souza E.M., Souza E.M.,
The complete genome sequence of Chromobacterium reveals
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=ATCC 12472 / DSM 30191;
MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
                                                                      ;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales,
Neisseriaceae, Chromobacterium.
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      Score 33; DB 2; Length 282;
                                                                      Indels
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Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AE016911, AAG58051.1; -...
GO; GO:0005529; C:tubulin; IEA.
GO; GO:0005525; F:GTP binding; IEA.
GO; GO:0003924; F:GTPaea activity; IEA.
GO; GO:0046785; P:microtubule polymerization; IEA.
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; Pred. No. 92;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   297 AA
                                                                   1; Mismatches
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InterPro; IPR008280; Tub_Ft8Z_C.
Pfam; PF01936; DUF88; 1.
ProDom; PP010896; DUF88; 1.
Complete proteome; Hypochetical protein.
SEQUENCE 297 AA; 32462 MW; PC0D2708D
                                        Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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   82.5%;
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(TrEMBLrel. 26, I
(TrEMBLrel. 26, I
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                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                           ||||||||
265 RLSSMLKK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
                                                                                                                                      1 RLSSMVKK 8
                                 Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=536;
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Query Match
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225 RLSQMVKKL 233

1 RLSSMVKKV 9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Philipsen P., Kleine K., Pohlamann R., Duesterhoeft A., Hamberg K., Hagemann J.H., Obermaier B., Urrestarazu L.A., Aert R., Albermann K., Aldemann J.H., Obermaier B., Urrestarazu L.A., Aert R., Albermann K., Altmann R., Beinhauer J., Boskovic J., Bultrago M.J., Bussereau F., Coster F., Couzet M., D'Angelo M., Dal Pero F., De Antoni A., Del Rey F., Crouzet M., D'Angelo M., Dal Pero F., De Antoni A., Del Rey F., Doignon F., Dondey H., Dubois E., Fiedler T., Fleig U., Floeth M., Gaffeau A., Gallardin C., Garcia-Cantalejo J.M., Glansdorff N., Antiz C., Gaillardin C., Marchert C.J., Heumann K., Heuss-Neitzel D., Hilbert H., Hinni K., Iraqui Houssaini I., Jacquet M., Jimenez A., Jonniaux J.-L., Karpfinger-Hartl L., Lanfranchi G., Lepingle A., Levesque H., Lyck R., Maffahi M., Mallet L., Maurer K.C. T., Mesenguy F., Mewes H.-W., Moestl D., Nasr F., Nicaud J.-M., A. Niedenthal R.K., Pandolfo D., Pierard A., Scherwhiza A., Urbanus J.H. M., Valle G., Van Dyck L., Verhasselt P., Nierendeels F., Vissers S., Voet M., Volckaert G., Wach A., Hambutt R., Mambutt R., Wedler H., Zollner A., Hani J.; Antendecide sequence of Saccharomyces cerevisiae chromosome XIV and its evolutionary implications.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Taycher E.
                     COQ2_YEAST STANDARD; PRT; 372 AA.
P3278; Q6B113;
01-0CT-1993 [Rel. 27, Created)
101-0CT-1993 [Rel. 27, Last sequence update)
25-0CT-2004 [Rel. 45, Last annotation update)
Para-hydroxybenzoate--polyprenyltransferase, mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Creation of the YFLEX clone resource: cloning of Saccharomyces cerevisiae ORFs in the Gareway recombinational cloning system."; Submitted (JUL-2004) to the BWBL/GenBank/DDBJ databases.
-i- FUNCTION: Catalyzes the prenylation of para-hydroxybenzoate with
                                                                                                                                                                                                                                                                                                                                                                                                       Ashby M.N., Kutsunai S.Y., Ackerman S., Tzagoloff A., Edwards P.A., "COQ2 is a candidate for the structural gene encoding para-hydroxybenzoate:polyprenyltransferase.";
J. Biol. Chem. 267:4128-4136(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marsischky G., Rolfs A., Richardson A., Kane M., Baqui M., Taycher J
Hu Y., Vannberg F., Weger J., Kramer J., Moreira D., Kelley F.,
Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an all-trans polyprenyl group.
-!- PATHWAY: Coenzyme Q biosynthesis; second step.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                          (EC 2.5.1.-) (PHB:polyprenyltransferase).
Name=COO2; OrderediocusNames=YNR041C; ORFNames=N3419;
Saccharomyces cerevisiae (Baker, 8 yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inner membrane.
-!- SIMILARITY: Belongs to the ubiA prenyltransferase family.
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=92156158; Pubmed=1740455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97313269; PubMed=9169873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 387:93-98(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4932;
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417 AA;
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Q6FR58;
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                                                                                                                                                                                                                                                                                                                                                    2 (Potential).
3 (Potential).
5 (Potential).
6 (Potential).
8 (Potential).
Allylic polyprenyl diphosphate-binding
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                              PROSITE; PS00943; UBIA; 1...
Isoprene biosynthesis; Mitochondrion; Transferase; Transit peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., FUNCTION, INDUCTION, AND TISSUE SPECIFICITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 1; Length 3/2.
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=14724626; DOI=10.1038/427212a;
Hallem E.A., Fox A.N., Zwiebel L.J., Carlson J.R.;
"Olfaction: mosquito receptor for human-sweat odorant.";
Nature 427:212-213(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anopheles genome sequencing consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 site (Potential).
A -> T (in Ref. 3).
4D9738CE248B4AD6 CRC64;
                                                                                                                                                                                                                                                                                     Mitochondrion (Potential)
                                                                                                                                                                                                                                                                                                      Para-hydroxybenzoate--
polyprenyltransferase.
                                                                               Germonline; 143386; -.
SGD; S000005324; COQ2.
GO; GO:0004659; F:prenyltransferase activity; IMP.
GO; GO:0006443; P:ubiquinone metabolism; IMP.
InterPro; IPR000537; UblA_prenyltrans.
InterPro; IPR006370; UblA_prenyltrans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OR1 ANOGA STANDARD; PRT; 417 AA. 08WTE7; 0701T3; 29-MAR-2004 (Rel. 43, Created) 9-MAR-2004 (Rel. 43, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                         (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                         Pfam; PF01040; UbiA; 1.
TIGRFAMS; TIGR01474; ubiA proteo; 1.
                               EMBL; AY693097; AAT93116.1; -. PIR; S20056; S20056.
Intact; P32378; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     273 273 1
372 AA; 41001 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.5%;
77.8%;
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EMBL; M81698; AAA34507.1; -. EMBL; Z71656; CAA96321.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 77.00,
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                                                                                                                                                                                                                                                                 Transmembrane.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                DATABASE: NAME=Protein Spotlight; NOTE=Issue 44 of February 2004; WWW="http://www.expasy.org/spotlight/articles/sptlt044.html".
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                                                                                                                                                                                           in disease vector mosquitoes after blood feeding.
SUBCELLULAR LOCATION: Integral membrane protein (Potential).
TISSUE SPECIFICITY: Female-specific antennae and maxillary palp
                                                                                                                                                                                                                                                                expression.
INDUCTION: Strong response to the odorant 4-methylphenol, a component of human sweat, when expressed in odorant receptor deficient Drosophila. In vivo, decreased expression in antennae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF02949; 7tm_6; 1.
G-protein coupled receptor; Multigene family; Olfaction; Receptor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                  after a blood meal.
SIMILARITY: Belongs to the G-protein coupled receptor Dr-or
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Pred. No. 1.3e+02;
1; Mismatches 1; Indels
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2 (Potential).
Extracellular (Potential)
3 (Potential).
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4 (Potential).
Extracellular (Potential)
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Extracellular (Potential)
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Cytoplasmic (Potential)
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EMBL; AAAB01008980; EAA13838.1; -.
GO; GO:0016021; C:Integral to membrane; NAS.
GO; GO:0015549; F:odorant binding; IDA.
GO; GO:0042048; F:olfactory receptor activity; IDA.
GO; GO:0042048; P:olfactory behavior; IDA.
InterPro; IPR004117; 7tm6 olfacrecept.
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IDENTIFICATION, AND TISSUE SPECIFICITY
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Best Local Similarity 77.8-
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NCBI_TaxID=562;
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Marsischky G., Rolfs A., Richardson A., Kane M., Baqui M., Taycher B.,
                                                                                                                                                                                                                                                                                                                                                                                                                     Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemire M., Lesur I., Ma L., Muller H., Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Zeniou-Meyer M., Zivanovic I., Bolocin-Fukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
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                                                                                                                                                                                              Eukaryotā; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TaxID=284593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Hypothetical 62.8 kDa protein in RPS16A-TIF34 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
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                       05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Similar to sp|P40215 Saccharomyces cerevisiae YMR145c NDH1.
ORFNames-CAGL0100748g;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00070; Pyr_redox; 1.-
SEQUENCE 530 AA; 59725 MW; 9BF95A03A0347248 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.5%; Score 33; DB 2; I
77.8%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OrderedLocusNames=YMR145C; ORFNames=YM9375.14C; Saccharomyces cerevisiae (Baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         560 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
   05-JUL-2004 (TrEMBLrel. 27, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wincker P., Souciet J.L.; "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 77.8
les 7; Conservative
                                                                                                                                                                   Candida glabrata CBS138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 387:90-93(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     316 RLKTMVKKV 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 430:35-44(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RLSSMVKKV 9
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                               STRAIN=CBS138;
                                                                                                                                                                                                                                                                                                                                                                                                 Genolevures;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YM23 YEAST
P40215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
YM23 YEAST
TO YM23 YEAST
TO P40215/I
DT 01-FEB
DT 01-FEB
DT 25-OFE
CO SECHAIO
OC SACCHAIO
OC
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Hu Y., Vannberg F., Weger J., Kramer J., Moreira D., Kelley F.,
Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                  Labaer J.;
"Creation of the YFLEX clone resource: cloning of Saccharomyces cerevisiae ORFs in the Gateway recombinational cloning system."; Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00070; Pyr_redox; 1. Trans: NAD; Oxidoreductase; FAD; Flavoprotein; Hypothetical protein; NAD; Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.0%; Score 32; DB 2; Length 107; 77.8%; Pred. No. 60; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 560;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Anbutsu H., Tsuda M.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AB182370; BAD24124.1; -.
Hypochatical protein; Plasmid.
SEQUENCE 107 AA; 12021 MW; 1B128007B7367B5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              560 AA; 62774 MW; 10B1795E12E29C34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGD; S000004753; NDE1.
GO; GO:0005739; C:mitochondrion; IDA.
GO; GO:0003954; F:NADH dehydrogenase activity; IDA.
GO; GO:0019655; P:ethanol fermentation; IMP.
GO; GO:0006116; P:NADH oxidation; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.5%; Score 33; DB 1; I
77.8%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001327; FAD pyr_redox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterobacteriaceae; Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z47071; CAA87359.1; -.
EMBL; AY692785; AAT92804.1; -.
PIR; S50401; S50401.
GermOnline; 142815; -.
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27,
27,
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Best Local Similarity 77.8-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 80.0
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q616B7;
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 RLKTMVKKV 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
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Gaps

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Length 288; 0; Indels

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TIGRFAMs; TIGR01099; galU; 1.
Complete proteome; Nucleotidyltransferase; Transferase.
SEQUENCE 288 AA; 31782 MW; FID28AC4A04EE3CB CRC64;
                                                                                                                                       80.0%; Score 32; DB 2; I
87.5%; Pred. No. 1.5e+02;
ive 1; Mismatches 0;
InterPro; IPR005835; NTP transferase.
Pfam; PF00483; NTP transferase; 1.
TIGRFAMs; TIGR01099; galU; 1.
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                   184 RLSSMVEK 191
                                                                                                                 Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                        1 RLSSMVKK 8
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=536;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Q7NVJ5;
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                                                                                                                                                                                                                                                                                                                                                     RESULT 15
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BR GO; GO:0005506; F:iron ion binding; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

R GO; GO:0016491; F:oxidoreductase activity; IEA.

R GO; GO:0016491; F:oxidoreductase activity; IEA.

R GO; GO:0016491; Redical activat.

R InterPro; IPR001345; CytC_heme_BS.

R InterPro; IPR001999; Radical_SAM.

R Ffan; PP04055; Radical_SAM.

R Ffan; PP04055; Radical_SAM.

R PROSITE; PS01090; CYTCCHROWE C; UNKNOWN 1.

R PROSITE; PS01087; RADICAL_ACTIVATING; 1.

R Complete protecome; Oxidoreductase.

SEQUENCE 169 AA; 19292 MW; CC7AB2511D3844C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium from permanently cold Arctic sediments."; from permanently cold Arctic sediments."; Environ. Microbiol. 6:887-902(2004).

EMBL; CR522871; CA637932.1; CR522871; CA637932.1; CR522871; CR522871; CA637932.1; CR522871; CA6379381; F:UTP-glucose.activity; IEA. GO; GO:0003983; F:UTP-glucose.l-phosphate uridylyltransferase. . .; IEA. GO; GO:0009058; P:biosynthesis; IEA. GO; GO:0006011; P:UDP-glucose metabolism; IEA.
                                                                                                EC
EC
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                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Anaerobic ribonucleoside-triphosphate reductase activating protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Desulfotalea psychrophila.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
Desulfobulbaceae; Desulfotalea.
NCBI_TaxID=84980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M., Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K. Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R. Klenk H.-P.;
                                                                                                                                                                    Clostridium tetani.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                         "The genome sequence of Clostridium tetani, the causative agent tetanus disease.";
                                                                                                                                                                                                                                                                                                       STRAIN=Massachusetts / E88;
MEDLINE=22457253; PubMed=12552129; DOI=10.1073/pnas.0335853100;
Brueggemann H., Baeumer S., Fricke W.F., Wiezer A., Liesegang H
Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
Gottschalk G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Probable UTP-glucose-1-phosphate uridylyltransferase.
OrderedLocusNames=DPPB68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288 AA
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                                                                                                                                            OrderedLocusNames=CTC00258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=LSv54 / DSM 12343;
PubMed=15305914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 75.0
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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85 RLASMIKK 92
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                                                                                                                                                                                                                                        NCBI_TaxID=1513;
                                                                                                                                                                                                                     Clostridium.
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Matches
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SEQUENCE FROM N.A.

STRAIN-ATCC 12472 / DSM 30191;

RX MEDLINE-22882809 bubmed=14500782; DOI=10.1073/pnas.1832124100;

RX VASCONCEGIOS A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,

RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,

RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,

RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,

RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,

RA Antonio R.V., Almeida E.M., Arataipe J., de Almeida R.A.

RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,

RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,

RA Carvalho C.M.B., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,

Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,

RA Carcaynski-Peas T.B., Cunha-Unnior N.C., Fegundee N., Falcao C.L.,

RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R., Ralcao C.L.,

RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,

RA Ferro M.I.T., Franco G.R., Maranhao A.O., Martins W.S.,

RA Gazinelli R.T., Mandio G.R., Maranhao A.O., Martins W.S.,

RA Madeira H.M.F., Mandio G.R., Maranhao A.O., Martins W.S.,

RA Madeira H.M.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,

RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seura E.M.,

Santos E.B.P., Santos F.R., Schneider M.P., Simen D., Soares C.M.A., Soares R.B.A., Souza E.M., Simen D., Soares C.M.A., Soares R.B.A., Souza E.M., Simen D., Soares C.M.A., Soares R.B.A., Souza E.M., Simen Proc. Natl Acad Scilus A.M. S. Shappon A.J.G.,

RA Vettore A., Wassem R., Zaha A., Simpson A.J.G.,

RA Vettore A., Wassem R., Zaha A., Simpson A.J.G.,

RA Vettore A., Wassem R., Zaha A., Simpson A.J.G.,

RA Perce. Valle Salve P. L. Schools P. C. Silve B. C.,

RA Perce. Valle Salve P. C. Silve B. C.,

RA Perce. Valle Salve P. C. Silve B. C.,

RA Perce. Valle Salve S. C., Silve R., Simbson A.J.G.,

RA Vettore A., Wassem R., Zaha A., Simpson A.J.G.,

RA Perce. Valle Salve P. C., Silve B. C.,

RA Perce. Valle Salve P. C. Silve 
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                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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Pred. No. 1.7e+02;
1; Mismatches 0; Indels
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Complete proteome; Lipoprotein.
SEQUENCE 330 AA; 35382 MW; 2AFAB050961AF87F CRC64;
                                                                                                                                              01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                  330 AA
                                                                                                     01-MAR-2004 (TrEMBLrel. 26, Created)
PRT;
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                                                                                                                                                                                                                                      Probable membrane lipoprotein.
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87.5%;
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                                                                                                                                                                                                                                                                                        OrderedLocusNames=CV2347;
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                  PRELIMINARY;
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247 LTSMVKKV 254

Search completed: July 13, 2005, 17:29:18 Job time : 65.2222 secs

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TYPE: PRT
ORGANISM: Homo sapiens
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US-09-502-600-32
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Sequence 4, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 110, App
Sequence 110, App
Sequence 110, App
Sequence 110, App
Sequence 79, Appli
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Sequence 7, Appli
Sequence 8, Appli
Sequence 13, Appl
Sequence 12, Appli
Sequence 4, Appli
Sequence 12, Appli
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                                                                                                                                                  (without alignments)
34.552 Million cell updates/sec
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Sequence 7
Sequence 1
                                                                                                                            July 13, 2005, 16:58:04; Search time 19.4444 Seconds
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-618-243-32

US-09-618-259-4

US-09-261-416-7

US-08-94-403-33

US-08-94-403-33

US-08-57-146-12

US-09-154-34-12

US-09-154-34-12

US-09-154-34-12

US-09-154-34-3

US-09-154-34-3

US-09-154-34-3

US-09-10-044-3

US-09-10-043-3

US-09-10-043-3

US-09-10-043-3

US-09-10-0716

US-09-918-243-110

US-09-918-243-110

US-09-918-243-176

US-09-918-243-87
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                                                                                                                                                                                                                                                                                                                                                           513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                    - protein search, using sw model
                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                         US-09-905-083A-32
                                                                                                                                                                                                                                                     1 RLSSMVKKV 9
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Match Length
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                                                                                  OM protein
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2462, Ap
4562, Ap
5171685
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APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: Ovarian Cancer
FILE REFERENCE: D6223CIP-C
CURRENT FILING DATE: 2000-02-11
CURRENT APPLICATION NUMBER: U5/09/502,600A
PRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 136
LENGTH: 9
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 31.32

Sequence 32. Application US/09918243

Patent No. 6627403

GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Mattin J.
APPLICANT: Santin, Alessandro
TITLE OF INVENTION:
FILE REFERENCE: D6223CIP/C/D/CIP
CURRENT APPLICATION NUMBER: US/09/918,243

CURRENT APPLICATION NUMBER: US
FRICR FILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 32

LENGTH: 9

TYPE: RRT

CORGANISM: Homo sapiens
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                                                  Sequence
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Patent No.
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100.0%; Score 40; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.18+05;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
, OTHER INFORMATION: Residues 123-131 of the SCCE protein
US-09-502-600-32
           US-08-261-086-4

US-08-261-086-6

US-09-248-7966-1383

US-09-328-352-7990

US-09-328-352-7990

US-09-248-7966-18044

US-09-107-433-4867

US-09-107-5328-4737

US-09-107-5328-6154

US-09-107-5328-6154

US-09-1107-5328-6154

US-09-1107-5328-6154

US-09-1107-5465

US-09-1134-000C-5465

US-09-1134-000C-5465

US-09-1134-001C-5465

US-09-1134-001C-5465

US-09-1134-001C-5465

US-09-1134-001C-5465
                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                    ; Sequence 32, Application US/09502600A
; Patent No. 6294344
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COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GRANADOS, EDWARD N.
KLASEL, JOHNEL R.
STEWART, KENT D.
STEWART, KENT D.
STROUPE, STRVEN D.
NUVENTION: AND WETHOOL USEFUL FOR DETECTING AND TREATING DISEASES
NVENTION: OF THE PROSTATE
                                                                                                                                                                                Sequence 8, Application US/09261416A
Patent No. 6291663
Patent No. 629163
Patent No. 6291632
Patent No. 62916331 Transmembrane Serine Protease
TITLE OF INVENTION: TAGG-12: A No. 629166331 Transmembrane Serine Protease
TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
PILE REPERENCE: D6192
CURRENT APPLICATION NUMBER: US/09/261,416A
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 8
LENGTH: 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: Serine protease catalytic domain of hepsin (Heps)
OTHER INFORMATION: homologous to similar domain in TADG-12
US-09-261-416-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 40; DB 3; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/944,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: 10. Abbott Laboratories STREET: 100 Abbott Park Road CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 33, Application US/08944483
; Patent No. 6232456
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                       69 RLSSMVKKV 77
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                          1 RLSSMVKKV 9
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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APPLICANT:
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US-09-261-416-8
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APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, J.
APPLICANT: 1999-03-03
AUMBER OF SEQ ID NOS: 14
APPLICANT: 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Serine protease catalytic domain of stratum corneum OTHER INFORMATION: chymotryptic enzyme (Scce) homologous to similar OTHER INFORMATION: domain in TADG-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: DOMAIN
OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
OTHER INFORMATION: enzyme (scce) catalytic domain
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                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Dimothy J.
APPLICANT: O'Brien, Lowell J.
TITLE OF INVENTION: No. 6642013e1 Extracellular Serine Protease
TITLE OF INVENTION: No. 6642013e1 Extracellular Serine Protease
CURRENT APPLICATION UNMER: US/99/618,259
CURRENT FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: US 09/127,444
PRIOR FILING DATE: 1998-08-21
NUMBER OF SEQ ID NOS: 72
SEQ ID NOS: 72
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                                                                                                               100.0%; Score 40; DB 4; Length 9; 100.0%; Pred. No. 4.1e+05; Attive 0; Mismatches 0; Indels
                   ) NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 123-131 of the SCCE protein
US-09-918-243-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
US-09-261-416-7
; Sequence 7, Application US/09261416A
; Patent No. 6291663
                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09618259; Patent No. 6642013; GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 9; Conservative
                                                                                                             Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 RLSSMVKKV 68
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                                                                                                                                                                                                                                                         1 RLSSMVKKV 9
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ORGANISM: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-618-259-4
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FEATURE:
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Gaps

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GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in TITLE OF INVENTION: TADG-15: An Ovarian Carcinomas
FILE REFERENCE: D6064
CURRENT APPLICATION NUMBER: US/09/027,337B
CURRENT FILING DATE: 1998-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Serine protease catalytic domain of Scce homologous to OTHER INFORMATION: similar domain in TADG-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels . 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: C.C...

TIP: 10036-2787

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DE PC COMPASSION | PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,344

TITING DATE: 16-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 40; DB 2; Length 225; 100.0%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: White & Case, Patent Department STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 16. SEP-198
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
NAME: Sterner, Richard J.
REGISTATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 35,372
RELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/09154344; Patent No. 5981256; GENERAL INFORMATION: APPLICANT: Hansson, Lennart
                                                                                                                                                                                Sequence 4, Application US/09027337B Patent No. 5972616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (212) 819-8783
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 9; Conservative
     95 RLSSMVKKV 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Unknown
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-154-344-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 4
LENGTH: 225
                                                                                                                                                     US-09-027-337-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/08557146

| Sequence 12, Application US/08557146
| Patent No. 5834290
| GENERAL INFORMATION:
| APPLICANT: Egeltud, Torbjorn
| APPLICANT: Hansson, Lennart
| TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
| TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
| TITLE OF INVENTION: Brayme (SCCE)
| NUMBER OF SEQUENCES: 17
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: White & Case, Patent Department
| STREET: 1155 Avenue of the Americas
| CITY: New York
| COUNTRY: U.S.A. |
| STATE: New York
| COUNTRY: U.S.A. |
| COMPUTER READABLE FORM: WEDIUM TYPE: Floppy disk
| COMPUTER: IBM PC compatible |
| OPERATING SYSTEM: PC-DOS/MS-DOS |
| COMPUTER: BATE: 14-DEC-1995 |
| CLASSIFICATION NUMBER: US/08/557,146 |
| PILING DATE: 14-DEC-1995 |
| ATTORNEY/AGENT INFORMATION: NAME: Sterner, Richard J. |
| REGISTRATION NUMBER: 1103326-181 |
| TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
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100.0%; Pred. No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

100.0%; Score 40;
Best Local Similarity 100.0%; Pred. No.
Matches 9; Conservative 0; Mismatch
                                                                                               6183.US.01
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGIGSTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: No. 6232456e
US-08-944-483-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
US-08-557-146-12
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LENGTH: 225 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 10v..
                                                                                                                                                                                TELEFAX: 847/938-2623
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1 RLSSMVKKV 9

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1: 253 amino acids
amino acid
                                                                  Query Match
Best Local Similarity 100.
Matches 9; Conservative
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  ; OTHER INFORMATION: SCCE US-09-654-600A-4
                                                                                                                                                                                                   95 RLSSMVKKV 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 RLSSMVKKV 131
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09644600

Patent No. 6451500

GENERAL INFORMATION:
APPLICANT: O'Brien Timothy J.
APPLICANT: Tanimoto, Hirotoshi
ITILE OF INVENTION: TADG-15: An Extracellular Serine Protease
ITILE OF INVENTION: TADG-15: An Extracellular Serine Protease
ITILE OF INVENTION: Overexpressed in Carcinomas
FILE REFERENCE: D606411P/D
CURRENT APPLICATION NUMBER: US/09/644,600

CURRENT APPLICATION NUMBER: 09/421,213
FRIOR APPLICATION NUMBER: 09/421,213
FRIOR APPLICATION NUMBER: 09/027,337
FRIOR FILING DATE: 1998-10-20
FRIOR APPLICATION NUMBER: 09/027,337
FRIOR FILING DATE: 1998-02-20
FRIOR APPLICATION NUMBER: 09/027,337
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                                                                                                                                                                            / Match 100.0%; Score 40; DB 2; Length 225; Local Similarity 100.0%; Pred. No. 1.5; Onservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 40; DB 4; Length 225; 100.0%; Pred. No. 1.5; tive 0; Mismatches 0; Indels
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US-09-654-600A-4
Sequence 4, Application US/09654600A
Patent No. 6649741
    LENGTH: 225 amino acids

TYPE: amino acids

TYPE: amino acids

TYPE: amino acids

TOPOLOGY: linear

MOLECULE TYPE: polypeptide
US-09-154-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 9; Conservative
SEQUENCE CHARACTERISTICS LENGTH: 225 amino acid
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COTHER INFORMATION: SCCE
US-09-644-600-4
                                                                                                                                                                                                                                                                                                               95 RLSSMVKKV 103
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                   1 RLSSMVKKV 9
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LENGTH: 225
                                                                                                                                                                                                                                                                                                                                                                                                    US-09-644-600-4
                                                                                                                                                                                 Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                     Recombinant Stratum Corneum Chymotryptic Enzyme (SCCE)
100.0%; Score 40; DB 4; Length 225; 100.0%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 253;
                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Recombinant Stratum Corneum TITLE OF INVENTION: Brighme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department STREET: 1155 Avenue of the Americas CITY: New York STATE: New York STATE: New York STATE: New York STATE: 10036-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 40; DB 2; Best Local Similarity 100.0%; Pred. No. 1.7; Matches 9; Conservative 0; Mismatches 0;
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US-08-824-874-3
Sequence 3, Application US/08824874
Patent No. 5962300
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
MUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION UNBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILLING DATE: 14-DEC-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                     US-08-557-146-2; Sequence 2, Application US/08557146; Patent No. 5834290; GENERAL INFORMATION:
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Gaps

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Sequence 2. Sequence 2. Sequence 2. Sequence 2. Sequence 2. Sequence 2. Sequence 2. Sequence 2. Sequence 2. Sequence 2. Sequence 3. Correspondence 3. Sequence 3. Correspondence 4. Sequence 3. Sequence 4. Sequence 4. Sequence 4. Sequence 5. Sequence 5. Sequence 5. Sequence 6. Sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 40; DB 2; Length 253; 100.0%; Pred. No. 1.7;
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Floppy disk
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,188
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTOMENYAGENT INFORMATION:
ANAMERICATION DATA:
ANAMERICATION DATA:
ATTOMENYAGENT INFORMATION:
ANAMERICATION DATA:
ANAMERICATION DA
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Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                        NAME: Sterner, Richard J.

REGISTRATION NUMBER: 35,372
REGISTRATION NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
FELEPHONE: (212) 819-8783
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
NOLECULE TYPE: protein
US-09-154-344-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RY: United States of America
46285
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REGISTRATION NUMBER: 38,082
REFRENCE/DOCKET NUMBER: X923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
TELEFAX: 317-276-3861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity luv...
9, Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 RLSSMVKKV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
         CLASSIFICATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,344
FILING DATA:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                         OCHEVIER: 15M COMPACTION OF CONTROLLER: 15M COMPACTOR OF CONTROLLER: 15M CONTR
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Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches
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APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
: 3174 Porter Drive
Palo Alto
                                                                                                                                                                                                                                                                                                                                     IBM Compatible
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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MEDIUM TYPE: Diskett
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LIBRARY: General S32504
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IMMEDIATE SOURCE:
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Sequence 98, Appli Sequence 3, Appli Sequence 49, Appli Sequence 49, Appl Sequence 49, Appl Sequence 49, Appl Sequence 63, Appl Sequence 95, Appl Sequence 11, Appli Sequence 110, Appl Sequence 244024, Sequence 4, Appli Sequence 45273, Sequence 49273, A Sequence 61611, A Sequence 6377, A Sequence 59862, A Sequence 59862, A Sequence 53750, A Sequence 53750, A

4 US-10-071-214-2 4 US-10-071-214-48 4 US-10-66-283-90 5 US-10-295-027-498 6 US-10-999-48 6 US-10-10-998-18-95 7 US-10-948-18-95 7 US-10-948-18-95 8 US-10-948-110 10S-09-918-243-110 10S-09-918-243-110 10S-09-918-243-110 10S-09-918-2440-24 10S-10-425-110-240-24 10S-10-425-114-61611 5 US-10-425-114-61611 5 US-10-425-114-61611 5 US-10-425-114-61611 5 US-10-425-114-61611 5 US-10-425-114-9367 6 US-10-425-114-59862 10S-10-425-114-59862 10S-10-425-114-59862 10S-10-425-114-59862 10S-10-425-114-59862 10S-10-425-114-59862 10S-10-425-114-59862 10S-10-425-114-59862 10S-10-425-114-59862

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TYPE: PRT
ORGANISM: Homo sapiens
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 137, App Sequence 4, Appli Sequence 4, Appli Sequence 104, Appl Sequence 104, Appl Sequence 104, Appl Sequence 104, Appl Sequence 102, Appl Sequence 102, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                             July 13, 2005, 17:29:45; Search time 64.8889 Seconds (without alignments) 53.584 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

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15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-905-083-32
US-10-312-521-32
US-10-831-075-32
US-10-831-075-137
US-09-766-294-4
US-10-461-787-4
US-09-789-210-33
US-10-600-181-104
US-10-600-181-102
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Listing first 45 summaries
                                                                                           OM protein - protein search, using sw model
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Sequence 79, Appl Sequence 87, Appl Sequence 79, Appl Sequence 87, Appl

Sequence 79,

US-10-372-521-79 US-09-905-083-79 US-09-905-083-87 US-09-918-243-79

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                                                                                   Sequence 32, Application US/09918243

Sequence 32, Application US/09918243

Patent No. US20020142317A1

GENERAL INFORMATION:

APPLICANT:

APPLICANT:

APPLICANT:

Cannon, Martin J.

APPLICANT:

APPLICANT:

APPLICANT:

APPLICANT:

CURRENT APPLICATION WUMBER: US/09/918,243

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 32

SEQ ID NO 32
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; OTHER INFORMATION: Residues 123-131 of the SCCE protein
US-09-918-243-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 40; DB 9; I. larity 100.0%; Pred. No. 1.6e+06; Conservative 0; Mismatches 0;
ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RLSSMVKKV
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RESULT 2

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FILE REFERENCE: D6223CIP/C/D/CIP3
                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 RLSSMVKKV 22
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NAME/KEY: CHAIN
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US-10-831-075-137
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          Sequence 32, Application US/09905083

Patent No. US20020146708A1

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: O'Arian Cancer;

FILE REFERENCE: D6223CIP/C/Div.

CURRENT APPLICATION NUMBER: US/09/905,083

CURRENT FILING DATE: 2001-07-13

PRIOR PLING DATE: 2000-02-11

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 32, Application US/10372521
; Sequence 32, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
; APPLICANT: Cannon, Martin J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT FILING DATE: 2003-02-1
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR PLILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 32
LENGTH: 9
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Publication No. US20040224891A1
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Martin, J.
APPLICANT: Santin, Alessandro
ITILE OF INVENTION: Methods for the early diagnosis of ovarian cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 40; DB 9; Length 9; 100.0%; Pred. No. 1.6e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Residues 123-131 of the SCCE protein US-10-372-521-32
                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Residues 123-131 of the SCCE protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CHAIN
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US-10-372-521-32
                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-905-083-32
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US-09-905-083-32
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Publication No. US20040224891A1

GENERAL INFORMATION:

APPLICANT: Cannon, Martin J.

APPLICANT: Santin, Alessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

FILE REFERENCE: D6223CIP/C/D/CIP3

CURRENT FILING DATE: 2004-04-23

FRIOR APPLICATION NUMBER: US/10/831,075

CURRENT FILING DATE: 2003-02-21

FRIOR FILING DATE: 2003-02-21

NUMBER OF SEQ ID NOS: 140

SEQ ID NO 137

LENGTH: 30

LENGTH: 30
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                                                                                                                                                                                                                                                                                                                                           Length 9;
                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Residues 123-131 of the SCCE protein US-10-831-075-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CHAIN
CHER INFORMATION: Residues 110-139 of the SCCE protein US-10-831-075-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09796294
Patent No. US2002037581A1
GENERAL INPORMATION:
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: Extracellular Serine Protease;
FILE REFERENCE: D6020CIP3
CURRENT APPLICATION NUMBER: US/09/796,294
CURRENT FILING DATE: 2001-02-28
PRIOR FILING DATE: 2000-07-18
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 4
LENGTH: 144
                                                                                                                                                                                                                                                                                                                                           100.0%; Score 40; DB 16; 100.0%; Pred. No. 1.6e+06;
                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
CURRENT APPLICATION NUMBER: US/10/831,075
CURRENT FILING DATE: 2004-04-23
PRIOR PILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 140
SEQ ID NO 32
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
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Gaps
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                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/944,483
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
STRANDEDMESS: single
TOPOLOGY: linear
MOLECULE TYPE: None
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-789-210-33
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TELEFAX: 847/938-2623
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Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Shenoy, Suresh G.
Shimkets, Richard A.
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Ji, Weizhen
Miller, Charles E.
Rastelli, Luca
Stone, David J.
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Malyankar, Uriel M.
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Anderson, David W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: <Unknown>
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STATE: IL
COUNTRY: USA
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APPLICANT:
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APPLICANT:
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APPLICANT
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RUSSELL, JOHN C.
STEWART, KENT D.
STROUPE, STENDE DE PROTEASE REACENTS
TITLE OF INVENTION: NOVEL SERINE PROTEASE REACENTS
OF THE PROSTATE
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Sequence 4, Application US/10461787

Publication No. US20030199010A1

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: No. US20030199010A1e1 Extracellular Serine Protease;
FILE REPERENCE: D602CIP2.

CURRENT APPLICATION NUMBER: US/10/461,787

CURRENT APPLICATION NUMBER: US/09/618,259

PRIOR APPLICATION NUMBER: US 09/127,444

PRIOR PILING DATE: 2000-0-18

PRIOR PILING DATE: 1998-08-21

NUMBER OF SEQ ID NOS: 72

SEQ ID NOS: 72
                                                    NAME/KEY: DOMAIN
OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
OTHER INFORMATION: enzyme (scce) catalytic domain
US-09-796-294-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic OTHER INFORMATION: enzyme (scce) catalytic domain
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                                                                                                                                                      Query Match 100.0%; Score 40; DB 9; Length 144; Best Local Similarity 100.0%; Pred. No. 1.9;
                                                                                                                                                                                              0; Indels
                                                                                                                                                                                            0; Mismatches
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CORRESSONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 110 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COLPITTS, TRACEY L. FRIEDMAN, PAULA N. GRANADOS, EDWARD N.
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; Sequence 33, Application US/09789210
; Publication No. US20040241646A1
; GENERAL INFORMATION:
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                                                                                                                                                                                            9; Conservative
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                                                                                                                                                                                                                                   1 RLSSMVKKV 9
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ORGANISM: unknown
              ORGANISM: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: DOMAIN
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PRIOR APPLICATION NUMBER: 60/326, 483
PRIOR FILING DATE: 2001-10-02
PRIOR FILING DATE: 2001-10-02
PRIOR FILING DATE: 2002-04-19
PRIOR PILING DATE: 2002-04-19
PRIOR PELING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327, 917
PRIOR APPLICATION NUMBER: 60/328, 029
PRIOR PILING DATE: 2002-10-19
PRIOR APPLICATION NUMBER: 60/328, 029
PRIOR APPLICATION NUMBER: 60/328, 029
PRIOR APPLICATION NUMBER: 60/328, 026
PRIOR APPLICATION NUMBER: 60/381, 038
PRIOR PILING DATE: 2002-05-16
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2002-04-17
PRIOR PILING DATE: 2002-04-17
PRIOR PILING DATE: 2002-04-19
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APPLICANT: Miler, Charles E.
APPLICANT: Rastelli, Luca
APPLICANT: Stone, David J.
APPLICANT: Stone, David J.
APPLICANT: Stone, David J.
APPLICANT: Stoney, Suresh G.
APPLICANT: Shinkets, Richard A.
APPLICANT: Leach, Mark E.
APPLICANT: Leach, Mark E.
APPLICANT: Berghs, Constance
TILE OF INVENTION: OVVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
                                                          Gaps
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                                                          0; Indels
                      100.0%; Pred. No. 3.1;
                                                          0; Mismatches
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; Publication No. US20040038223A1
; GENERAL INFORMATION:
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Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
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Malyankar, Uriel M.
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Anderson, David W.
Zhong, Mei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
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                  Best Local Similarity 100.
Matches 9; Conservative
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Li, Li
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ORGANISM: Homo sapiens
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APPLICANT: Leach, Martin D.
APPLICANT: Age, Michele L.
APPLICANT: Age, Michele L.
APPLICANT: Bege, Michele L.
APPLICANT: BAD2-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT PILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR APPLICATION NUMBER: 60/381,039
PRIOR FILING DATE: 2002-10-09
PRIOR PILING DATE: 2002-10-09
PRIOR PILING DATE: 2002-06-16
PRIOR PILING DATE: 2002-04-17
PRIOR PILING DATE: 2001-10-06
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APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
TITLE OF INVENTION: Overexpressed in Carcinomas
FILE REFRENCE: D6064CIP/D
CURRENT PELINGS DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US/09/654,600A
PRIOR APPLICATION NUMBER: 09/021
PRIOR APPLICATION NUMBER: 09/021
PRIOR APPLICATION NUMBER: 09/021
PRIOR PILING DATE: 1909-10-20
PRIOR FILING DATE: 1999-10-20
NUMBER: OF SEQ ID NOS: 98
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Matches 9; Conservative
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COTHER INFORMATION: SCCE
US-10-600-187-4
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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LENGTH: 225
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SEQ ID NO 104
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Shimkets, Richard A.
APPLICANT: Rothenberg, Mark B.
APPLICANT: Leach, Martin D.
APPLICANT: Age, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
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                                                                                                                                     100.0%; Score 40; DB 15; Length 250; 100.0%; Pred. No. 3.5;
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CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR PLING DATE: 2001-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R FILING DATE: 2002-04-19
R APPLICATION NUMBER: 60/327,917
R FILING DATE: 2001-10-09
APPLICATION NUMBER: 60/381,642
R FILING DATE: 2002-05-17
R APPLICATION NUMBER: 60/328,029
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APPLICATION NUMBER: 60/381,038
FILING DATE: 2002-05-16
APPLICATION NUMBER: 60/328,056
FILING DATE: 2001-10-09
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FILING DATE: 2002-04-19
APPLICATION NUMBER: 60/327,435
FILING DATE: 2001-10-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 94, Application US/10262511 Publication No. US20040038223A1 GENERAL INFORMATION:
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Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
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Miller, Charles E.
Rastelli, Iuca
Stone, David J.
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Malyankar, Uriel M.
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APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
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Zerhusen, Bryan D.
Anderson, David W.
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Catterton, Elina
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Pena, Carol B. A.
Shenoy, Suresh G.
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                            TYPE: PRT

CRGANISM: Homo sapiens
US-10-262-511-92
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Best Local Similarity
Matches 9; Conserv
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LENGTH: 250
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PRIOR PILING DATE: 2002-04-19

PRIOR APPLICATION NUMBER: 60/327,917

PRIOR APPLICATION NUMBER: 60/381,642

PRIOR PELING DATE: 2002-05-17

PRIOR PELING DATE: 2002-10-19

PRIOR PELING DATE: 2002-10-19

PRIOR PELING DATE: 2002-10-19

PRIOR PELING DATE: 2001-10-09

PRIOR APPLICATION NUMBER: 60/328,056

PRIOR APPLICATION NUMBER: 60/328,056

PRIOR PELING DATE: 2002-04-17

PRIOR PELING DATE: 2002-04-19

PRIOR PELING DATE: 2002-04-19

PRIOR PELING DATE: 2002-04-19

PRIOR APPLICATION NUMBER: 60/373,260

PRIOR PELING DATE: 2002-04-19

PRIOR PELING DATE: 2002-04-19

PRIOR APPLICATION NUMBER: 60/373,436

PRIOR PELING DATE: 2001-06-19

PRIOR APPLICATION NUMBER: 60/377,435

PRIOR APPLICATION NUMBER: 60/327,435

PRIOR APPLICATION NUMBER: 60/327,435

PRIOR APPLICATION NUMBER: 60/327,435

PRIOR PELING DATE: 2001-10-09

PRIOR PELING DATE: 2001-10-09

PRIOR APPLICATION NUMBER: 60/327,435

PRIOR PELING DATE: 2001-10-09

PRIOR PELING DAT
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
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                                                               DB 15; Length 247;
                                                                                                                           0; Indels
                                                            100.0%; Score 40; DB
100.0%; Pred. No. 3.4
tive 0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
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PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
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Publication No. US20040038223A1
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Spytek, Kimberly A.
Edinger, Shlomit R.
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Ort, Tatiana
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Anderson, David W.
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APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
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Shenoy, Suresh G.
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Catterton, Elina
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Agee, Michele L.
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Miller, Charles
Rastelli, Luca
                                                         Query Match
Best Local Similarity 100.
Matches 9; Conservative
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US-10-262-511-102
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100.0%; Pred. No. 3.5;
vative 0; Mismatches 0; Indels
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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APPLICANT: Hillman, Jennifer L.
ITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                               Sequence 98, Application US/09888615
Patent No. US20020064856A1
GENERAL INPORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: WHYTE, DAVID
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SEQ ID NO 98
LENGTH: 253
                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 3, Application US/09764762
; Patent No. US20020068341A1
; GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 94
LENGTH: 252
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ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                Ouery Match
Best Local Similarity 100.0
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                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-10-262-511-94
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TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 9; Conserv
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US-09-764-762-3
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                                                                            APPLICATION NUMBER: 09/210,084
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION:
APPLICATION NUMBER: US/09/764,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE: 532504
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: July 13, 2005, 18:23:33 Job time : 69.8889 secs
                       FILING DATE: 16-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                         TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                              PRIOR APPLICATION DATA:
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LIBRARY: GenBank
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ALIGNMENTS

Human pep Human pol Rat OST10

ADF59165 ABB78636 ADL91113 ADL91117 ADL91127 AAR75642 ADL91107 ADL91076 ADL91059

Adr68796
Adr68797
Adr68797
Adb6378
Adb63578
Adb63582
Abb63582
Abb63582
Abb63582
Abb63582
Abg76617
Adg761113
Adg791117
Adg91117
Adg911076
Adg911076

Human gas Human gas Human gas Peptide # Peptide # Human bra

AAB63582 ABB43858 AAM37771

AAM64837 ABG46617

AAB63580

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The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide
                                                                                                                                                                                                                                                                                            Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia.
                                                                                                                                                                                                                                                                               Human stratum corneum chymotrypsin enzyme peptide #3 (residues 5-13).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diagnosing cancer comprises detecting stratum corneum chymotrypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 40;
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                                                                                                                                                                                                                             AAE08238 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                07-FEB-2001; 2001WO-US003977
                                                                                                                                                                                                                                                                                                                                                                                                11-FEB-2000; 2000US-00502600
                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 (UYAR-) UNIV ARKANSAS
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WO200159158-A1.
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AAE08238;
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AAE08238
Human NOV
Human NOV
Human NOV
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                                                       July 13, 2005, 16:12:23 ; Search time 76.6667 Seconds (without alignments) 45.402 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                  Human
Novel
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Abg23378
Add62900
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        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                  2105692 seqs, 386760381 residues
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Maximum Match 100%
Listing first 45 summaries
                                         - protein search, using sw model
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ADA05736
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ABB84406
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ABU07471
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Gapop 10.0 , Gapext 0.5
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DB 4; Length 9;

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us-09-905-083a-33.rag

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Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                                                                                             Novel human diagnostic protein #23369.
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                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.
                                                                                  (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                                                                              WO200175067-A2.
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                                                                                    18-FEB-2002
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                                          ABG23378;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel method for vaccinating an individual against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating an individual with a SCCE peptide, which elicits an immune response in the individual with a SCCE peptide, which elicits an immune response in the individual. A peptide of the invention acts as a stratum corneum chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating an individual against SCCE, particularly an individual having, suspected or at risk of getting ovarian, lung, prostate, pancreatic or colon cancer. The oligonucleotide is useful for treating a neoplastic state in an individual, such as ovarian, breast, lung, colon, prostate, or an individual such as ovarian, breast, lung, colon, prostate, or peptides are also useful in the monitoring and development of immunotherapies for ovarian and other malignancies. The present sequence represents a peptide fragment of serine protease SCCE (stratum corneum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for vaccinating an individual against SCCE, and in monitoring and developing immunotherapies for ovarian and other malignancies.
                                                                                                                                                                                                                                                                                                                                                                   Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:33.
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                                                                                                                                                                                                                                                                                                                                                                                                           serine protease; stratum corneum chymotrytic enzyme; SCCE;
immune response; ovarian cancer; lung cancer; prostate cancer;
pancreatic cancer; colon cancer.
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                                          0; Indels
                 Pred. No. 1.8e+06;
                                          Mismatches
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100.08;
                                                                                                                                                                                                                                   ADR68794 standard; peptide; 9 AA.
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Best Local Similarity luv.
                                        9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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ABG23378
ID ABG2
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ADRIA 2
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain caction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of [II]. The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cutivity of (II) susful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (III) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in a polymucleotide sequences have applications of mutations diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in
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100.0%; Pred. No. 12;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID NO 53737; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
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The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more
                                                                                                                                                                                                                                                                                              (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                WPI; 2003-381626/
N-PSDB; ADA05735.
                                                                                                                                                                                                                                                                                                                                                                                   pharmacogenomics
                                                                              WO2003029424-A2
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12-0CT-2001)
17-0CT-2001)
18-0CT-2001)
18-0CT-2001)
24-0CT-2001)
24-0CT-2001)
29-0CT-2001)
                                                                   Homo sapiens
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16-MAY-2002;
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17-MAY-2002;
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containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule above; (6) an entible above each comprising the presence or amount of the above polypeptide or nucleic acid molecule in a cent of presence or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a comprising a nucleic acid molecule in a first mammalian subject; (9) a cerening for incenting a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (11) a method of cor preventing a pathology associated with the above polypeptide in a corporation and activity of the polypeptide described above; (12) a method for modulating cor preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide in a corporation and antilipaemic activities, and can be used in gene therapy. The collypeptide is useful in manufacturing a medicament for treating a cyndrome associated with a human disabase. The polypeptide or the nucleic corporation and benched for the activity of producining the above polypeptide is useful in manufacturing a medicament for treating a cyndrome associated with a human disabase. The polypeptide or the nucleic corporation and proved the corporation and particles and antilipaemic activities, and can be used in gene therapy. The colline associated with a human disabase. The polypeptide or the nucleic corporation and and particles or prevent metabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
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tive 0; Mismatches
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2001US-0327435P.
2001US-0327449P.
2001US-0327917P.
2001US-0328029P.
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05-OCT-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peyman JA, Kekuda R, Ju J, Li L, Guo X;
, Edinger SR, Ellerman K, Malyankar UM;
sen BD, Anderson DW, Zhong M, Catterton E;
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                                                                                                                        human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
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a CEA, Shenoy SG;
ML, Berghs C, Di
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                                                                                Human NOV18c protein SEQ ID NO:96
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2001US-0328849P.
2001US-0329414P.
2001US-0330142P.
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2001US-0327917P.
2001US-0328029P.
2001US-0328044P.
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2001US-0349575P.
2001US-0346357P.
2002US-0373260P.
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2002US-0373817P.
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2001US-0327435P,
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2001US-0339266P.
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2002US-0374977P.
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                                06-NOV-2003 (first entry)
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05-OCT-2001; 2 09-OCT-2001; 2 09-OCT-2001; 2

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Gaps

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Peyman JA, Kekuda R, Ju J, Li L, Guo X;

A. Edinger SR, Ellerman K, Malyankar UM;

Ben BD, Anderson DW, Zhong M, Catterton E;

Bli L, Stone DJ, Pena CEA, Shenoy SG;

JME, Leach MD, Agee ML, Berghs C, Dipippo VA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rastelli L, Stone DJ, Pena CEA,
enberg ME, Leach MD, Agee ML, Be
EA, Rieger DK, Spaderna SK;
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Miller CE, RABLELLE
PFR RA, Rothenberg ME, Leace
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Patturajan M, Spytek KA, Edinge
Ort T, Gorman L, Zerhusen BD,
                                2001US-0330309P.
2001US-0341058P.
2001US-0339266P.
2001US-0343629P.
                                                                                                                                                 2002US-0381042P.
2002US-0381642P.
2002US-0383656P.
2002US-0383831P.
                                                                                2002US-0373260P.
2002US-0373815P.
2002US-0373817P.
                2001US-0329414P.
2001US-0330142P.
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2002US-0373884P.
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SPYTEK K A.
EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eisen A, Gangolli EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EISEN A.
GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
                                                                                                                                                                                                                                                                                                            GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                                            MILLER C E.
STONE D J.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M ELEACH M D.
                                                                                                                                                                                                                                                                                                                                                                                                                              AGEE M L.
BERGHS C.
DIPIPPO V A.
                                                                                                                                                                                                          MILLET I.
PEYMAN J A.
KEKUDA R.
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N-PSDB; ADN62899.
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                                                                                                                                                                                                    SMITHSON G.
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                                                                                                                                                                                                                                           LI L.
GUO X.
              15-OCT-2001
17-OCT-2001
28-OCT-2001
24-OCT-2001
24-OCT-2001
29-OCT-2001
29-OCT-2001
01-NOV-2001
                                                                                                                                 16-MAY-2002;
16-MAY-2002;
                                                                                                                                                                                    25-JUN-2002;
                                                                                                  19-APR-2002;
                                                                                17-APR-2002;
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(EISE/)
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(RAST/)
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Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.

Claim 1; SEQ ID NO 96; 395pp; English

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The invention relates to isolated NOVX polypeptides and polynucleotides.

NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and conjuncted with decreased by a usefain or activity of NOVX by supplementing the patient our protectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polymucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators anti-NOVX polypeptide antibodies, agonists and antagonists may also be used to modulate NOVX polymucleotide expression and activity of NOVX cused to modulate NOVX polymucleotide expression and activity of NOVX cused to modulate NOVX polymucleotide expression and activity of NOVX cused to modulate NOVX polymucleotide expression and activity of NOVX cused to modulate NOVX polymucleotide expression and activity of NOVX polymetides and polymucleotides may be used in this way to prevent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, disorders, and the various dyslipidaemias metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antipaemic; gene therapy; human disease; metabolic disorder; diabetes; obseity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represents the amino acid sequence of a human NOVX protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001US-0326483P.
2001US-0327435P.
2001US-032743P.
2001US-0329179P.
2001US-032803P.
2001US-0328034P.
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 198 AA;
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09-OCT-2001; 2
09-OCT-2001; 2
09-OCT-2001; 2
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2001US-0341058P.
2001US-0339266P.
2001US-0343629P.
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2002US-0373826P.
2002US-0373884P.
                                        2002US-0373260P
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              2001US-0330309P
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                                                                                   2002US-0381642P
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                                                                                                     2002US-00262511
                                                                                                               (CURA-) CURAGEN CORP.
                                                                                                                                                        WPI; 2003-381626/36.
                                                                                                                                                            N-PSDB; ADA05731
                                                                                                                                                                                    pharmacogenomics
        17-0CT-2001;
18-0CT-2001;
22-0CT-2001;
24-0CT-2001;
29-0CT-2001;
                                                      19-APR-2002;
                                                                    16-MAY-2002;
16-MAY-2002;
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(MILL/) (PEYM/) Matches ADN62896 The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising in one or more containers, the composition described above; in one or more comprising the mucleic acid molecule described above; (3) an isolated nucleic acid molecule of the invention; (4) a vector comprising the mucleic acid molecule described above; (5) a cell comprising the mucleic acid molecule described above; (5) a cell comprising the propertied described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a disease associated with altered levels of expression of the above comprising a special devels of expression of the above comprising the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aborent physiological interactions of the polypeptide; (11) a method of confidential interactions of the polypeptide; (11) a method of a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preduced with the polypeptide; (12) a method for modulating confidences have antidiabetic, anorectic, antibacterial, virucide, mammal; and (14) a method for producing the above polypeptide; NOVX sequences have antidiabetic, anorectic, antibacterial, virucide, and antilipaemic activities, and be essent for treating a medicament for treating a syndrone associated with a numbar of and antilipaemic activity and produce the produced the polypeptide of the poly New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or Dipippo VA; acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various Catterton E; Gno X; Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X. Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM, Okt T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipil Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK; Claim 1; Page 169-170; 586pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopojetic disorder; dyslipidaemia; metabolic syndrome X;
dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
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                                                                                                                                6; Length 250;
                                                                                                                                                                       0; Indels
                                                                                                                              100.0%; Score 40; DB
ilarity 100.0%; Pred. No. 22;
Conservative 0; Mismatches
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15-0CT-2001; 20010S-0329414P.
18-0CT-2001; 20010S-0330142P.
22-0CT-2001; 20010S-0341058P.
24-0CT-2001; 20010S-0341058P.
24-0CT-2001; 20010S-0343252P.
29-0CT-2001; 20010S-0345575P.
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2001US-0327449P.
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2002US-0391335P
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MILLET I.
PEYMAN J A.
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                                                                                                                                                    Similarity
9; Conserv
                                                           present invention
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                                                                                              Sequence 250 AA;
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Best Local S
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They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.

Sequence 250 AA;

SSXS

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Gaps

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8; Length 250; 0; Indels

100.0%; Score 40; DB 100.0%; Pred. No. 22; ive 0; Mismatches

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MALYANKAR U M.
             SPYTEK K A.
EDINGER S R.
ELLERMAN K.
           PATTURAJAN M.
                                                                                                            WPI; 2004-213931/20.
                           GORMAN L.
KEKUDA R
                                                                                                               N-PSDB; ADN62895.
        GUO X
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(RIEG/)
(SPAD/)
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(LEAC/)
(AGEE/)
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(SHIM/)
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AAR67888 standard; protein; 253 AA.
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(first entry)
Query Match
Best Local Similarity 100.
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9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Egelrud T, Hansson L;
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LLLPLQILL 13
                                                                                                                                       LLLPLQILL 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specific inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SYMB-) SYMBICOM AB.
                                                                                                            1 LLLPLQILL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9500651-A1
                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
09-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35-JAN-1995.
                                                                                                                                                                                                                                                                                                         AAR67888;
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Best Local S
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                                                                                                                                                                                                                   RESULT 8
                                                                                                                                                                                                                                       AAR67888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated NOVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the abberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and activity of NOVX polypeptides. For example, NOVX polypeptides and conformable of the aberrant expression and polymucleotides may be used to treat disorders associated with decreased expression or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX bolymeticotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX. The used to modulate NOVX polypeptide antibodies and in this way to prevent, cused to modulate NOVX polypeptide antibodies may be used in this way to prevent, diagnose and treat: metabolic disorders, immune disorders, disorders, and the various dyslipidaemias, metabolic disorders, immune disorders, distorders, match bobsity, the metabolic syndrome X and the various dyslipidaemias, mad wait wasting disorders and with obesity, the metabolic syndrome X and wasting disorders associated with obesity, the metabolic syndrome S and cores.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smithson G, Miller KA, Edinger SR, Ellermann, Catterton E; Patturajan M, Spytek KA, Edinger SR, Ellermann M, Catterton E; Ort T, Gorman L, Zerhenber BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Anngolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 92; 395pp; English.
                                                                                                                                                                                                                                                       MILLER C E.
RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHINKETS R A.
ROTHENBERG M E.
ERACH M D.
BERGHS C.
BERGHS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EISEN A.
GANGOLLI E A.
                                                                                                                                                  ZERHUSEN B D.
ANDERSON D W.
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SPADERNA S K.
                                                                                                                                                                                               ZHONG M.
CATTERTON E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and related vectors, transformed cells and polypeptides, useful for treating skin disorders, e.g. acne or psoriasis, and for identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                             Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis; callosities; keratosis pilaris; ichthyoses; eczema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
Human stratum corneum chymotrophic recombinant enzyme (SCCE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, operably linked to a promoter that drives expression of heterologous sccoor its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or testing of a cosmetic or a pharmaceutical formulation, and for the development of a diagnostic method. It can also be used as a model for a skin disease or skin cancer. The invention is also useful for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a composition effective for the prevention or treatment of an abnormal byperkeratosis, eczema, acne and inherited skin diseases or pruritus, atopic dermatitis, eczema, acne and inherited skin diseases with the pidermal hyperkeratosis. The mammal of the invention is also useful as a model for further studies of itch mechanisms and the testing of potential compounds and compositions for relieve of various skin diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     where itch is a component. This sequence represents the N-terminal tragment of the human stratum corneum chymotryptic enzyme, SCCE synonymous with human kallikrein 7 (KLK7), used in the development of the transgenic mammals described in the invention
                                                                                                                                                                                                                                                                                                                                                     Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serihe protease; transgenic mammal, skin; skin disease; skin cancer; hyperkertatosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 40; DB 5; Length 253; 100.0%; Pred. No. 23; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB84406 standard; protein; 253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Page 37; 74pp; English
                                                    08-FEB-2002; 2002WO-IB001300.
                                                                                                   09-FEB-2001; 2001CA-02332655.
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Matches 9; Conservative
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LLLPLQILL 13
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                                                                                                                                                                                                                                                                                                        WPI; 2002-643380/69.
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                                                                                                                                                                             (EGEL/) EGELRUD T.
(HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 253 AA;
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15-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB84406;
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ABB84406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human amyloid precursor protein protease (AAW05383) is involved in the percessing or clearance of amyloid precursor protein to form beta-amyloid peptide. Its amino acid sequence was deduced from a cDNA clone (AAY39783) obtd. from a human lung library. Recombinant protease can be produced in transformed or transfected prokaryotic (partic. E. coli) or eukaryotic and testing of cpds. useful for treating or preventing contitions associated with beta-amyloid peptide, esp. Alzheimer's disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated human amyloid precursor protein protease - used to develop prods. for the treatment or diagnosis of associated conditions, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                  Amyloid precursor protein protease; Alzheimer's disease; diagnosis;
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                                                                                                                                                Human amyloid precursor protein protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Little SP;
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AAW05383 standard; protein; 253 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 44-45; 55pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-US004294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-00416257
                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dixon EP, Johnstone EM,
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9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT39783.
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                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                           WO9631122-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                              02-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-APR-1995;
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                                                                                                 31-DEC-1996
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                                                 AAW05383;
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                      Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of novel human protease #39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transgenic mammals described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10; Page 58-59; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU82740 standard; protein; 253 AA
                                                                                08-FEB-2002; 2002WO-IB001300.
                                                                                                                         09-FEB-2001; 2001CA-02332655
09-FEB-2001; 2001DK-00000218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
                                                                                                                                                                                                                                                    Egelrud T, Hansson L;
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                                                                                                                                                                                                                                                                                         WPI; 2002-643380/69
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                                                                                                                                                                                   (EGEL/) EGELRUD T.
(HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                 N-PSDB; ABQ76226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 253 AA;
  WO200262135-A2.
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                                         15-AUG-2002
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The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. restenosis and coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. diseases, migraines, pain, sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypotension, hypertension, psychotic disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's useful for treating viral infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel
                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
viral infection; human immunodeficiency virus; HIV; non-viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prostate cancer; gene expression; differential regulation; molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer grading; cancer assessing; cancer monitoring.
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                                                                                                                                                                                                                                                               Caenepeel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein differentially regulated in prostate cancer #43.
                                                                                                                                                                                                                                                               Sudarsanam S, Manning G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU07440 standard; protein; 253 AA.
                   ocular disease; cytostatic; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human proteases of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Fig 2N; 313pp; English.
                                                                                                                                                         26-JUN-2001; 2001WO-US020171.
                                                                                                                                                                                          26-JUN-2000; 2000US-0214047P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JAN-2003 (first entry)
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9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 LLIPLOILL 13
                                                                                                                                                                                                                                                               Whyte D,
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                                                                                                                                                                                                                                                                                                                WPI; 2002-139913/18.
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                                                                                                                                                                                                                            (SUGE-) SUGEN INC
                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABK31782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 253 AA;
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                                                                                     WO200200860-A2
                                                                                                                                                                                                                                                               Plowman G, W}
Charydczak G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                    Homo sapiens.
                                                                                                                       03-JAN-2002
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Best Local
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genes which are differentially regulated in prostate cancer, useful
                                                                                Claim 1; Page 293-294; 416pp; English.
                                 (ORIG-) ORIGENE TECHNOLOGIES INC.
            08-APR-2002; 2002WO-US010824.
                    06-APR-2001; 2001US-0281731P.
                                                                                                                                                                                                                                      regulated in prostate cancer
                                                  2003-058520/05.
                                                       N-PSDB; ABX10343
                                                                                                                                                                                                                                              Sequence 253 AA;
     17-OCT-2002.
                                          Sun Z,
                                                                Novel
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. 0 0; Mismatches 9; Conservative Query Match Best Local Similarity Matches

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ABU07471; RESULT 14
ABU07471
ID ABU07
XX
AC ABU07

The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises concerts and a subject having a prostate cancer, which involves contextion in a subject having a prostate cancer. Crasses which are differentially-regulated in prostate cancer. Freferably, the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer. Preferably, the expression levels of at least 10 genes are determined. (I) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells with a test agent under conditions effective for the test agent to modulate a biological activity of the polypeptide and prostate cancer cells with a test agent under conditions effection, of the test agent to modulates the biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, proventing or treating, determining predisposition to diseases and cancer sepecially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer. Crasses products are used in the diagnostic test to assay for presence of cancer. The polypeptide encoded by (I) can be used as target for therapy or drug diagnostic appropriate encoded by (I) can be used as target for therapy or drug efforts and groups of genes, expressed in pathways and thus concer. The identifications concerned by a polypeptide and droups of genes, expressed in pathways and the definition of functional markers and groups of genes, expressed in pathways which are useful in diagnostic, the representation of physiologically relevant to prostate cancer. The identifications of pathways which are useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.

pathways which are useful in diagnostic, therapeutic, and clinical applications. This is the amino acid sequence of a protein diferentially

Gaps ö 100.0%; Score 40; DB 6; Length 253; 100.0%; Pred. No. 23; Indels

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ABU07471 standard; protein; 253 AA.

(first entry) 28-JAN-2003

Protein differentially regulated in prostate cancer #74.

Prostate cancer, gene expression, differential regulation, molecular marker, drug target, cancer detection, cancer diagnosis, cancer staging, cancer grading, cancer assessing, cancer monitoring.

WO200281638-A2.

17-OCT-2002.

08-APR-2002; 2002WO-US010824.

06-APR-2001; 2001US-0281731P. 06-APR-2001; 2001US-0281732P.

(ORIG-) ORIGENE TECHNOLOGIES INC.

Jay G; Sun Z,

WPI: 2003-058520/05. N-PSDB; ABX10375. Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.

Claim 1; Page 351; 416pp; English.

The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (I) Is useful for assessing a therapettic or preventive of the number is indicative of the probability that the sample comprises or prostate cancer. (C determining the expression levels in a sample comprising prostate cancer. (C target genes which are differentially-regulated in prostate cancer. Preferably, the expression levels of at least 10 genes are determined. (C is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer calls with a test agent under conditions effective for the test agent to modulate a biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (I is useful as modecular markers, as drug targets, and for detecting, daynosing, staging, and etermining predisposition to diseases and conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer of conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer of cancer, its stage of development, the nature of genetic defect, etc. The polypeptide encoded by (I) can be used as target for therapy or drug discourser, its stage of development, the number of genetic defect, etc. The polypeptide encoded by (I) can be used as target for therapy or drug discourser, its stage of development, the pulypeptide and groups of genes, expression to determine the polypeptide encoded by (I) can be used for expression of specific applications to treat prostate cancer. The identification of in therapeutic pathways which are useful in diagnostic, therapeutic, and clinical applications. This is the amino acid sequence of a protein diferentially in prostate cancer

Sequence 253 AA;

Gaps ö 100.0%; Score 40; DB 6; Length 253; ilarity 100.0%; Pred. No. 23; Conservative 0; Mismatches 0; Indels Best Local Similarity Matches 9; Conserv Query Match

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The invention relates to a novel isolated polynucleotide. The polynucleotides of the invention have cytostatic activity, and may have a use in gene therapy, and in a vaccine. The composition and methods are useful in diagnosing and/or treating cancer, particularly ovarian cancer. The composition may also be used as a vaccine to prevent cancer. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotide and polypeptide useful for diagnosing and/or treating cancer, particularly ovarian cancer, and as a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cytostatic; gene therapy; vaccine; cancer; ovarian cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 157-158; 169pp; English
                                                                                                                                                                                                                                                                        ABR58471 standard; protein; 253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-OCT-2002; 2002WO-US031467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-OCT-2001; 2001US-0327135P. 30-MAY-2002; 2002US-0384531P.
                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUL-2003 (first entry)
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mannion J;
                                                1 LLLPLQILL 9
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                                                                                                                                                                                                                                                                                                                                                         ABR58471;
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ABR58471
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AC ABR58
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Gaps

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Search completed: July 13, 2005, 17:19:51 Job time: 77.6667 secs

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1 LLLPLOILL 9

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

July 13, 2005, 16:54:03; Search time 13.5556 Seconds (without alignments) 63.882 Million cell updates/sec Run on:

US-09-905-083A-33 Title:

1 LLLPLQILL 9 Perfect score: Sequence: Scoring table:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. (Score	Match	Query Match Length DB	DB	ID	Description
	40	1	1	7	A53968	serine proteir
	36	90.0	146	7	H75201	hypothetical p
	34	85.0	277	7	H84314	cytochrome aa
	34	85.0		~	833603	surfactant pro
	34	85.0		Н	JN0450	conglutinin p
	34	85.0		7	145878	conglutinin -
	34	85.0		7	AE0614	propable compe
	34	85.0	845	~	D97163	cation transpo
	33	82.5	196	7	G65039	hypothetical

				H		111111111111111111111111111111111111111
-	40	100.0	25	~	A53968	serine proteinase
7	36	90.0		7	H75201	hypothetical prote
m	34	S		~	H84314	aa
4	34	ď.		~	833603	surfactant protein
5	34	85.0	371	Н	JN0450	conglutinin precur
9	34	85.0	371	7	145878	in
7	34	85.0	754	~	AE0614	probable competenc
80	34	85.0	845	~	D97163	cation transport P
6	33	82.5	196	7	G65039	hypothetical prote
0	33	82.5	282	~	E70890	hypothetical prote
1		82.5	370	~	AB3334	
7	33		398	~	C91063	cal
m		82.5	413	7	AC0834	슅
4	33	82.5	426	7	C83103	hypothetical prote
'n	33	82.5	470	~	A90083	al
9	33	82.5	475	н	A69149	en tra
7	33	82.5		7	A46362	
80	32	80.0		~	S25656	surface
6	32	80.0	235	-	RWHUT8	T-cell surface gly
20	32	80.0	238	-	LNRTMA	ij
-	32	80.0		Н	KYHUCM	chymase (EC 3.4.21
~	32	80.0		~	F91095	type III secretion
<u>س</u>	35	80.0		N	B85941	hypothetical prote
4	32	80.0		N	C97402	probable acyltrans
n.	32	80.0	264	~	AC2620	1-acyl-sn-glycerol
9	32	80.0	266	~	JC7300	tax-responsive ele
7	32	80.0	267	~	JC4857	hepatocarcinogenes
80	32	80.0	491	~	JC6197	stromelysin 3 (EC
σ	32	80.0	492	~	A44399	stromelysin 3 (EC

Na+/H+-exchanging	peptidyl-dipeptida	apolipoprotein C-I	interleukin-2 prec	conserved hypothet	alpha-2u-globulin	hypothetical prote	nitrate ABC transp	probable secreted	hypothetical prote	hypothetical prote	probable permease	ABC transporter, m	hypothetical prote		hypothetical prote
A12088	A31759	A38685	A31278	G75555	S10125	T43766	F69260	T35589	T38931	C84914	A98157	AH3130	D83934	C84306	A71875
~	-	N	~	~	~	~	~	~	C)	~	~	~	N	7	7
543	1306	100	155	159	184	189	244	249	569	303	372	372	392	447	493
80.0	80.0	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5
32	32	31	31	31	31	31	31	31	31	31	31	31	31	31	31
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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A53968
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serine proteinase SCCE precursor - human

N;Alternate names: stratum corneum chymotryptic enzyme C;Species: Homo sapiens (man) C;Date: 07-Jul.1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004 C;Accession: A53968

Filansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T. J. Biol. Chem. 269, 19420-19426, 1994
A,Filte: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme A; Reference number: A53968; MUID:94308225; PMID:8034709
A; Reference number: A53968
A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-253 «HAN»
A; Residues: 1-253 «HAN»
A; Cross-references: UNIPROT:P49862; GB:L33404; NID:g521214; PIDN:AAC37551.1; PID:g532504

C,Genetics: A,Gene: GDB:PRSS6; SCCE A,Cross-references: GDB:377730

A;Map position: 7q35-7q35 C;Superfamily: trypsin; trypsin homology F;30-245/Domain: trypsin homology <TRY>

Gaps ö Length 253; Indels ; 0 DB 2; 100.0%; Score 40; DB 100.0%; Pred. No. 2; tive 0; Mismatches Best Local Similarity 100. Matches 9; Conservative Query Match

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1 LLLPLQILL 9 ò ď

5 LLLPLQILL 13

RESULT 2

hypothetical protein PAB0088 - Pyrococcus abyssi (strain Orsay)

C,Species: Pyrococcus abyssi C,Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C,Accession: H75201
R,anonymous, Genoscope
R,anonymous, Genoscope
A,Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struct
A,Reference number: A75001

A; Accession: H7520

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-146 <KAW>

A;Cross-references: UNIPROT: 09V2D5; GB: AJ248283; GB: AL096836; NID: g5457433; PIDN: CAB4906: A;Experimental source: strain Orsay

C, Genetics:

A,Gene: PAB0088 C,Superfamily: Pyrococcus abyssi hypothetical protein PAB0088

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A; Molecule type: mRNA
A; Residues 1.371 cKA2, a cKA2, A; A; Residues 250 and 270 as Glu
A; Note: The authors translated the codon GAT for residues 250 and 270 as Glu
R; Lu, J.; Laursen, S.B.; Thiel, S.; Jensenius, J.C.; Reid, K.B.M.
Biochem. J. 292, 1157-162, 1993
A; Title: The CDNA cloning of conglutinin and identification of liver as a primary site of A; Reference number: S33235; MUID:93277452; PMID:7684896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1,122, "W.1, 174-217,'A', 219-271,'V', 273-371 <LUU>
A;Residues: EMBL:X71774; NID:g395267; PIDN:CAA50665.1; PID:g395268
A;Experimental source: liver

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Bur. J. Biochem. 215, 793-799, 1993

Strictus Structural similarity between lung surfactant protein D and conglutinin. Two dis A;Reference number: S35044; WUID:93358905; PMID:8354286

A;Accession: S35044
                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues 1.371 cSUZ-
A;Cross.references: UNIPROT:P23805; DDBJ:D14085; NID:g285643; PIDN:BAA03170.1; PID:g28564
A;Experimental source: liver
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Biochem. J. 293, 15-19, 1993
A;Title: Research Communication. Localization of the receptor-binding site in the collect
A;Reference number: S34054; WUID:93319501; PMID:8328957
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C;Comment: This protein mediates the agglutination of erythrocytes with antibody and comm
C;Comment: This protein is a Ca2+-dependent serum lectin specific for N-acetylglucosamine
                                                                                                                                                                                                                                                                                                                                                               R;Kawasaki, N.; Itoh, N.; Kawasaki, T.
Biochem. Biophys. Res. Commun. 198, 597-604, 1994
A;Title: Gene organization and 5'-flanking region sequence of conglutinin: A C-type mamma
A;Reference number: JC296; MID:94128104; PMID:8297370
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A;Residues: 75-86, X', 88-89, X', 91, I' <LUA>
A;Residues: 75-86, X', 88-89, X', 91, I' <LUA>
A;Reperimental source: lung
N.M.; Leon, Mommun. 143, 645-651, 1987
Biochem. Biophys. Ree. Commun. 143, 645-651, 1987
A;Title: The carbohydrate specificity of conglutinin and its homology to proteins in A;Reference number: A29416; MUID:87184551; PMID:3566740
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A.Residues: 21-54;75-86,'X',88-89,'X',91,'X',93-94;208-209,'X',211-227 <KAW>
A.Experimental source: serum
                         Biochem. Biophys. Res. Commun. 191, 335-342, 1993
A;Title: Cloning and sequencing of a CDNA coding for bovine conglutinin.
A;Reference number: JN0450; MUID:93213261; PMID:8460993
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        R;Suzuki, Y.; Yin, Y.P.; Makino, M.; Kurimura, T.; Wakamiya,
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A;Residues: 21-209, 'S', 211-371 <LEE>
R;Kawasaki, N.; Yokota, Y.; Kawasaki, T.
Arch: Bicchem: Bicophys. 305, 533-540, 1993
A;Title: Differentiation of conglutination activity and A;Reference number: $36879; MUID:93384312; PMID:8373191
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A;Introns: 67/1; 106/1; 142/1; 178/1; 217/1; 245/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                  cytochrome aa3 controlling protein [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 09-Jul-2004
C;Accession: H8414
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabld Jung, K.H.; Alam, M.; Preitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Danialels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID:20504483; PMID:11016950
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333603
surfactant protein D - bovine
c;Species: Bos primigenius taurus (cattle)
c;Species: Dos primigenius taurus (cattle)
c;Accession: 333603
R;Lim, B.L.; Lu, J.; Reid, K.B.M.
Immunology 78, 159-165, 1993
A;Title: Structural similarity between bovine conglutinin and bovine lung surfactant pro
A;Reference number: S33603; MUID:93170856; PMID:8436402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: UNIPROT: Q9HP13; GB:AE004437; NID:g10581096; PIDN:AAG19884.1; GSPDB: G
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N'Contains: conglutinin-N
C'Species: Bos primigenius taurus (cattle)
C'Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C'Date: 10-Sep-1999 yesquence revision 10-Sep-1999 $text change 09-Jul-2004
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C,Superfamily: pulmonary surfactant protein D; C-type lectin homology F;248-367/Domain: C-type lectin homology <LCH>
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Pred. No. 33;
3; Mismatches
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Pred. No. 44;
1; Mismatches
    Score 36; DB
Pred. No. 7;
                                              Pred. No. 7;
2; Mismatches
90.08;
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66.7%;
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77.8%;
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JN0450
conglutinin precursor - bovine
                                                                                       7; Conservative
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97 VLLPLQVIL 105
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LLLPLSVLL 10
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LLLPLQIII 75
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Molecule type: DNA
Residues: 1-277 <STO>
                                              Best Local Similarity Matches 7; Conser
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A; Status: prelimina
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C;Genetics:
A;Gene: ccp
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cation transport P-type ATPase CAC2137 [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 C;Accession: D97163 G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. Jacteriol: 183, 4823-4838, 2001 A;Tile: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clost A;Reference number: A96900; MUID:21359325; PMID:21359325
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C;Species: Escherichia coli
C;Species: Bscherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: G65039
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G65039
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C;Species: Mycobacterium tuberculosis
C;Species: TJ-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: E70890
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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A;Experimental source: Clostridium acetobutylicum ATCC824
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A;Cross-references: GB:AE000347; GB:U00096; NID:g2367142; PIDN:AAC75661.1; PID:g1788965;
A;Experimental source: strain K-12, substrain MG1655
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           Gaps
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87.5%; Pred. No. 1e+02;
live 1; Mismatches
              Mismatches
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Matches 7; Conservative
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              Conservative
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                                                                                                                                                     371 LLLPLOVAL 379
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670 LLPIQILL 677
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                                                                              1 LLLPLQILL
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A;Molecule type: DNA
           7;
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A;Gene: CAC2137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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C; Superfamily: pulmonary surfactant protein D; C-type lectin homology C (Keywords: calcium binding; glycoprotein; hydroxylysine; hydroxyproline P;1-20/Domain: signal sequence #status predicted <SIG> P;1-21/Product: conglutinin #status predicted <MAT> P;46-214/Region: collagen-like P;75-371/Product: conglutinin-N #status predicted <MAZ> P;75-371/Product: conglutinin-N #status predicted <MAZ> P;75-371/Product: conglutinin-N #status predicted <P;75-371/Product: conglutinin-N #status predicted <P;75-371/Product: conglutinin-N #status predicted <P;75-371/Product: conglutinin-N #status predicted site: 5-hydroxyproline (Lys) #status predicted site: 5-hydroxyproline (Lys) #status experime P;78,96,108,111,129,132,147,153,171,195/Modified site: 4-hydroxyproline (Pro) #status experime predicted site: carbohydrate (Asn) (covalent) #status experimental
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C.Species: Bos primigenius taurus (cattle)

C.Species: Bos primigenius taurus (cattle)

C.Jate: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004

C.Jate: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004

C.Jate: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004

R.Liou, L.S.; Sastry, R.; Hartshorn, K.L.; Lee, Y.M.; Okarma, T.B.; Tauber, A.I.; Sastry

Gene 141, 277-281, 1994

A.Title: Bovine conglutinin (BC) mRNA expressed in liver: cloning and characterization charact
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A;Cross-references: UNIPROT:P23805; GB:L18871; NID:g495012; PIDN:AAA20126.1; PID:g495013
A;Cross-references: UNIPROT:P23805; GB:L18871; NID:g495012; PIDN:AAA20126.1; PID:g495013
C;Superfamily: pulmonary surfactant protein D; C-type lectin homology
F;248-369/Domain: C-type lectin homology <LCH>
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Pred. No. 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                       85.0%; Score 34; DB 1; Length 371; 77.8%; Pred. No. 44; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Length 371;
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Pred. No. 44;
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C;Superfamily: competence protein ComEC
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77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
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LLLPLSVLL 10
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Best Local Similarity
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Matches 7; Conserv
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probable membrane protein corB [imported] - Salmonella enterica subsp. enterica serovar 1 c; Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: Ac0834
B;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, t. ; Connerton, P; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AC0834
A;Status: preliminary
A;Residues: 1-413 < PAR>
A;Residues: 1-413 < PAR>
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CiDate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
CiAccession: C83103
Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q9HW63; GB:AE004850; GB:AE004091; NID:g9950560; PIDN:AAG07726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AL513382; PIDN:CAD05858.1; PID:g16503833; GSPDB:GN00176
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein PA4338 [imported] - Pseudomonas aeruginosa (strain PAO1)
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Pred. No. 80;
1; Mismatches
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              77.8%; Pred. No. 74; ive 1; Mismatches
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1; Mismatches
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Pred. No.
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C,Superfamily: hypothetical protein H10107
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C, Genetics:
A, Gene: PA4338
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77.8%;
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Best Local Similarity 77.8-
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Best Local Similarity 77.0
Best Local 7; Conservative
           Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                    101 LLAPLOILM 109
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-426 <STO>
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B.Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv1978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      daunorubicin resistance transmembrane protein [imported] - Brucella melitensis (strain 1 C;Species: Brucella melitensis
C;Species: Brucella melitensis
C;Species: Dr.Peb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AB3334
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, M.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
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A;Residues: 1-398 - CHAY>
A;Cross-treferences: UNIPROT: Q8X9C3; GB:BA000007; PIDN:BAB36898.1; PID:g13362946; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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C;Date: 18-Uul-2001 #sequence_revision 18-Uul-2001 #text_change 09-Uul-2004

C;Accession: C91063

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gend

A;Reference number: A99629; MUD:21156231; PMID:11258796

A;Accession: C91063

A;Accession: C91063

A;Molecule type: DNA
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A;Cross-references: UNIPROT:Q8YHY9; UNIPROT:Q8FZX1; GB:AE008917; PIDN:AAL51837.1; PID:g1
A;Experimental source: strain 16M
A, Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID: 98295987; PMID: 9634230
A; Accession: E70890
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-282 < COL>
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                                                                                                                                                                                                                                                                                                                                                   Length 282
                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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Pred. No. 53;
1; Mismatches
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C,Superfamily: hypothetical protein HI0107
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Best Local Similarity 77.6
Matches 7; Conservative
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Molecule type: DNA
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A; Status: preliminar
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C;Genetics:
A;Gene: BMEI0656
A;Map position: I
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C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: A90083
R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an englaved algal nucleus.
A;Reference number: A99082; MUD:11323671; PMID:11323671
A;Accession: A90083
A;Status: preliminary
A;Molecule type: DNA
A;Coss-references: UNIPROT:Q9SEA5; GB:AF165818; NID:g6690603; PIDN:AAF24211.1; GSPDB:GN
C;Genetics:
C;Genetics:
A;Genome: nucleomorph
C;Keywords: nucleomorph
C;Keywords: nucleomorph
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Search completed: July 13, 2005, 17:31:28 Job time : 15.5556 secs

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SEQUENCE FROM N.A.
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KLK7_HUMAN
ID _KLK7_HUMAN
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                                                                                             July 13, 2005, 16:15:23; Search time 62.2222 Seconds (without alignments) 74.069 Million cell updates/sec
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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QBNSN9
QBNCA9
QBRSD6
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PK11 MOUSE
IHA TRIVU
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Q91MZ4
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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Perfect score:
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Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A.,
Egelrud T.;
"Cloning, expression, and characterization of stratum corneum
chymotryptic enzyme. A skin-specific human serine proteinase.";
J. Biol. Chem. 269:19420-19426(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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01-OCT-1996 (Rel. 34, Last sequence update)
02-OCT-2004 (Rel. 45, Last annotation update)
Kallikrein 7 precursor (EC 3.4.21.-) (Stratum corneum chymotryptic enzyme) (hSCCE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain;
Kishi T., Michael I.P., Diamandis E.P.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databages.
EMBL; AY646152; AAT66047.1; ...
SEQUENCE 66 AA; 7171 MW; 82EIC392BC822FDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Kallikrein 7 splice variant 3.
Homo sapiens (Human).
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                              Q7D7M8
Q6GNT6
Q8THY9
Q8THY9
Q8FX1
Q7AB12
Q8XFY3
Q7CZS
Q7CZS
Q7CZS
Q9HW63
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Name=KLK7; Synonyms=PRSS6, SCCE;
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              UnterPro; IPR0012017, F. Epidemina uniterientiation; IAS.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001214; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Promo Pr00069; Trypsin; I.
SWART; SW00020; Tryp SPC; I.
PROSITE; PS00134; TRYPSIN_DOW; I.
PROSITE; PS00135; TRYPSIN_SER; I.
PROSITE; PS00135; TRYPSIN_SER; I.
Direct protein sequencing; Glycoprotein; Hydrolase; Serine protease; Signal; Zymogen.

22
                                                                                                                                                                                                                                     Hansson L., Backman A., Ny A., Edlund M., Edholm E., Tornell J., Wallbrandt P., Egelrud T.;
"Epidermal overexpression of stratum corneum chymotryptic enzyme in mice; a model for chronic ithchy dermatlis.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95314630; PubMed=7794273;
Skytt A., Stroemqvist M., Egelrud T.;
"Primary substrate specificity of recombinant human stratum corneum
                                                                                                        PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
Moss P., Peeper B., Wang K.,
"Sequencing and expression analysis of the serine protease gene
cluster located in chromosome 19q13 region.";
             Yousef G.M., Scorilas A., Diamandis E.P.;
"Molecular characterization, mapping and tissue expression of
human stratum corneum chymotryptic enzyme gene.";
Submitted (DEC.1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM; 604438; -. GO; GO: 0008236; F:serine-type peptidase activity; TAS. GO; GO:0008544; P:epidermal differentiation; TAS.
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EMBL, AF243527, AAG33360.1;
EMBL, AF332583, AAK69624.1,
FIR, A53368, A53968.
HSSP, P00760, 1EZX.
MEROPS; S01.300, -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L33404; AAC37551.1;
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H-InvDB; HIX0015373; -.
                                                                                                                                                                                          Gene 257:119-130(2000).
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TISSUE=Keratinocytes;
                                                                              [3]
SEQUENCE FROM N.A.
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MEDINE-228825; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDINE-228825; PubMed=12477932; DOI=10.1073/pnas.242603899; A trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., A tausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Ra Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., A blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., A Braha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M., A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M., A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A Hitching M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rakeeley R.W., Touchman J.W., Green B.D., Dickson M.C., A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., K. Williald M.J., Madan M., Schmutz J., Myers R.M., Butterfield Y.S., Ryvinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., R. "Generation and initial analysis of more than 15,000 full-length human
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                          (By similarity).
(By similarity).
(By similarity).
                                                                                                                                                                                                                                                                                                                       . .) (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                       y Match 100.0%; Score 40; DB 1; Length 253; Local Similarity 100.0%; Pred. No. 10; hes 9; Conservative 0; Mismatches 0; Indels
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                        2D68B6B15A76A668 CRC64;
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GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004209; F:trypsin activity; IEA.
GO; GO:0004209; F:trypsin activity; IEA.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Stratum corneum chymotryptic enzyme, preproprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Charge relay system (I
Charge relay system (I
By simlarity.
N-linked (GlCNAc...
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Kallikrein 7.
                                                                                                                                                                                                                                                                                                                                                            27525 MW;
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176
201
246
253 AA;
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DISULFID
DISULFID
DISULFID
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DISULFID
DISULFID
CARBOHYD
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6 LLLPLQLLL 14
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es 8; Conserv
                                                                                                                   NCBI_TaxID=10090;
                                                                             Fkbp11 protein.
                                                                                    Name=Fkbp11;
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                                      QBR5D6
QBR5D6;
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Q6PKE2;
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Matches
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                       RESULT 5
                               Q8R5D6
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                                                                                            Gaps
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                                                                                                                                                                                                                     Mus muscrius (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                           100.0%; Score 40; DB 2; Length 253; 100.0%; Pred. No. 10;
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Pred. No. 7.6;
                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
Submit BC021345; AAH21345.1; -
MGD; MGI:1913370; Fkbp11.
MGD; MGI:1913370; Ekbp11.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:001601; C:integral to membrane; TAS.
SEQUENCE 73 AA; 7819 MM; 93E8P53399BF3C11 CRC64;
     PERMIT PROGRES, TYPESIN; 1.
PRINTS, PRO072; CHYMOTRYPSIN.
SMART; SM00020; TYPY SPC; 1.
PROSITE; PS0240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
HYDROLTE; PS0134; TRYPSIN EN; 1.
HYDROLASE; PS0135; TRYPSIN EN; 1.
HYDROLASE; PS0125; STRIP EN; 2068B6A41B22A668 CRC64;
                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                73 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Salivary gland;
InterPro; IPR009003; Pept_Ser_Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences."
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Best Local Similarity 85...
8; Conservative
                                                                                           9; Conservative
                                                                                                                                                                PRELIMINARY;
                                                                                                                       5 LLLPLQILL 13
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                                                                                                          1 LLLPLOILL 9
                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                        Fkbp11 protein.
                                                                                                                                                                                                              Name=Fkbp11;
                                                                           Query Match
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                                                                                           Matches
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=CZECH II; TISSUE=Mammary tumor;

Ratuanberg R.L., Feingold E.A., Wagner L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I.; Wang J., Haieh F.,

And Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninoi P., Parange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley N., Sodergen B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Gdreen E.D., Dickson M.C.,

Ray, Milland M.I., Salska U., Samailus D.E., Schnerch A., Schein J.E.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.; Strausberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS50059; FKBP PPIASE; 1.
SEQUENCE 104 AA; 11005 MW; 0534D57467566914 CRC64;
                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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104 AA
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STRAIN=CZECH II; TISSUE=Mammary tumor;
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PRT;
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PRELIMINARY;
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                                                                                                                                                                                                                             Mus musculus (Mouse)
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ID Q6
AC Q6
DT 05
DT 05
DT 05
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CHAIN
      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=FVB/N; TISSUE=Nammary tumor;

MEDLINE=238825; PubMed=1247932; DOI=10.1073/pnas.242603899;

A Straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Itschul S.F., Zebebrg B. Duetow K.H., Schaefer C.F., Bhat N. K.,

A Itschul S.F., Zebebrg B. Buetow K.H., Schaefer C.F., Bhat N. K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Tonshiyuki S., Carninci P., Prange C.

Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wakernan K.J., Malek J.A., Gunaratne P.H.,

Raba S.S., Morley K.C., Hale S., Garriactine D., Prange C.

Richards S., Worley K.C., Hale S., Garriactus S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T "Generation and initial analysis of more than 15,000 full-length human
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05-JUL-2004 (Rel. 44, Last annotation update)
FKGO binding protein 11 precursor (EC 5.2.1.8) (Peptidyl-prolyl cistrans isomerase) (PPIase) (Rotamase) (19 kDa FK506-binding protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CS7BL/6J; TISSUB=Embryo; MEDLINE=23546B3; PubMed=12466B31; DOI=10.1038/nature01266; MEDLINE=223546B3; PubMed=12466B31; DOI=10.1038/nature01266; Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T. Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schrill L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-2001, c. Submitted (JAN-2001, c. EMBL; BC002311; AAH02311.1; -. EMBL; BC002311; AAH02311.1; -. EMBL; BC002311; AAH02311.1; -. GO; GO:0005615; C:extracellular space; TAS. GO; GO:0016021; C:integral to membrane; TAS. Interpro; IPR001179; FKBP_PPIASE. Interpro; IPR001179; FKBP_PPIASE; 1. PR0SITE; PS50059; FKBP_PFIASE; 1. PR0SITE; PS50059; FKBP_PFIASE; 1. APRICE 138 AA; 15\overline{15}\text{05}\text{07}\text{07}\text{07}\text{09}\text{09}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}\text{01}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FK11 MOUSE STANDARD; E
Q9D1M7; Q9CRE4;
28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 LLLPLOLLL 14
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                                                                                              NCBI_TaxID=10090;
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ID FK11 MOUSE

ID FK11 MOUSE

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Balke 3.A. Deaged D. Bousie V. Chelle C. Cocata A. Cousins S.,

Acasserland T. Garinich S. Hirokawa N., Joseson I. J., Jarvis E. D.,

Romagowa A. Cauthuch S. Hirokawa N., Joseson I. J., Jarvis E. D.,

Romagowa A., Kurochkin I. V., Bernick C. Cocata K. A. Cough J. S.,

Romagowa A., Kurochkin I. V., Bernick C. Cocata K. A. Cough J. S.,

Romagowa A., Kurochkin I. V., Bernick E. M. King B. L.,

Romagowa A., Kurochkin I. V., Bernick E. D., Tomia B. D.,

Romagowa A., Rucochkin I. V., Lenhard B., Lyons P. A.,

Rapict D.R., Walkaris L., Taylor M. S.,

Rapick E. M., Schmider C., Semple C.A. Serou M., Schmida K.,

Rapick E. Wanger L., Wallestedt C., Wang Y., Watanaba Y., Walls C.,

Ramadia A., Sachmider C., Semple C.A., Serou M., Shimada K.,

Ranna S., Wanger L., Wallestedt C., Wang Y., Watanaba Y., Walls C.,

R. Milmig L.G., Wangwa Y., Kuroch M., Nahamara M., Sakarum M., Sach

R. Milmig L.G., Wangwa Y., Kuroch M., Nahamara M., Sakarum M., Sach

R. Milmig L.G., Wangwa W., Marker L. Mang Y., Wang I.,

R. Mangaris C., Wangwa W., Shuroch M., Sakarum M., Wang I.,

R. Mangaris C., Wangwa W., Shuroch M., Sakarum M., Wang I.,

R. Mangaris C., Wangwa W., Shuroch M., Sakarum M., Wang I.,

R. Mangasi G. He Mandawa W., Romo M., Nahamara M., Sakarum M., Wang I.,

R. Mangasi G. He Mandawa M., Marercon R., John M., Kogawa I.,

R. Mangasi G. He Mandawa M., Marercon R., Shinaga C.,

R. Mangasi G. He Mandawa M., Marercon R., Shinaga C.,

R. Mangasi G. He Mandawa M., Marercon R., Shinaga C.,

R. Mangasi G. He Mandawa M., Marercon R., Shanga C., Manga C.,

R. Mangasi G. He Mandawa M., Sakari M., Sakarum M., Sakarum M.,

R. Mangasi G. He Mandawa M., Sakari M., Sakarum M., Sakarum M.,

R. Mangasi G. He Mandawa M., Sakarum M., Sakarum M., Sakarum M.,

R. Mangasi G. M., Wangan M., Sakarum M., Sakarum M.,

R. Mangasi G. M., Wangan M., Sakarum M., Sakarum M.,

R. Mangasi G. M., Wangan M., Sakarum M., Sakarum M.,

R. Mangara M., Wangan M., Sakarum M., Sakarum M.,

R. Mangasi M., Wangan M., Sakarum M., Sakarum M.,

R. Mangasi M., Wangan M., Sakaru
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Witochondrion
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                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
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021527
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R GO; GO:000576; C:extracellular; ISS.
GO; GO:001106; F:extracellular; ISS.
R GO; GO:001106; F:extracellular; ISS.
R GO; GO:000803; F:growth factor activity; ISS.
R GO; GO:000803; F:growth factor activity; ISS.
R GO; GO:000515; P:protein binding; ISS.
R GO; GO:000515; P:protein binding; ISS.
R GO; GO:000150; P:cell cycle arrest; ISS.
R GO; GO:000154; P:cell differentiation; ISS.
R GO; GO:000156; P:cell differentiation; ISS.
R GO; GO:000166; P:cell airferentiation; ISS.
R GO; GO:000787; P:cell cycle differentiation; ISS.
R GO; GO:0001287; P:cell-cell signaling; ISS.
R GO; GO:0001287; P:rethrocyte differentiation; ISS.
R GO; GO:00042541; P:hemoglobin biosynthesis; ISS.
R GO; GO:0006917; P:induction of apoptosis; ISS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vulpecula).";

J. Mol. Endocrinol. 21:141-152(1998).

-!- FOUCTION: Inhibins and activine inhibit and activate,
respectively, the secretion of follitropin by the pituitary gland.
Inhibins/activins are involved in regulating a number of diverse functions such as hypothalamic and pituitary hormone secretion, gonadal hormone secretion, germ cell development and maturation, erythroid differentiation, insulin secretion, nerve cell survival, embryonic axial development or bone growth, depending on their subunit composition. Inhibins appear to oppose the functions of
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE-99027340; PubMed-9801457; Vanmontfort D., Fidler A.E., Heath D.A., Lawrence S.B., Tisdall D.J., Greenwood P.J., McNatty K.; Greenwood P.J., McNatty K.; epok sequence analysis, gene expression and protein localisation of the inhibin alpha subunit of Australian brushtail possum (Trichosurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: Dimeric, linked by one or more disulfide bonds. Inhibin is a dimer of alpha and beta-A. Inhibin B is a dimer of alpha and
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                       Trichosurus vulpecula (Brush-tailed possum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
                                                                                                       ö
                                                                       95.0%; Score 38; DB 1; Length 201; 88.9%; Pred. No. 20; tive 1; Mismatches 0; Indels
57 144 PPlase, FKBP-type.
53 5 -> F (in Ref. 1; BAB31559)
198 198 S -> R (in Ref. 1; BAB31559)
201 AA; 22137 MW; 94D955C57264BD82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the TGF-beta family.
                                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                       361 AA
                                                                                                                                                                                                                                                                                                            Inhibin alpha chain precursor.
                                                                                                      Conservative
                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                            LLIPLOLLE 14
                                                                                                                                 1 LLLPLQILL 9
                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activins.
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8
                                                                                                                                                                                                                                                                                                                           Name=INHA;
                                                                                                                                                                                                                                    IHA TRIVU
077755;
               CONFLICT
CONFLICT
SEQUENCE
                                                                      Query Match
 DOMAIN
                                                                                                                                                                                                                   Matches
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GO, GO:0045578; P:negative regulation of B-cell differentiation; ISS. GO:0045786; P:negative regulation of cell cycle; ISS. GO:0046802; P:negative regulation of follicle-stimulating. .; ISS. GO; GO:004507; P:negative regulation of interferon-gamma bio. .; ISS. GO; GO:004507; P:negative regulation of macrophage different. .; ISS. GO; GO:004226; P:negative regulation of phosphorylation; ISS. GO; GO:0001541; P:negative regulation of phosphorylation; ISS. GO; GO:0001541; P:neurogeneation of phosphorylation; ISS. GO; GO:0001541; P:positive regulation of follicle-stimulating. .; ISS. InterPro; IPR001839; TGPb.

FPERM; PF00019; TGP_beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sigmodontine rodents..;
Mol. Biol. Evol. 15:35-49(1998).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
EMBL; U83808; AAB87168.1; -.
GO; GO:0005739; C:mitochondrion; IEA.
GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
GO; GO:001491; F:oxidoreductase activity; IEA.
GO; GO:001491; F:oxidoreductase activity; IEA.
GO; GO:00120; P:mitochondrial electron transport, IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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By similarity.
Inhibin alpha chain.
By similarity.
By similarity.
By similarity.
Interchain (By similarity).
Interchain (By similarity).
Interchain (GloNac. .) (Potential).
Inlinked (GloNac. .) (Potential).
Inlinked (GloNac. .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \label{eq:median} $$\operatorname{MEDLINE=98152303}, $$\operatorname{PubMed=9491603}, $$\operatorname{Engel S.R.}, $$\operatorname{Hogan K.M.}, $$\operatorname{Taylor J.F.}, $$\operatorname{Davis S.K.}, $$\\"Molecular systematics and paleobiogeography of the South American
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Arvicolinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -linked (GlcNAc. . .) (Pc
D661CDF93CDAA87D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 021527;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-2003 (TrEMBLrel. 25, Last annotation update)
NADH dehydrogenase subunit 4 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clethrionomys gapperi (Southern red-backed vole).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003918; NADHub oxred4.
InterPro; IPR001750; Oxidored q1.
InterPro; IPR000260; Oxidored q2.
Pfam; PF00361; Oxidored q1: 1.
Pfam; PF01059; Oxidored q5_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0669; INHIBINA.
PRODOM; PD000357; TGPb; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF BETA 1; 1.
Glycoprotein; Growth Factor; Hor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01059; Oxidored q5 N; 1. PRINTS; PR01437; NUOXDRDTASE4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38945 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LLLPLQILL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144
266
361 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; G
SIGNAL 1
PROPEP 22
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PubMed=14704707; DOI=10.1038/nbt923;
PubMed=14704707; DOI=10.1038/nbt923;
Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L., Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R., Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C., Harrison F.H., Gibson J., Harwood C.S.; resey y Torres J.L., Peres C., Photosynthetic bacterium Rhodopseudomonas palustris.";
Nat. Biotechnol. 22:55-64[2004].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leishmania tarentolae (Sauroleishmania tarentolae).
Bukaryota; Euglenozoa, Kinetoplastida; Trypanosomatidae; Leishmania;
lizard Leishmania.
                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the ABC transporter family.
-!- SIMILARITY: Belongs to the ABC transporter family.
BMBL; AYS89043; AAT02643.1; --
GO; GO:00166021; C:integral to membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004565; F:ATPase activity, coupled to transmembrane m.
GO; GO:0000166; F:mucleotide binding; IEA.
GO; GO:0006810; P:transport; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhodopseudomonas palustris.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Rhodopseudomonas.
MCBI_TaxID=1076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.5%; Score 35; DB 2; Length 181;
87.5%; Pred. No. 73;
1.ve 1; Mismatches 0; Indels
                                                                                                                       Indels
Endonuclease.
SEOUENCE 205 AA; 22733 MW; 6FBFE7178F6C9EFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome; Hypothetical protein.
SEQUENCE 181 AA; 19632 MW; CDB44D8210E565D1 CRC64;
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0-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 27, Last sequence update) (TrEMBLrel. 27, Last annotation update)
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                                                                        Score 36; DB
Pred. No. 52;
                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           05-JUL-2004 (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last seq 05-JUL-2004 (TrEMBLrel. 27, Last ann
                                                                        90.0%;
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                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                     176 ILLPLOLLL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
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                                               Query Match
Best Local Similarity
7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                           SEQUENCE
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Q6PPA4
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M EDLINE-22511545; PubMed=12622808;

M EDLINE-22511545; PubMed=12622808;

M EDLINE-22511545; PubMed=12622808;

M C Cohen G.N.; Barbe V.; Flament D., Galperin M., Heilig R., Lecompte O.,

D Cohen G.N.; Barbe V.; Ripp R., Thierry J.-C.,

N Prieur D., Querellou J., Ripp R., Thierry J.-C.,

N Prieur D., Querellou J., Zivanovic Y., Forterre P.;

Tarchaeon Pyrococcus abygain.";

Tarchaeon Pyrococcus abygain.";

Mol. Microbiol. 47:1495-1512(2003).

EMBL; AJ248283; CAB49063.1; -..

MR PRI, H75201, H75201.

R InterPro; IPRO08537; DUP819.

R Pfam; PPO5684; DUP819.

C Complete proteome; Hypothetical protein.

C Complete Exoteome; Hypothetical protein.
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Sukaryota, Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnolliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, BAC clone:OSJNBB0065C04.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP004744; BAD45874.1; -
                                                                                              Length 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.0%; Score 36; DB 2; Length 146; 77.8%; Pred. No. 37;
                                                                                                                                                Indels
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                                               208 AA; 23967 MW; 8AF1788697AED6A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Endonuclease V protein-like.
Name=OSJNBD0065C04.45;
    Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
                                                                                           92.5%; Score 37; DB 2;
88.9%; Pred. No. 33;
vative 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                 PRT;
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
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Matches 7; Conservative
                                                                                                                                                8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                         98 LLVPLQILL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 LLLPLQIII 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein.
                                                                                                                                                                                               1 LLLPLQILL 9
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                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical prot
ORFNames=PAB0088
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SEQUENCE
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Q91T40
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A Kara P.D., Afonso C.L., Wallace D.B., Kutish G.F., Abolnik C., Lu Z.,

A Vreede F.T., Taljaard L.C.F., Zask A., Viljoen G.J., Rock D.L.;

A vreede F.T., Taljaard L.C.F., Zask A., Viljoen G.J., Rock D.L.;

T "Comparative sequence analysis of the South African vaccine strain and
two virulent field isolates of Lumpy skin disease virus.";

Arch. Virol. 148:1335-1356(2003).

REMBL, AF400137; AAN02576:1; -..

RO; GO:000151; C:ubiquitin ligase complex; IEA.

GO; GO:000151; C:ubiquitin-protein ligase activity; IEA.

GO; GO:000157; F:zinc ion binding; IEA.

RO; GO:000157; P:zinc ion binding; IEA.

RO; GO:000157; P:zinc ion binding; IEA.

RO; GO:0015657; P:protein ubiquitination; IEA.

REMBL; RNOR7; SNO0744; RINGV; 1.

N Metal-binding; Zinc; Zinc-finger.

SEQUENCE 162 AA; 18835 MW; OEA24745C3818222 CRC64;
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Lumpy skin disease virus (LSDV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21329495; PubMed=11435593;
DO1=10.1128/JVI.75.15.7122-7130.2001;
Tulman E.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
"Genome of lumpy skin disease virus.";
J. Virol. 75:7122-7130(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                 87.5%; Score 35; DB 2; Length 152
77.8%; Pred. No. 5.7e+02;
ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                 1527 AA; 167943 MW; E942681FFC675AAE CRC64;
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88.9%; Pred. No. 1e+02;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 AA
                                                                                                                                                                                                                           PROSITE; PSS0929; ABC TMIF; 2.
PROSITE; PS00211; ABC TRANSPORTER_1; 2.
PROSITE; PS00301; ABC TRANSPORTER_2; 2.
PROSITE; PS00030; RRM_RNP_1; UNKNÖMN_1.
ATP-binding.
SEQUENCE 1527 AA; 167943 MW; E94268:
                     InterPro; IPR011527; ABC_membrane_1.
InterPro; IPR001140; ABC_TM transpt.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00064; ABC_membrane; 1.
Probom; PD00006; ABC_tran; 2.
Probom; PD00006; ABC_tran; 2.
Probom; PD00006; ABC_tran; 2.
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01-DEC-2001 (TrEMBLrel. 19, Last seq
InterPro; IPR003593; AAA_ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 77.8
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Best Local Similarity
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SEQUENCE FROM N.A.
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Matches
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LLLPLTIL 98

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MEDLINE=22710395; PubMed=12827464;

MEDLINE=227103974; PubMed=12827464;

MEDLINE=22710395; PubMed=1282764;

MEDLINE=22710395; PubMed=1282764;

MEDLINE=22710395; PubMed=1282764;

MEDLINE=22710395;

MEDLINE=23710395;

MEDLINE=2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Neethling;
Stiphnovich C., Vreede F.T., Kara P.D., Wallace D.B., Nel L.H.,
Viljoen G.J.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 1e+02;
0; Mismatches 1; Indels
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162 AA; 18782 MW; 5F914A4080F729EE CRC64;
091T40 PRELIMINARY; PRT; 162 AA. 091T40; 0-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Hypothetical protein (LAP/PHD-finger protein).
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                                                                                                                                                                                                                                                                                                                                                                                                Lumpy skin disease virus (LSDV)
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8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Capripoxvirus.
NCBI_TaxID=59509;
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37, Appl 8, Appli 11785, A 4, Appli 4, Appli

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Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence

70-767-39889

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TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-918-243-33
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셤
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Sequence 33, Appl
Sequence 3, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 7716, Appli
Sequence 7216, Appli
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Sequence 6, Appli
Sequence 112, Appli
Sequence 17, Appl
Sequence 16, Appli
Sequence 3, Appli
Sequence 3, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                 (without alignments)
34.552 Million cell updates/sec
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Sequence 36,
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Sequence 36
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Sequence 2
Sequence 1
                                                                                                                             July 13, 2005, 16:58:04; Search time 19.444 Seconds
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                                                                                                                                                                                                                                                                                                                                                                               513545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-502-600-33

US-09-918-243-33

US-08-957-146-2

US-08-824-874-3

US-09-154-344-2

US-09-154-344-2

US-09-154-344-2

US-09-106-138-2

US-09-106-138-2

US-09-764-762-3

US-09-764-762-3

US-09-949-016-7716

US-09-918-243-12075

US-09-918-243-135-19

US-09-918-243-19

US-08-918-243-19

US-08-918-243-19

US-08-918-243-19

US-08-339-152A-19

US-08-339-152A-17

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US-07-940-605A-12
                                                                                                                                                                                                                                                                                                                                       513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                          - protein search, using sw model
                                                                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                      US-09-905-083A-33
                                                                                                                                                                                                                                       1 LLLPLQILL 9
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Match Length
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                                                                                                                               Run on:
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7, Appli
7, Appli
4177, Ap
3902, Ap
21399, A
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Patent No. 6294344

GENERAL INFORMATION:

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of

TITLE OF INVENTION: Ovarian Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapa
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APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alebsandro.
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer FILE REFERENCE: D6223CIP/C/D/CIP
CURRENT APPLICATION NUMBER: US/09/918,243
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 33
LENGTH: 9
                                                                                                                                                                                                                                                                                                                   Sequence Sequence
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Residues 5-13 of the SCCE protein US-09-502-600-33
US-09-270-767-55106
US-09-393-634-37
US-09-489-0394-11785
US-09-489-0394-11785
US-09-489-0394-12646
US-08-001-711-4
US-08-09-299-7
US-09-407-427-7
US-09-513-9990-4177
US-09-513-9990-4177
US-09-513-9900-4177
US-09-513-9900-4177
US-09-619-388-10
US-09-869-388-10
US-09-869-388-10
US-09-869-388-10
US-09-869-388-10
US-09-869-388-10
US-09-869-388-10
                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: D6223CIP-C
CURRENT FILING DATE: 2000-02-11
CURRENT APPLICATION NUMBER: US/09/502,600A
PRIOR APPLICATION NUMBER: 09/039,211
PRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 136
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 33, Application US/09918243
Patent No. 6627403
GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 9; Conserv
                                                         Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1 CLASSIFICATION:
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TOPOLOGY: lin
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US-08-824-874-3
                ADDRESSEE:
STREET: 317
CITY: Palo
STATE: CA
                                                                                                                  ZIP: 94304
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                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                  US-08-557-146-2
; Sequence 2, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Egelrud, Torbjorn
; TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Rezyme (SCCE)
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
; STREET: 1155 Avenue of the Americas
; CITY: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Detentin release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: 424
ATORNEY/AGENT INFORMATION:
NAME: Sterior, Richard J.
REGISTRATION NUMBER: 35,372
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEPHONE: (212) 819-8783
TELEPHONE: REQUIRENTERIESTICS:
SEQUENCE CHARACTERISTICS:
                                                                                               Query Match

100.0%; Score 40; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
              NAME/KEY: CHAIN
OTHER INFORMATION: Residues 5-13 of the SCCE protein US-09-918-243-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08824874
Patent No. 5962300
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: protein
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Best Local Similarity
Matches 9; Conserv
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US-08-824-874-3
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MUDDESSEE: Incrye pherenceuticals, Inc.

STREET: 3174 Porter Drive
CTIY: Palo Alco
CTIV: Palo
CTIV: Palo Alco
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100.0%; Score 40; DB 3; Length 253; 100.0%; Pred. No. 3.6;
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OPERATING SYSTEM: DOS
SOFTWARE: FRAELSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                         US-09-210-084-3
; Sequence 3, Application US/09210084
; Patent No. 6197511;
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/210,084 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
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Patent No. 6472195
GENERAL INFORMATION:
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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TYPE: amino acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
Query Match
Best Local Similarity 100.
Matches 9; Conservative
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Matches 9; Conservative
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                                                                                                                             5 LLLPLQILL 13
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IMMEDIATE SOURCE:
                                                                                    1 LLLPLOILL
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CLONE: 532504
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US-09-764-762-3
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Fatent No. 6093397

GENERAL INFORMATION:

APPLICANT: Dixon, Eric P.

APPLICANT: Little, Sheila P.

TITLE OF INVENTION: AMPLIOID PRECURSOR PROTEIN PROTEASE AND TITLE OF INVENTION: RELATED NUCLEIC ACIDS

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Eli Lilly and Company

STREET: Lilly Company

CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 40; DB 2; Length 253; 100.0%; Pred. No. 3.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMABER: US/08/930,188
                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSITICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
TELEPHONE: 317-277-1090
TELEPHONE: 317-276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                             1103326-181
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COUNTRY: United States of America
US 08/557,146
                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFRENCE/DOCKET NUMBER: 11033
TELECHONE: (212) 819-878
TELEPHONE: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 mmino acids
  APPLICATION NUMBER: US 08 PILING DATE: 14-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                     : 253 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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MOLECULE TYPE: protein
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0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hillman, Jennifer L.
Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
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Ouery Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                         single
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PCT-US96-04294-2
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                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-949-016-7716
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APPLICANT: Dixon, Eric P.
APPLICANT: Dixon, Edward M.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND TITLE OF INVENTION: RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 253;
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                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OMPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NAMES: US/09/764,762
FILING DATE: 16-Jan-2001
CLASSIFICATION OF 'CURROWS'
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/210,084
FILING DATE: LUCKOWS 'CURROWS'
ATTONEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 9F-0252 US
TELEPHONE: 415-85-0555
TELEPHONE: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04294
               ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 40; DB 4
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 9; Conservative 0; Mismatches
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CLONE: 532504
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 253 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
CORRESPONDENCE ADDRESS:
                                                                                                  COUNTRY: USA
ZIP: 94304
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8; Conservative
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US-09-918-243-36
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          Matches
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Patent No. 629434

GENERAL INFORMATION:
APPLICANT: O'Enie, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer
FILE REFERENCE: D6223CIP-C
CURRENT APPLICATION NUMBER: US/09/502,600A
PRIOR APPLICATION NUMBER: 09/039,211
PRIOR APPLICATION NUMBER: 09/039,211
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 35
LENGTH: 9
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APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: Ovarian Cancer
FILE REFERENCE: D6223CIP-C
CURRENT FILING DATE: 2000-02-11
CURRENT APPLICATION NUMBER: U9/09/502,600A
PRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 136
LENGTH: 9
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Pred. No. 30;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Residues 6-14 of the SCCE protein US-09-502-600-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:

OTHER INFORMATION: Residues 4-12 of the SCCE protein US-09-502-600-36
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12075
LENGTH: 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36, Application US/09502600A Patent No. 6294344
                                                                                                          ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12075
                                                                                                                                                                                      95.0%;
88.9%;
                                                                                                                                                                                        Query Match
Best Local Similarity 88.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                               429 LLLPLOLLL 437
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                                                                                                                                                                                                                                                                           1 LLLPLOILL 9
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Best Local Similarity
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US-09-502-600-36
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| Sequence 36, Application US/09918243
| Patent No. 6627403
| GENERAL INFORMATION:
| APPLICANT: Cannon, Martin J.
| APPLICANT: Cannon, Martin J.
| APPLICANT: Santin, Alessandro:
| TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer:
| FILE REFERENCE: DE23CIP(C/C/D/CIP):
| CURRENT APPLICATION NUMBER: US/09/918,243
| CURRENT FILING DATE: 2001-07-30
| PRIOR FILING DATE: 2001-07-13
| NUMBER OF SEQ ID NOS: 136
| SEQ ID NO 36
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapa
                                                                                                                                                                                                                                                                                                 APPLICANT: Cannon, Martin J.
APPLICANT: Santon, Martin J.
APPLICANT: Santon, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
FILE REFERENCE: D6223CIP/C/D/CIP
CURRENT APPLICATION NUMBER: US/09/918,243
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 35
LENGTH: 9
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  0; Indels
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OTHER INFORMATION: Residues 4-12 of the SCCE protein US-09-918-243-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Residues 6-14 of the SCCE protein US-09-918-243-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 90.0%; Score 36; DB 4; Le Best Local Similarity 100.0%; Pred. No. 4.1e+05; Matches '8; Conservative 0; Mismatches 0;
0; Mismatches
                                                                                                                                                                            US-009-918-243-35; Application US/09918243; Sequence 35, Application US/09918243; Patent No. 6627403; Patent INFORMATION: APPLICANT: O'Brien, Timothy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 90.0
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LLPLOILL 9
                                              1 LLLPLQIL
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July 13, 2005, 17:29:45; Search time 64.8889 Seconds (without alignments) 53.584 Million cell updates/sec
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/cgnz 6/ptocate 1/puppaa/USO9B PUBCOMB.pep: *
/cgnz 6/ptocate 1/pubpaa/USO9B PUBCOMB.pep: *
/cgnz 6/ptocate 1/pubpaa/USO9 NEW PUB.pep: *
/cgnz 6/ptocate 1/pubpaa/USIOM_PUBCOMB.pep: *
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/ Cgn2_6/prodate//pubpaa/USO8_PUBCOMB.pep:*
/ Cgn2_6/prodate//pubpaa/USO8_PUBCOMB.pep:*
/ Cgn2_6/prodate//pubpaa/USO9_PUBCOMB.pep:*
/ Cgn2_6/prodate//pubpaa/USO9_PUBCOMB.pep:*
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/ Cgn2_6/prodate//pubpaa/USO0_PUBCOMB.pep:*
/ Cgn2_6/prodate//pubpaa/USO0_PUBCOMB.pep:*
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

(cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

(cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*)

(cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*)
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1726220 seqs, 386332138 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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40
1 LLLPLQILL 9
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 33, Appl	Sequence 33, Appl	Sequence 33, Appl	Sequence 33, Appl	Sequence 96, Appl	Sequence 92, Appl	Sequence 98, Appl	Sequence 3, Appli	Sequence 2, Appli	Sequence 48, Appl	Sequence 90, Appl
ID	US-09-918-243-33	US-09-905-083-33	US-10-372-521-33	US-10-831-075-33	US-10-262-511-96	US-10-262-511-92	US-09-888-615-98	US-09-764-762-3	US-10-071-214-2	US-10-071-214-48	US-10-264-283-90
98	6	σ	15	16	15	15	σ	σ	14	14	14
% Query Match Length DB	6	σ	6	σ	198	250	253	253	253	253	253
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	40	40	40	40	40	40	40	40	40	40	40
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1 LLLPLQILL

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RESULT 2

2 40	100.0	253	15	US-10-295-027-498	Sequence 498, App
40	100.0	253	19	1	63
40	100.0	253	16	-10-643-795A-95	e 95
40	100.0	253	17	US-10-948-518-95	95
40	100.0	253	17	-10-868-490A-	ų,
40	100.0	257	15	US-10-344-394-38	38
	95.0	70	15	US-10-424-599-207950	~
	90.0	σ	0	-916-	35
	0.06	σ	σ	918-243-3	36
36	90.0	σ	σ	US-09-905-083-35	Sequence 35, Appl
	0.06	σ	σ	US-09-905-083-36	36
	0.06	σ	15	US-10-372-521-35	9
	90.0	σ	15	US-10-372-521-36	m
	0.06	σ	16	US-10-831-075-35	m
36	90.0	σ	16	US-10-831-075-36	m
36	0.06	187	16	US-10-437-963-110905	-
35	87.5	66	16	5-34	'n
35	87.5	173	16	8-10-437-963-119	Sequence 119305,
34	85.0	53	σ,	US-09-864-761-46097	4
34	85.0	61	16	US-10-425-115-218429	ø
34	85.0	187	15	US-10-425-114-57128	5712
34	85.0	201	10	US-09-956-622A-39	
34	85.0	229	16	0	2273
34	85.0	369	18	10-	ĕ
34	85.0	369	18	US-10-820-155-64	Sequence 64, Appl
34	85.0	369	18	-10-	7
34	85.0	371	18	US-10-820-155-3	m
34	85.0	371	18	US-10-820-155-4	4
34	85.0	371	18	н	24,
34	85.0	371	18	US-10-820-155-54	
34	85.0	845	15	-10-282-1	518
33	82.5	46	15	-10-424-599-2	26594
33	82.5	28	16	US-10-437-963-156728	Sequence 156728,

ALIGNMENTS

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0; Mismatches
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CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR APPLICATION NUMBER: 60/373,917
PRIOR PILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR APPLICATION NUMBER: 60/381,039
PRIOR PILING DATE: 2002-10-09
FILE REFERENCE: D6223CIP/C/D/CIP3
CURRENT APPLICATION NUMBER: US/10/831,075
CURRENT FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 10/372,521
PRIOR FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 140
LENGTH: 9
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Publication No. US20040038223A1
GENERAL INFORMATION:
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Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
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Shenoy, Suresh G.
Shimkets, Richard A.
Rothenberg, Mark E.
Leach, Martin D.
Agee, Michele L.
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Miller, Charles E.
Rastelli, Luca
Stone, David J.
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Anderson, David W.
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Catterton, Elina
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APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
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                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 9; Conservative
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Gorman, Linda
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Li, Li
                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1 LLLPLQILL
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APPLICANT:
APPLICANT:
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APPLICANT:
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                 ## Sequence 33, Application US/09905083

| Patent No. US20020146708A1
| GENERAL INFORMATION:
| APPLICANT: O'Brien, Timothy J.
| TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer
| TITLE OF INVENTION: Ovarian Cancer
| TITLE OF INVENTION: Ovarian Cancer
| TITLE OF INVENTION: WINDER: US/09/905,083
| CURRENT APPLICATION NUMBER: US/09/905,083
| PRIOR APPLICATION NUMBER: US/09/905,000
| PRIOR FILING DATE: 2000-07-11
| NUMBER OF SEQ ID NOS: 136
| SEQ ID NO 33
| TYPE: PRT
| ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 33, Application US/1037251

Sequence 33, Application No. US20030223973A1

SERVERAL INFORMATION:
SEQUENCANT: O'Brien Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alesandro
ITILE OF INVENTION: Methods for the early diagnosis of ovarian cancer;
FILE REFERENCE: D6226TPF/C/D/CIP2
CURRENT APPLICATION NUMBER: US/10/372,521
CURRENT FILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-07-30

NUMBER OF SEQ ID NOS: 136

LENGTH: 9

LENGTH: 9
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APPLICANT: O'Brien, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
ITILE OF INVENTION: Methods for the early diagnosis of ovarian cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 40; DB 9; Length 9; 100.0%; Pred. No. 1.6e+06;
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                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CHAIN
OTHER INFORMATION: Residues 5-13 of the SCCE protein
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Best Local Similarity 100.
Matches 9; Conservative
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LILPLOILL 9
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        US-09-905-083-33
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
                                                                                                                                                     ö
                                                                                                          Length 9;
                                                                                                                                                  Indels
FEATURE:

NAME/KEY: CHAIN

OTHER | FORMATION: Residues 5-13 of the SCCE protein US-10-831-075-33
                                                                                                      100.0%; Score 40; DB 16; 100.0%; Pred. No. 1.6e+06;
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Query Match
Best Local Similarity 10v...
Seconservative
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TYPE: PRT
ORGANISM: Homo sapiens
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US-09-888-615-98
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Best Local Similarity
Matches 9; Conserv
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              PRIOR PLILAN JATES 201-10-09
PRIOR PLILAN LANDER: 60/3128,056
PRIOR PLILAND NUMBER: 60/3128,056
PRIOR PLILAND NUMBER: 60/313,260
PRIOR PLILAG DATE: 2002-04-19
PRIOR PLILAG DATE: 2002-04-19
PRIOR PLILAG DATE: 2002-04-19
PRIOR PLILAG DATE: 2001-04-19
PRIOR PLILAG DATE: 2001-10-05
PRIOR PLILAG DATE: 2001-10-
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
THER REPERENCE: 2402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
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PRIOR APPLICATION NUMBER: 60/326,483
PRIOR PILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR PILING DATE: 2002-05-17
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Publication No. US20040038223A1
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Patturajan, Meera
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Leach, Martin D.
Agee, Michele L.
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Malyankar, Uriel M
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Miller, Charles E.
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Anderson, David W.
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Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
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FILING DATE: 2002-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
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Best Local Similarity 100.
Matches 9; Conservative
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Li, Li
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ORGANISM: Homo sapiens
US-10-262-511-96
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PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-10-09
PRIOR PILING DATE: 2002-05-16
PRIOR PLING DATE: 2002-05-16
PRIOR PLING DATE: 2002-05-16
PRIOR PLING DATE: 2002-05-16
PRIOR PLING DATE: 2001-10-09
PRIOR PLING DATE: 2001-010-09
PRIOR PLING DATE: 2002-04-17
PRIOR PLING DATE: 2002-04-17
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
PRIOR PLING DATE: 2002-04-19
PRIOR PRIOR DATE: 2002-04-19
PRIOR PLING DATE: 2002-04-19
PRIOR DATE: 20
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CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: Patentin Ver: 2.1
SOFTWARE: 253
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TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
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APPLICANT: WHYTE, DAVID
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: WANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROFEASES
FILE REFERENCE: 038602/1214
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APPLICANT: HANSSON, Lennart
APPLICANT: BGELRUD, Torbjorn
TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
FILE REFERENCE: HANSSON=3A
CURRENT APPLICATION NUMBER: US/10/071,214
CURRENT FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: US 60/267,422
RIOR APPLICATION NUMBER: US 60/267,422
RIOR APPLICATION NUMBER: DK PA 2001 00218
PRIOR PILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Deduced amino acid sequence from the C-terminal part of SCCE from OTHER INFORMATION: homo sapiens.
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Publication No. US20030144494A1

GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF OVARIAN CANCER;
FILE REPERENCE: 210121.590
CURRENT APPLICATION NUMBER: US/10/264,283
CURRENT FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 111
SOFTWARE: Corixa Invention Disclosure Database
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Best Local Similarity 100.0%; Pred. No. 33;
Matches 9; Conservative 0; Mismatches 0; Indels (
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US-10-295-027-498
; Sequence 498, Application US/10295027
                                                                                                                                                                                                                                                                                  Sequence 48, Application US/10071214 Publication No. US20030066099A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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US-10-264-283-90
                                        1 LLLPLQILL 9
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US-10-264-283-90
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LENGTH: 253
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| Sequence 2, Application US/10071214 |
| Sequence 2, Application US/20030066099A1 |
| Sequence 2, Application No. US20030066099A1 |
| Publication No. US20030066099A1 |
| Publication No. US20030066099A1 |
| APPLICANT: HANSSON, Lennart |
| APPLICANT: BGELRUD, Toxbbjorn |
| TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN |
| FILE REPERENCE: HANSSON=3A |
| CURRENT APPLICATION NUMBER: US 60/267,422 |
| PRIOR APPLICATION NUMBER: US 60/267,422 |
| PRIOR PILING DATE: 2001-02-09 |
| PRIOR FILING DATE: 2001-02-09 |
| PRIOR PILING DATE: 2001-02-09 |
| NUMBER OF SEQ ID NOS: 50 |
| SEQ ID NOS: 50 |
| SEQ ID NO 2 |
| LENGTH: 253 |
| LENGTH: 253
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                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Diskete

COMPUTER: IBM Compatible

COMPUTER: IBM Compatible

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/764,762

FILING DATE: 16-Jan-2001

CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 09/210,084

FILING DATE: CURKNOWN-

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 36,749

RESPERENCE/DOCKET NUMBER: 96-0252 US

TELEPROMUNICATION INFORMATION:

                             ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLONE: 532504
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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CORRESPONDENCE ADDRESS:
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100.0%; Score 40; DB 15; Length 253; larity 100.0%; Pred. No. 33; Conservative 0; Mismatches 0; Indels (
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-04-12
PRIOR PILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 163
SOFTWARE: Patentin Ver. 2.1
LENGTH: 253
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APPLICANT: GRETCHEN FRANTZ
APPLICANT: KENNETH J. HILLAN
APPLICANT: PAUL POLAKIS
APPLICANT: ANDREW POLSON
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SUSAN D. SPENCER
THOMAS D. WU
ZEMIN ZHANG
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TYPE: PRT
CRGANISM: Homo sapiens
US-10-408-765A-639
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ORGANISM: Homo sapiens
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Matches 9; Conserv
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Sequence 49, Application US/10173999
Publication No. US20040005563A1
Sequence 40. Sequence 40. Sequence 40. Sequence 40. Sequence 40. Sequence 40. Sequence 40. Sequence 40. Sequence 40. Sequence 40. Sequence 40. Sequence 40. Sequence 40. Sequence 40. Sequence 40. Sequence 40. Sequence 40. Sequence 50. Sequence 50
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                                                                                                                                                                                                                    APPLICANT: Glah, Kurf C.
APPLICANT: Glah, Kurf C.
APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Mackov, Rosan R.
APPLICANT: Mareon, Susan R.
TYTLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Diagnosis of Cancer, CURENT Eos Biotechnology, Inc.
APPLICANT: Bos Biotechnology, Inc.
APPLICANT: Bos Biotechnology, Inc.
TYTLE OF INVENTION: Methods of Screening for Modulators of Cancer, CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-12
PRIOR FILING DATE: 2001-11-12
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-24
PRIOR FILING DATE: 2001-11-24
PRIOR FILING DATE: 2001-11-24
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-02-08
PRIOR FILING DATE: 2002-02-03
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NUMBER OF SEQ ID NOS: 1386
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    Publication No. US20030232350A1
                                                                                   APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
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Best Local Similarity 100.
Matches 9; Conservative
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COGGANISM: Homo sapiens
US-10-295-027-498
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LENGTH: 253
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APPLICANT: GACALIANS Soumitra S.
APPLICANT: Rahy, Boin D.
APPLICANT: Rahy, Boin D.
APPLICANT: Chang, Bing
APPLICANT: Chang, Bing
APPLICANT: Taylor, Steven W.
APPLICANT: Warnock, Dale B.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
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Search completed: July 13, 2005, 18:23:37 Job time : 68.8889 secs

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26 47 100.0 253 6 ABR58471 Abb58471 Human str 2 28 47 100.0 253 7 Abb68833 Adb80484 Ovarian C 28 47 100.0 253 7 Abb68833 Adb80484 Ovarian C 29 47 100.0 253 7 Abb68833 Adb83980 Cancer/an 30 47 100.0 253 8 Abb06515 Adb80515 Add106515 Human tum 31 47 100.0 253 8 Abb72880 Add106515 Human ova 33 47 100.0 253 8 Abb72880 Adr22326 Human ova 34 43 91.5 9 8 Abb6825 Ada608255 Human str 36 43 91.5 9 8 Abb68801 Adr68811 Human str 37 43 91.5 9 8 Abb68811 Adr68811 Adr68811 Human str 38 40 85.1 243 5 Abb84419 Adr68811 Adr68811 Human str 39 83.0 228 8 Abb04134 Adr68814 Ad	SULT 1 208239 AAE08239 standard; peptide; 9 A AAE08239; 01-NOV-2001 (first entry) Human stratum corneum chymotrypsin en Stratum corneum chymotrypsin en cancer; ovarian; breast; lung; antisense therapy; malignant hy	5-0050260 5AS. 5AS. comprises i 127pp; tes to di tes to di nin corne in di cati in in corne in di cati in merer. Th spant hyp spant in which in which
Copyr protein se July 13 US-09-9 ore: 47 UVNE Dle: BLOSUM6 Gapop 1 2105692 or of hits sa seq length:	Maximum Bs eq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database: A Geneseq 16Dec04:* 1: geneseqp1990s:* 2: geneseqp1990s:* 3: geneseqp2000s:* 5: geneseqp2001s:* 6: geneseqp2001s:* 7: geneseqp2001s:* 8: geneseqp2003bs:* 8: geneseqp2003bs:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the acore of the result being printed, and is derived by analysis of the total score distribution.

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immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                          antidiabetic; anorectic; antibacterial; virucide;
                                                                             Human NOV18e protein SEQ ID NO:100.
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2002US-0381037P.
2002US-0381038P.
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2002US-0373260P.
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                                              (first entry)
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N-PSDB; ADA05739.
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09-0CT-2001; 2
12-0CT-2001; 2
15-0CT-2001; 2
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22-OCT-2001;
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24-OCT-2001;
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01-NOV-2001;
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                 ADA05740;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for vaccinating an individual against SCCE, and in monitoring and developing immunotherapies for ovarian and other malignancies.
                                                                                                                                                                                                                                                  Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:34.
                 Gaps
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                 Indels
 Pred. No. 1.8e+06;
                 Mismatches
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100.08;
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Best Local Similarity 1000.
9; Conservative
                9; Conservative
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Matches 9; Conserv
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton B;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
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ADA05740 standard; protein; 97 AA.

RESULT 3
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         containers, the composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of secreening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (11) a method of treating a pathology associated with the polypeptide; (11) a method or modulating or preventing ansociated with the polypeptide; (12) an enthod for producing the above polypeptide in a method for producing the above polypeptide in useful in manufacturing a medicament for treating a sanctated with a human disease. The polypeptide or the nucleic acid molecule may be used to dispance, treat or prevent metabolic disorders such as Albahimer disorders and antilipaemic acide can above polypeptide in the proper acide can above polypeptide or prevent in the prosent sequenc
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05-OCT-2001; 3
09-OCT-2001; 2
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton B;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease
12-OCT-2001; 20010S-0328849P.
15-OCT-2001; 20010S-0329414P.
17-OCT-2001; 20010S-0330142P.
18-OCT-2001; 20010S-0330309P.
22-OCT-2001; 20010S-033026P.
24-OCT-2001; 20010S-0330266P.
                                                                                                                                                                                                                                                                         2002US-0373884P.
2002US-0374977P.
2002US-0381037P.
                                                                                                                                              29-OCT-2001; 2001US-0349575P.
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2002US-0373826P.
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GANGOLLI E A.
RIEGER D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPYTEK K A.
EDINGER S R.
ELLERMAN K.
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CATTERTON E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZERHUSEN B D.
ANDERSON D W.
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PEYMAN J A.
KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-213931/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMITHSON G.
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STONE D J.
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BERGHS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GORMAN L.
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The invention relates to isolated NoVX polypeptides and polymucleotides.

NoVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NoVX polypeptides. For example, NoVX polypeptides and activity of NoVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NoVX polypeptides by binding with the cells own genes and preventing their expression. NoVX polypucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NoVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators captivity of NoVX. The production of antibodies and in assays to identify and subject of antibodies and antagonists and condulate NoVX polypeptide expression and activity of NoVX polypeptides and polymucleotide expression and activity of NoVX polypeptides and polymucleotide expression and activity of MoVX polypeptides and polymucleotide expression and activity of adagonse and treat: metabolic disorders, diabetes, obesity, infectious disputes, anomaty and the machanisms and the amine associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence of a human NoVX protein.
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                                  Claim 1; SEQ ID NO 100; 395pp; English.
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23-AUG-2000; 2000US-00649167,
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Best Local Similarity 100.
Matches 9; Conservative
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39 VLVNERWVL 47
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reaction (PCR) primers, or isolated polymersele than the first of equences. (I) is useful as hybridisation probes, polymerse chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymotelectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging colypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of supplement. (II) and its binding partners are useful in medical imaging colypeptide and polymotelectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this pattent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in the printed specification.
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                                                                                                                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                        Claim 20; SEQ ID NO 53737; 103pp; English
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2001US-0327435P.
2001US-0327449P.
2001US-0328029P.
2001US-0328044P.
2001US-0328044P.
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Best Local Similarity 100...
9, Conservative
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09-OCT-2001; 2
09-OCT-2001; 2
09-OCT-2001; 2
                                                                                 biodiversity.
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Claim 1; Page 171; 586pp; English.
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                                                                                     (CURA-) CURAGEN CORP.
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                                                                                                                         N-PSDB; ADA05737
                                                                                                                                           pharmacogenomics
             22-OCT-2001; 24-OCT-2001; 24-OCT-2001;
                        29-OCT-2001;
                                      19-APR-2002;
                                                                              01-OCT-2002;
                                   19-APR-2002;
                                          19-APR-2002;
                                              19-APR-2002;
                                                  22-APR-2002;
                                                         16-MAY-2002;
                                                                17-MAY-2002;
                                                                           -JUN-2002
                                                            16-MAY-2002
                            01-NOV-2001
                                                                    28-MAY-2002
                                                                       29-MAY-2002
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human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopojetic disorder; dyslipidaemia; metabolic syndrome X;
                    probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
dyslipidaemias. The nucleic acids can also be used as hybridisation
                                                                                                                                                100.0%; Score 47; DB 6; Length 181; 100.0%; Pred. No. 2.3;
                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     ADN62902 standard; protein; 181 AA
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2001US-0327449P.
2001US-0328024P.
2001US-0328044P.
2001US-0328044P.
2001US-0338049P.
2001US-0339266P.
2001US-0339266P.
2001US-0343629P.
2001US-0343629P.
2001US-034362P.
2001US-034362P.
2001US-034362P.
2001US-0343637P.
2001US-0343815P.
2002US-0373815P.
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2002US-0373884P.
2002US-0374977P.
2002US-0381037P.
2002US-0381038P.
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                                                                                                                        Query Match
Best Local Similarity 100.v.
Best Aconservative
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PEYMAN J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMITHSON G.
                                                                                                                                                                                                                                1 VLVNERWVL
                                                                                                                                                                                                                                                                          39 VLVNERWYL
                                                                  present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  wasting disorder
                                                                                                        Sequence 181 AA;
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12-OCT-2001; 2
15-OCT-2001; 2
17-OCT-2001; 2
18-OCT-2001; 2
22-OCT-2001; 2
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09-OCT-2001;
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29-OCT-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human NOV18d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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(e.g. NOV1). Also described: (1) a composition comprising a polypeptide
described above and a carrier; (2) a kit comprising, in one or more
containers, the composition described above; (3) an isolated nucleic acid
molecule which encodes a NOVX protein of the invention; (4) a vector
comprising the ancience acid molecule described above; (5) a cell
comprising the bove vector; (6) an antibody that immunospecifically
binds to the polypeptide described above; (7) methods for determining the
presence or amount of the above polypeptide or nucleic acid molecule in a
sample; (8) methods for determining the presence of or predisposition to
a disease associated with altered levels of expression of the above
CC a disease associated with altered levels of expression of the above
CC a pathology asphology that is related to an aberrant expression or
aberrant physiological interactions of the polypeptide (11) a method of
cc screening for a modulator of activity or of latency or predisposition to
a pathology associated with the polypeptide; (12) a methods of treating
cc a pathology associated with the polypeptide in a
cc a pathology associated with the above polypeptide in a
cc a mammal; and (14) a method for producing the above polypeptide in a
cc an antidiabetic, anoretic, anothererial, virucide,
cc mammal; and (14) a method for producing the above polypeptide in a
cc antidiabetic, anotropic, neuroprotective, antiparkinsonian
cc an antilipament activities, and can be used in gene therapy. The
polypeptide is useful in manufacturing a medicament for treating a
syndrome associated with a human disease. The polypeptide or the nucleic
disorders such as diabetes or obesity, infections, cancer,
cc disorders such as diabetes or obesity, infections, cancer
cc disorders such as diabetes or obesity, infections, cancer
cc disorders such as diabetes or as Alzheimer's disease or Parkinson's
cd disease, immune disorders, haematopoletic disorders and various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dipippo VA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Catterton E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipipp Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                     2001US-0330142P.
2001US-0330309P.
2001US-0339266P.
2001US-0349575P.
2001US-0349575P.
2001US-0346357P.
2002US-0373260P.
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2002US-0381038P.
2002US-0381042P.
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2002US-0373826P.
2002US-0373884P.
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2002US-0383831P.
2002US-0391335P.
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The invention relates to isolated NOVX polypeptides and polynucleotides.

NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and activity of NOVX by supplementing the patient our polynucleotides may be used to treat disorders associated with decreased polynucleotides may be used to treat disorders associated with decreased production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polynucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the confidence of the production of antibodies and in assays to identify modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (agonists and antagonists) of the expression and activity of NOVX. The anti-NOVX polypeptide antibodies, agonists and antagonists may also be used to modulate NOVX polymcleotide expression and activity of NOVX polypeptides. The anti-NOVX polypeptide antibodies may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polymcleotides may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, haematopoietic disorders, and the various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dipippo VA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Malyankar UM;
I M, Catterton E;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyanka Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catt Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 98; 395pp; English.
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Patturajan M, Spytek KA,
Dit I, Gorman L, Zerhuman
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GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
                                                                                                                                                                      GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
                                                                                                                                                                                                                                                                        MILLER C E.
RASTELLI D.
STONE D J.
PENA C E A.
SHENOY S G.
SHENOY S G.
SHENOY B G.
ROTHENBERG M E.
                                                                                                                                        MALYANKAR U M.
                                                                    PATTURAJAN M.
                                                                                    SPYTEK K A.
EDINGER S R.
ELLERMAN K.
                                                                                                                                                                                                                                                                                                                                                                                                                 AGEE M L.
BERGHS C.
DIPIPPO V A.
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                                                                                                                                                                                                                                          CATTERTON E.
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 KEKUDA R.
                                                                                                                                                                                                                            ZHONG M.
                                                   GUO X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GANG/)
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(SHEN/)
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                                                                                                                                                                                                                                                                                         immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                Gaps
They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
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                                                                                                                                                                                                                                                                                numan; NOVX; antidiabetic; anorectic; antibacterial; virucide;
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                                                          8; Length 181;
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                                                      100.0%; Score 47; DB 8
100.0%; Pred. No. 2.3;
ive 0; Mismatches
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                                                                                                                                                                                     ADA05736 standard; protein; 198 AA.
                                                                                                                                                                                                                                                         Human NOV18c protein SEQ ID NO:96.
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18-0CT-2001; 2001US-0330309P.
22-0CT-2001; 2001US-0341058P.
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05-OCT-2001; 2001US-0327449P.
09-OCT-2001; 2001US-0327917P.
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                                                                                                                                                                                                                                  (first entry)
                                                                   Similarity 100.
9; Conservative
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                                                                                                     1 VLVNERWYL
                                                                                                                              39 VLVNERWVL
                                 Sequence 181 AA;
                                                                                                                                                                                                                                                                                                                                                                                      NO2003029424-A2.
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-OCT-2001;
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19-APR-2002;
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                                                         Query Match
Best Local
                                                                              Matches
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DIPIPPO V A
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                                                                                           Homo sapiens.
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16-MAY-2002;
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(KEKU/)
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(AGEE/)
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(DIPI/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHIM/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROTH/)
               The present invention describes NoVX proteins, where X can be 1 to 55

(e.g. NOV1). Also described: (1) a composition comprising a polypeptide
described above and a carrier; (2) a kit comprising, in one or more
containers, the composition described above; (3) an isolated nucleic acid
molecule which encodes a NOVX protein of the invention; (4) a vector
comprising the nucleic acid molecule described above; (5) a cell
comprising the above vector; (6) an antibody that immunospecifically
binds to the polypeptide described above; (7) methods for determining the
gresence or amount of the above polypeptide or nucleic acid molecule in a
sample; (8) methods for determining the presence of or predisposition to
a disease associated with altered lavels of expression of the above
polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
method of identifying an agent that binds to the polypeptide described
above; (10) a method for identifying a potential therapeutic agent for
use in treating a pathology that is related to an aberrant expression or
berrant physiological interactions of the polypeptide; (11) a method of
screening for a modulator of activity or of latency or predisposition to
a pathology associated with the polypeptide; (12) a method for modulating
the activity of the polypeptide described above; (13) methods of treating
cor preventing a pathology that above polypeptide. NoVX
sequences have antidiabetic, anorectic, antibacterial, virucide,
mammal; and (14) a method for producing the above polypeptide. NoVX
sequences have antidiabetic, anorectic, nutibacterial, virucide,
mammal; and (14) a method for producing the above polypeptide or producing a medicament for treating a
polypeptide is useful in manufacturing a medicament for treating a
polypeptide is useful in menufacturing a redicament for treating a
polypeptide is useful in menufacturing a redicament for treating a
polypeptide is useful in menufacturing a redicament for treating a
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Patturajan M, Spytek KA, Edinger SR, Ellerman, N, ...., Catterton E; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
                                                                                                                                                New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                            Claim 1; Page 170; 586pp; English
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                                                                                                    WPI; 2003-381626/36.
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Best Local Similarity
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                                                                                                                     N-PSDB; ADA05735
                                                                                                                                                                                               pharmacogenomics
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anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder;
        Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X; wasting disorder.
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2001US-0327917P.
2001US-0328029P.
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2002US-0381642P.
2002US-0383656P.
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18-OCT-2001; 2001US-0330309P.
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2001US-0349575P.
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SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
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PATTURAJAN M.
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ANDERSON D W.
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EDINGER S R.
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PEYMAN J A.
KEKUDA R.
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RASTELLI L.
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STONE D J.
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                                                                                                                      US2004038223-A1
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The invention relates to isolated NOVX polypeptides and polynucleotides. NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and polynucleotides may be used to treat disorders associated with decreased expression or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polynucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators
                                                                                                                          Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (agonists and antegonists) of the expression and activity NOVX. The anti-NOVX polypeptide antibodies, agonists and antagonists may also be anti-NOVX polypeptide antibodies, agonists and antagonists may also be used to modulate NOVX polynucleotide expression and activity of NOVX polypeptides. The anti-NOVX polypeptide antibodies may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polynucleotides may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious disorders, ancer-associated cachexia, neurodegenerative disorders, ancer-associated cachexia, neurodegenerative disorders, and the various dyslipidemmiss, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers.
                                                                                                                                                                                                                                                                                                                                                                                                 Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 96; 395pp; English.
EISEN A.
GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
                                                                                                                                                                                                                                                                                                                    WPI; 2004-213931/20.
                                                                                                                                                                                                                                                                                                                                               N-PSDB; ADN62899
                        (GANG/)
(RIEG/)
(SPAD/)
  (EISE/)
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Sequence 198 AA;

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Gaps
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0
100.0%; Score 47; DB 8; Length 198; ilarity 100.0%; Pred. No. 2.5; Conservative 0; Mismatches
                            Local Similarity
nes 9, Conserv
                Query Match
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Matches
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||||||||| 58 VLVNERWVL 66 1 VLVNERWVL 9

ADA05744 standard; protein; 224 AA. RESULT 10

06-NOV-2003 (first entry)

ADA05744;

Human NOV18g protein SEQ ID NO:104.

human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease;

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neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
                                                                                                                        05-OCT-2001; 2001US-0327435P.
05-OCT-2001; 2001US-0327449P.
09-OCT-2001; 2001US-0328044P.
09-OCT-2001; 2001US-0328044P.
09-OCT-2001; 2001US-0328044P.
12-OCT-2001; 2001US-0328044P.
15-OCT-2001; 2001US-0328044P.
15-OCT-2001; 2001US-0338044P.
16-OCT-2001; 2001US-0338049P.
24-OCT-2001; 2001US-0348629P.
24-OCT-2001; 2001US-0348629P.
24-OCT-2001; 2001US-0348629P.
24-OCT-2001; 2001US-0348629P.
24-OCT-2001; 2001US-0348629P.
24-OCT-2001; 2001US-0348639P.
24-OCT-2001; 2001US-034863P.
19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373816P.
19-APR-2002; 2002US-0373816P.
16-MAY-2002; 2002US-0373818P.
16-MAY-2002; 2002US-0373819P.
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17-MAY-2002; 2002US-0381642P.
28-MAY-2002; 2002US-0383656P.
25-MAY-2002; 2002US-0383831P.
25-UJN-2002; 2002US-0391335P.
01-OCT-2002; 2002US-0391335P.
                                                        402003029424-A2
                                      Homo sapiens
                                                                            10-APR-2003
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(CURA-) CURAGEN CORP.

Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton B; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Bisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

2003-381626/36. N-PSDB; ADA05743.

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New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics

Claim 1; Page 172; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of cor predisposition to a disease associated with altered levels of expression of the above

us-09-905-083a-34.rag

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polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide. NovX sequences have antidiabetic, anoredic, antibacterial, virucide, and antilipaemic activities, and can be used in gene therapy. The and antilipaemic activities, and can be used in gene therapy. The colypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease immune disorders, when the acide as hybridisation corporater, invancion. The present sequence represents a human NoVX from the present invancion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
                                                                                                                                                                                                                                                                                                                   Gaps
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2001US-032743P.
2001US-0327917P.
2001US-0328029P.
2001US-0328044P.
2001US-0328646P.
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2001US-0343629P
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                                                                                                                                                                                                                                                                                                       Local Similarity 100.
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                                                                                                                                                                                                                                                  present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wasting disorder
                                                                                                                                                                                                                                                                        Sequence 224 AA;
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09-0CT-2001;
09-0CT-2001;
12-0CT-2001;
15-0CT-2001;
17-0CT-2001;
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24-OCT-2001;
24-OCT-2001;
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05-OCT-2001;
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The invention relates to isolated NOVX polypeptides and polynucleotides. NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and polynucleotides may be used to treat disorders associated with decreased expression or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules
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17-APR-2002; 2002US-0373260P.
19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373817P.
19-APR-2002; 2002US-0373864P.
19-APR-2002; 2002US-0373864P.
22-APR-2002; 2002US-0374977P.
16-MAY-2002; 2002US-0381037P.
16-MAY-2002; 2002US-0381042P.
17-WAY-2002; 2002US-0381042P.
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2002US-0383831P.
2002US-0391335P.
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SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E.
LEACH M D.
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ZERHUSEN B D.
ANDERSON D W.
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EDINGER S R.
ELLERMAN K.
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PATTURAJAN M.
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PEYMAN J A.
KEKUDA R.
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CATTERTON E.
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RASTELLI L.
STONE D J.
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BERGHS C.
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                                                                                                                                                                                                                                                                                                                                                                                                                           (SPYT/)
(EDIN/)
(ELLE/)
(MALY/)
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(ZERH/)
(ANDE/)
(ZHON/)
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(ROTH/)
(LEAC/)
(AGEE/)
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(EISE/)
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may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX pulvaleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX. The anti-NOVX polypeptide antibodies, agonists and antagonists may also be used to modulate NOVX polypeptide antibodies may also be used to phypeptides. The anti-NOVX polypeptide antibodies may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polymocleotides may be used in this way to prevent, diagnostic agents for detecting the presence of NOVX in samples. NOVX diagnose and treat: metabolic disorders, diabetes, obesity, infectious discusses, Alzheimer's Disease, Parkinson's Disorder, immune disorders, hemenatopoietic disorders, and the various dyslipidaemias, metabolic may an infinite disorders associated with obesity, the metabolic syndrome X and may be used in this and various cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel extracellular serine protease, termed tumor antigen-derived gene 15 protein overexpressed in carcinomas and DNA encoding it, for diagnosis, treatment, prevention of cancer, particularly breast, ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                    They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 47; DB 8; Length 224; 100.0%; Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumour antigen-derived gene 15; serine protease;
Stratum Corneum Chymotryptic Enzyme; SCCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB98502 standard; protein; 225 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 VLVNERWYL 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 224 AA;
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The present invention relates to human tumour antigen-derived gene 15 (ThDE-15) protein and coding sequence (see AAH3601 and ABB98500). TABG-15 is an extracellular serine protease. It was found that TADG-15 is over-expressed in ovarian tumours. TADG-15 protein or its fragments of 9-20

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residues that lack TADG-15 protease activity are useful for vaccinating an individual against TADG-15, having, suspected of having or at risk of getting cancer. Furthernore, the TADG-15 gene can be used as a diagnostic or therapeutic target in cancer. The present sequence was used in a sequence homology alignment with the catalytic domain of TADG-15
                                                                                                                                                                                                                                                                                                                                         human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; metrodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                                             Gaps
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                                                                                                    100.0%; Score 47; DB 4; Length 225; 100.0%; Pred. No. 2.9;
                                                                                                                             0; Indels
                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                    Human NOV18f protein SEQ ID NO:102.
                                                                                                                                                                                                                                            ADA05742 standard; protein; 247 AA
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2001US-0327443P

2001US-0328024P

2001US-03280644P

2001US-03280644P

2001US-0328056P

2001US-0329144P

2001US-0339142P

2001US-0330142P

2001US-0330142P

2001US-034058P

2001US-034058P

2001US-034362P

2001US-034362P

2001US-034362P

2001US-034362P

2001US-034362P

2001US-034362P

2001US-0343637P

2002US-037386P
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2002US-0373884P.
2002US-0374977P.
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                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                               Local Similarity 100.
                                                                                                                                                                       30 VLVNERWVL 38
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                                                                                                                                                      1 VLVNERWVL
                                                                             Sequence 225 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003029424-A2
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09-0CT-2001; 2
112-0CT-2001; 2
15-0CT-2001; 2
17-0CT-2001; 2
18-0CT-2001; 2
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09-OCT-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                     Query Match
                                                                                                                            Matches
                                                                                                                                                                                                                   RESULT 13
ADA05742
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wasting disorder.
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                                                                                                                                    Homo sapiens.
   Human NOV18f.
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                                                                                                                                                                                                  26-FEB-2004.
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(ELLE/)
(MALY/)
(ORTT/)
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(RAST/)
(STON/)
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(PATT/)
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(SHEN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JIWMIC)
 The present line present the composition comprising a polypeptide described above and a carrier; (2) a kit comprising in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a Movy protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule date of the invention; (5) a cell comprising the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above; (10) a method of identifying an agent that binds to the polypeptide agent for above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating the activity of the polypeptide described above; (13) methods of treating a mammal; and (14) a method for production, and mammal; and (14) a method for production, and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in mannifacturing a medicament for treating a purposition of any antilipaemic activity and can be used in gene therapy. The polypeptide is useful in mannifacturing a medicament for treating a purposition of any antilipaemic and can be used in gene therapy. The polypeptide is useful in mannifacturing a medicament for treating a purposition of the polypeptide and the polypeptide in the polypeptide is useful in mannifacturing a medicament for treating and antilipaemic and antilipaemic and antilipaemic and antilipae
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                                                                                                Dipippo VA;
                                                                                                                                                                                              New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
                           Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Jiw, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                The present invention describes NOVX proteins, where X can be 1 to 55
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                                                                                                                                                                                                                                                                               Claim 1; Page 172; 586pp; English
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(CURA-) CURAGEN CORP.
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N-PSDB; ADA05741.
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tes 9; Conserv
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                                                                                                                                                                                                                                                  pharmacogenomics
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ID ADN6
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AC ADN6
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human, NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer: cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder haematopoletic disorder; dyslipidaemia; metabolic syndrome X;
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12-0CT-2001; 2001US-0328849P.
15-0CT-2001; 2001US-0339149P.
17-0CT-2001; 2001US-0330142P.
18-0CT-2001; 2001US-0330142P.
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2001US-0346357P.
2002US-0373260P.
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09-OCT-2001; 2001US-0328029P
09-OCT-2001; 2001US-0328044P.
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2001US-0343629P.
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2002US-0381038P
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2002US-0383831P
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EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
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RASTELLI D.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M ELEACH M D.
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PEYMAN J A.
KEKUDA R.
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CATTERTON E.
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The invention relates to isolated NOVX polypeptides and polynucleotides.

NOVX polypeptides and polynucleotides are used to prevent, diagnose or activity of NOVX polypeptides. For example, NOVX polypeptides and activity of NOVX polypeptides associated with decreased polynucleotides may be used to treat disorders associated with decreased expression or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX binding with the cells own genes and preventing their expression. NOVX binding with the cells own genes and preventing their expression. NOVX binding with the cells own genes and preventing their expression. NOVX binding with the cells own genes and preventing their expression. NOVX binding with the cells own genes and preventing their expression. NOVX binding with the cells of samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX.

Dilypeptides. The anti-NOVX polypeptide antibodies may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polymucleotides may be used in this way to prevent, diagnose and treat: metabolic disorders, obesity, infectious disorders, and the various disbetes, obesity, infectious clasorders, and the various disbetes, obesity, infectious thermal pages associated with obesity, the metabolic syndrome X and the used as any present and the used as any present and the used as any present.

The properties associated with obesity, the metabolic syndrome x and the page and the used as any present.
                                                                                                                                                                                                   Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     represents the amino acid sequence of a human NOVX protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 102; 395pp; English
                                                                           EISEN A.
GANGOLLI E A.
                                                                                                                           RIEGER D K.
SPADERNA S K.
                                                   DIPIPPO V A.
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-213931/20.
AGEE M L.
BERGHS C.
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                                                                                                   (GANG/)
(RIEG/)
(SPAD/)
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Gaps ö 100.0%; Score 47; DB 8; Length 247; 100.0%; Pred. No. 3.2; ative 0; Mismatches 0; Indels Best Local Similarity 100. Matches 9; Conservative 44 VLVNERWVL 52 1 VLVNERWVL 9 Query Match

ADA05732 standard; protein; 250 AA ADA05732; RESULT 15 ADA05732

Human NOV18a protein SEQ ID NO:92. 06-NOV-2003 (first entry) CX BX BX BX

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immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obseity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
                                                       immune disorder; haematopoietic disorder; dyslipidaemia
                                                                                                                                                                                                                                                                                   18-OCT-2001; 2001US-0330309P.
22-OCT-2001; 2001US-0330309P.
24-OCT-2001; 2001US-0343629P.
24-OCT-2001; 2001US-0349575P.
01-NOV-2001; 2001US-0349575P.
17-APR-2002; 2001US-0349575P.
19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373826P.
16-MAY-2002; 2002US-0381034P.
16-MAY-2002; 2002US-0381034P.
16-MAY-2002; 2002US-0381034P.
16-MAY-2002; 2002US-0381034P.
17-MAY-2002; 2002US-0381034P.
17-MAY-2002; 2002US-0381034P.
17-MAY-2002; 2002US-0381036P.
                                                                                                                                                                                                       09-0CT-2001; 2001US-0327917P.

09-0CT-2001; 2001US-0328029P.

09-0CT-2001; 2001US-0328054P.

12-0CT-2001; 2001US-032845P.

15-0CT-2001; 2001US-032845P.

15-0CT-2001; 2001US-032844P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2002US-0383831P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002; 2002US-00262511
                                                                                                                                                 02-OCT-2002; 2002WO-US031373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAY-2002;
                                                                               Homo sapiens
                                                                                                                            10-APR-2003,
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(CURA-) CURAGEN CORP.

Dipippo VA; Catterton E; Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton Ji W, Miller CE, Rastelli L, Stone DJ, Pena GEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipig Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK; Guo X;

WPI; 2003-381626/36. N-PSDB; ADA05731.

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New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.

Claim 1; Page 169-170; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the

presence or amount of the above polypeptide or nucleic acid molecule in a disease associated with altered levels of expression of the above polypeptide of a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method of modulating the activity of the polypeptide above; (13) methods of treating or or preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide in a mammal; and (14) a method for producing the above polypeptide; Novx sequences have antidiabetic, anorectic, antibacterial, virucide, immunomodulator, cytostatic, noctropic, neuroprotective, antiparkinsonian and antilipaemic activities, and can be used in gene therapy. The cylypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic cidisorders such as diabetes or obestiv; infections, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various cypobes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NoVX from the

Sequence 250 AA;

Gaps ö Query Match

100.0%; Score 47; DB 6; Length 250;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 0; Indels

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Search completed: July 13, 2005, 17:19:52 Job time: 77.6667 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

July 13, 2005, 16:54:03; Search time 13.5556 Seconds Run on:

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63.882 Million cell updates/sec

US-09-905-083A-34 Perfect score: Title:

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Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Deectivity		u	complement factor	tissue kallikrein	neuropsin - mouse	hypothetical prote	3.4	m	_				serine proteinase	A20R protein - vac	probable 49.1K pro	A22R protein - var	hypothetical prote	A21R protein - var		hypothetical prote		3.4.	(EC 3.4.	trypsin (EC 3.4.21	8	⊞			haptoglobin Hpp -	
£		A53968	DBHU	KQPG	IS6559	T25594	T01779	S31384	S44184	S49129	T05892	F82825 .	A45161	D42519	T37408	C72166	T28563	C36850	T47075	T25570	S31778	S31776	S31775	S49489	A25852	JC2479	95	I36945	694	147078
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ribosomal protein	hypothetical prote	haptoglobin precur	haptoglobin - chim	haptoglobin - chim	haptoglobin precur	haptoglobin - blac	haptoglobin-relate	haptoglobin - chim	haptoglobin precur	branched-chain-ami	coagulation factor	acrosin (EC 3.4.21	hypothetical prote	unknown protein [i	probable membrane
E70472	A83757	HPDG	136941	136942	нрнил	900005	HPHUR	I36944	HPHU2	T46034	KFBO	S11674	G96695	C86443	S54045
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274	282	329	345	346	347	347	348	349	406	410	416	421	453	505	539
74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5	74.5
35	35	35	35	32	35	32	35	32	32	32	32	35	35	35	35
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

serine proteinase SCCE precursor - human

WiAlternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
C;Date: 07-0u1-1995 #sequence_revision 07-Ju1-1995 #text_change 09-Ju1-2004
C;Accession: A53968 #sequence_revision 07-Ju1-1995 #text_change 09-Ju1-2004
B;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Bgelrud, T.
J. Biol. Chem. 269, 19420-19426, 1994
A;File: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A;Reference number: A53968; MuID:94308225; PMID:8034709

A)Sratus: preliminary
A,Molecule type: mRNA
A,Residues: 1-253 «HAN»
A)Cross-references: UNIPROT:P49862; GB:L33404; NID:g521214; PIDN:AAC37551.1; PID:g532504
C)Genetics:

A;Gene: GDB:PRSS6; SCCE
A;Cross-references: GDB:377730
A;Map position: 7435-7435
C;Superfamily: trypsin; trypsin homology
F;30-245/Domain: trypsin homology

Gaps ö Query Match 100.0%; Score 47; DB 2; Length 253; Best Local Similarity 100.0%; Pred. No. 0.26; Matches 9; Conservative 0; Mismatches 0; Indels

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RESULT 2

Complement factor D (EC 3.4.21.46) precursor [validated] - human (fragment)
NyAlternate names: adipsin; C3 convertase activator
C5pecies: Homo sapiens (man)
C5pecies: Homo sapiens (man)
C5pecies: A40197; A00936; A60571; S66645
R7White, R.Y.; Damm, D.; Hancock, N.; Rosen, B.S.; Lowell, B.B.; Usher, P.; Flier, J.S.;
J. Biol. Chem. 267, 9210-9213, 1992
A;Title: Human adipsin is identical to complement factor D and is expressed at high level
A;Accession: A40197; MUID:92250520; PMID:1374388
A;Accession: A40197
A;Molecule type: mRNA
A;Cossion: A40197
A;Cossion: A40936; MUID:85000441; PMID:6383466
A;Reference number: A00936; MUID:85000441; PMID:6383466

a

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F;41,89,184/Active site: His, Asp, Ser #status experimental F;78/Binding site: carbohydrate (Asn) (covalent) #status experimental F;225/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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77.8%;
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Best Local Similarity 77.8.
Section 7; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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219 VLINERW 225
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: CESP: C32E8.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuropsin - mouse
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C;Comment: The protein consists of two chains, A and B, held together by disulfide bonds C;Comment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release I C;Comment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release I C;Superfamily: trypsin homology
C;Superfamily: trypsin homology crRy>
F;1-224/Domain: trypsin homology crRy>
F;1-224/Domain: trypsin homology crRy>
F;1-80/Product: tissue kallikrein chain A #status experimental <MPTA>
F;3-92/Product: tissue kallikrein chain B #status experimental <MPTB>
F;3-144,26-42,121-190,155-169,180-205/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 19-20, XX', 23-27, XX', 30-31,'XX', 34,'X', 36-40 <MIY>
R;Balke, N.; Holtkamp, U.; Hoerl, W.H.; Tschesche, H.
PEBS Lett. 371, 300-302, 1995
A;Title: Inhibition of degranulation of human polymorphonuclear leukocytes by complement A;Reference number: S66645; MUID:96013156; PMID:7556615
                                         A; Residues: 19-44, 'G', 46-51, 'Q', 53-75, 'TH', 78, 'P', 80-83, 'XXXITIE', 90-172, 86-91, 185-235,' A; Note: a few residues were assigned from the previously published sequence of Reid et a Ryimyata, T.; Oda, O.; Inagi, R.; Sugiyama, S.; Miyama, A.; Maeda, K.; Nakashima, I.; Ya Ma, Immunol. 27, 537-644, 1990
A; Tille: Molecular and functional identification and purification of complement component A; Reference number: A60571; MUID:90370044; PMID:2395435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Status: preliminary
A,Molecule type: protein
A,Residues 19-44, '0',46-48 <BAL>
C,Comment: Factor D cleaves factor B when the latter is complexed with factor C3b, activ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 1-49, GML, 53-134, D', 136-156, 'H', 158, 'B', 160-224, 'B', 226-232 <TSC>
A; Residues: 1-49, GML, 53-134, D', 136-156, 'H', 158, 'B', 160-224, 'B', 226-232 <TSC>
A; Note: the residue identified as 225-Asx is bound to carbohydrate; therefore, we have so that the contact of the cont
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N;Alternate names: glandular kallikrein; kininogenin
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 31-Dec-1993 #text_change 31-Mar-2000
C;Accession: A00938; A92895
R;Tschesche, H.; Mair, G.; Godec, G.; Fiedler, F.; Ehret, W.; Hirschauer, C.; Lemon, Av. Exp. Med. Biol. 120, 245-260, 1979
A;Title: The primary structure of porcine glandular kallikreins.
A;Accession: A00938
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A; Map position: Xpter-Xqter
C; Superfamily: trypsin; trypsin homology
C; Superfamily: trypsin; trypsin homology
C; Keywords: complement alternate pathway; hydrolase; plasma; serine proteinase
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-246/Product: complement factor D. (fragment) #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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F;44-60,141-207,172-188,197-222/Disulfide bonds: #status predicted
F;59,105,201/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.0%; Score 39; DB 1; Length 246;
88.9%; Pred. No. 7.8;
ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 88.5
. . . 8; Conservative
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    A; Molecule type: protein
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                                                                                                                                                                                                                                                                                                                           A;Accession: A60571
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R;Chen, Z.L.; Yoshida, S.; Kato, K.; Momota, Y.; Suzuki, J.; Tanaka, T.; Ito, J.; Nishinc J.; Neurosci. 15, 5086-5097, 1995
A;Title: Expression and activity-dependent changes of a novel limbic-serine protease gene A;Reference number: 156559; MUID:95348817; PMID:7623137
A;Accession: 156559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:061955; GB:D30785; NID:g1648847; PIDN:BAA06451.1; PID:g102009
C;Superfamily: trypsin; trypsin homology
F;33-252/Domain: trypsin homology <TRY>
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CiDate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
CiDate: 12-Sep9 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
CiAccession: T25594
R;Gattung, S.
Rsbattung, S.
Rbbatticed to the EMBL Data Library, February 1997
A;Description: The sequence of C. elegans cosmid C32E8.
A;Reference number: Z20056
                                                                                                                                                                                                                                                                                                                     C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: 156559
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     Length 232
                                                        Indels
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Score 38; DB 1;
Pred. No. 11;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary, translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-417 <GAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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Pred. No. 21;
1; Mismatches
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Mismatches
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Pred. No.
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A;Introns: 22/3; 51/2; 92/1; 297/1; 354/1
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NiAlternate names: chymotrypsin-like proteinase MNHYMI
C;Species: Anopheles gambiae (African malaria mosquito)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: S49129; S44185
R;Mueller, H.
submitted to the EMBL Data Library, November 1992
A;Description: Cloning of blood meal induced serine protease genes of the mosquito Anophe A;Reference number: S35412
A;Reference number: S35412
A;Reference number: S35412
A;Residues: 1-259 cMUE
A;Residues: 1-250 cMUE
A;Residues: 1-200 cMUE
A;Residues: 1-200 cMUE
A;Residues: 1-200 cMUE
A;Residues: 1-200 cMUE
A;Residue
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 13-Aug-1999
C;Accession: T05892
R;Bevan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Bancroft, I.; Mewet
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A;Cross-references: EMBL:Z18888; NID:g509416; PIDN:CAA79326.1; PID:g509417
C;Genetics:
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A;Residues: 1-259 <MU2>
A;Cross-references: EMBL:Z32645; NID:g474026; PIDN:CAAB3568.1; PID:g474028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.7%; Score 37; DB 1; Length 258; 75.0%; Pred. No. 19; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.7%; Score 37; DB 1; Length 259; 75.0%; Pred. No. 19;
                                                                                          A; Introns: 78/2; 209/3
C;Superfamily: trypsin; trypsin homology
C;Superfamily: trypsin; trypsin digestion; serine proteinase
C;Keywords: hydrolase; protein digestion; serine proteinase
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-32/Domain: signal sequence #status predicted <PRO>
F;32-258/Domain: trypsin homology <TRY>
F;59-75,182-198,208-232/Disulfide bonds: #status experimental
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F;33-250/Domain: trypsin homology <TRY>
F;59-75,182-198,208-232/Disulfide bonds: #status experimental
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C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; protein digestion; serine proteinase
E;1-17/Domain: signal sequence #status predicted <SIG>
F;18-32/Domain: activation peptide #status predicted <PRO>
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63 LLNDRWVL 70
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63 LLNDRWVL 70
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Best Local Similarity
Matches 6; Conserv
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9
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Matches
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N;Alternate names: chymotrypsin-like proteinase ANCHYM2
C;Species Anopheles gambiae (African malaria mosquito)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: S44184; S49130
C;Accession: Catteruccia, F.; Crisanti, A.
Shwaller, H.M.; Catteruccia, F.; Crisanti, A.
Submitted to the EMBL Data Library, April 1994
A;Description: An Anopheles gambiae locus containing the sequences of two closely relate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Mueller, H.
submitted to the EMBL Data Library, November 1992
A;Description: Cloning of blood meal induced serine protease genes of the mosquito Anoph
A;Reference number: $35412
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A;Residues: 1-258 <MUE>
A;Cross-references: UNIPROT:Q17025; EMBL:Z32645; NID:g474026; PIDN:CAA83567.1; PID:g4740
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C;Species: Pleuronectes platessa (plaice)
C;Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
                      Species: Pleuronectes platessa (plaice)
Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 16-Jul-1999
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C;Superfamily: trypsisir, trypsin homology
C;Keywords: hydrolaes; protein digestion; serine proteinase
P;23-242/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; protein digestion; serine proteinase
F;23-242/Domain: trypsin homology <TRY>
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19;
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Pred. No. 19;
2; Mismatches
                                                                                                                                                                                                                                                                               Status: preliminary; translated from GB/EMBL/DDBJ
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submitted to the EMBL Data Library, November 1990
A;Reference number: S30567
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               C;Species: Pleuronectes platessa (plaice)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-199
C;Accession: T01779
R;Leaver, M.J.; George, S.G.
submitted to the EMBL Data Library, March 1996
A;Reference number: 214422
A;Accession: T01779
A;Stetus: preliminary; translated from GB/EMBL/DD
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.7%; Score 37; DB 66.7%; Pred. No. 19; iive 2; Mismatches
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66.7%;
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Matches 6; Conservative
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50 VLINNQWVL 58
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Best Local Similarity
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A,Molecule type: mRNA
A,Residues: 1-250 <LEA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: S31384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S31384
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GB:L05175; NID:g206691; PIDN:AAA42056.1; PID:g206692
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A;Note: host Homo sapiens (man)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 09-Jul-2004
C;Accession: D42519
R;Johnson, G.P.
B;Johnson, G.P.
A;Reference number: A33172
A;Reference number: A33172
A;Reference number: A3049
A;Reference number: A3049
A;Residues: 1-426 <JOH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.6%; Score 36; DB 2; Length 426; 55.6%; Pred. No. 50; 1; Indels tive 3; Mismatches 1; Indels
A; Reference number: A45161; MUID: 93077530; PMID: 1447189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P20995
C;Superfamily: vaccinia virus probable 49.1K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D42519
A20R protein – vaccinia virus (strain Copenhagen)
                                                                                                                                                                                                                                                                                                               Score 36; DB 2
Pred. No. 29;
3; Mismatches
                                                                                                                                               A,Cross-references: UNIPROT:003238; GB:LCC; Superfamily: trypsin; trypsin homology C; Keywords: hydrolase; serine proteinase F;21-245/Domain: trypsin homology <TRY>
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                                                                                                                                                                                                                                                                                                                     76.6%;
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Best Local Similarity 66.7
Matches 6; Conservative
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Matches 5, Conservative
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Best Local Similarity 55.6
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VLVNERWVL
                             A;Accession: A45161
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-258 <SMY>
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A;Introns: 72/3; 142/3; 227/2; 344/3; 372/3; 941/2; 1016/3; 1038/3; 1055/1; 1095/2; 1155
A;Note: F6H11.110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C)Accession: F82825
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Astricle: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: F82825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rismpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Ba.Netto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

Bubmitted to Genbank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Unqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.M.; Athuthors: Martins, E.G.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, A.Y.; Mench, C.; G. Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Aluthors and Silva, A.C.R.; da Silva, A.M.; Sawasak Aluthors and Silva, A.C.R.; da Silva, A.M.; Salva and A.R.; Tauhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zakeference number: AS9328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         serine proteinase (EC 3.4.21.-) RNK-Met-1 - rat (fragment)
(Species Rattue norvegicus (Norway rat)
(Species Rattue norvegicus (Norway rat)
(Species 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
(SAccession: A45161
(Sanyth, M.J.; Willrout, T.; Trapani, J.A.; Ottaway, K.S.; Sowder, R.; Henderson, L.E.;
(Ssnyth, M.J.; Willrout, T.; Trapani, J.A.; Ottaway, K.S.; Sowder, R.; Henderson, L.E.;
(Sindth, M.J.; Willrout, T.; Trapani, J.A.; Ottaway, R.S.; Sowder, R.; Henderson, L.E.;
(A); Sincl. Chem. 267, 24418-24425, 1992
(A); Title: Purification and cloning of a novel serine protease, RNK-Met-1, from the granul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q9PGL9; GB:AE003881; GB:AE003849; NID:g9105093; PIDN:AAF8309
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 1.1e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 72
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                                                                                                                  A,Residues: 1-1421 <BEV>
A,Cross-references: EMBL:AL021684
A,Experimental source: cultivar Columbia; BAC clone F6H11
   submitted to the Protein Sequence Database, April 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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Pred. No. 7.7;
3; Mismatches
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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                             A;Reference number: Z15456
A;Accession: T05892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-72 <SIM>
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                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                       C; Genetics:
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C;Species: vaccinia virus
A;Vaziety: strain Ankara
C;Vatety: strain Ankara
C;Vatety: strain Ankara
C;Accession: T37408
R;Antoine, G.; Scheiflinger, F.; Falkner, F.G.; Dorner, F.
submitted to the EMBL Data Library, March 1997
A;Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strair
A;Reference number: Z20877
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A;Residues: 1-426 <ANT>
A;Cross-references: UNIPROT:057228; EMBL:U94848; PIDN:AAB96523.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 426;
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probable 49.1K protein - vaccinia virus (strain Ankara)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: vaccinia virus probable 49.1K protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 2;
Pred. No. 50;
3; Mismatches
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A,Status: preliminary, translated from GB/EMBL/DDBJ
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RESULT 15 C72166

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R;Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar submitted to GenBank, March 1998
A;Description: Analysis of the complete coding sequence of DNA of alastrim variola minor A;Reference number: A72150
A;Accession: C72166
A;Scatus: preliminary
A;Molecule type: DNA
A;Residues: 1-426 <SHC>
A;Accossruerie references: UNIPROT:Q89166; GB:Y16780; NID:g5830555; PIDN:CAB54724.1; PID:g5830655; C;Genetics: C;
A22R protein - variola minor virus (strain Garcia-1966)
C;Species: variola minor virus
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 09-Jul-2004
C;Accession: C72166
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C, Superfamily: vaccinia virus probable 49.1K protein
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130 VLLNNRWIM 138
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Search completed: July 13, 2005, 17:31:29 Job time: 14.5556 secs

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P49862 homo sapien OB15n3 homo sapien OB15n3 homo sapien OB16n3 rabidopsis OB378 ctenocephal OF328 ctenocephal OF328 ctenocephal OF52 sus scrofa O61955 sus scrofa O61959 solanum tub O95ny8 solanum tub P9113 caenorhabdi O95ny8 solanum tub P9113 caenorhabdi O70nh8 chromobacte O67pwl symbiobacte O67pwl symbiobacte O69204 dissostichu O788v dissostichu O788v dissostichu O788v dissostichu O9946k oncochenia P35034 pleuronecte O97098 anopheles a
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                                                                        July 13, 2005, 16:15:23; Search time 62.2222 Seconds (without alignments) 74.069 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                      1612378
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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09JFW3
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09XY58
07SZE2
066PG8
KLK PIG
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NRPN_RAT
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Maximum Match 100%
Listing first 45 summaries
                                                   OM protein - protein search, using sw model
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Q9SNY9
P91123
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Q67PW1
Q9PTS1
Q8UUJ1
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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Match Length DB
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Perfect score:
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Maximum DB e
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VSP4_TRIMU VSP5_TRIMU VSP7_TRIMU

013062 trimeresuru Q71qi5 trimeresuru Q71qi7 trimeresuru Q71qi0 trimeresuru Q901ja agkistrodon Q17025 anopheles g Q9xy53 attenocephal Q7szel gloydius sa Q27x89 anopheles g Q8uk2 crotalus ad Q9d£68 trimeresuru Q8qhk3 crotalus at	Ø	253 AA. ppdate) update) (Stratum corneum chymotryptic	Vertebrata; Euteleostomi; i; Hominidae; Homo.	3. Wallbrandt P., Carlstein A., on of stratum corneum an serine proteinase.";	P.; and tissue expression of the rayme gene."; ank/bDBJ databases.	00)00382-6; t R., Lei H., McCuaig J., he serine protease gene on.";	<pre>I M., Edholm E., Tornell J., corneum chymotryptic enzyme in attitis."; ank/DDBJ databases.</pre>	ud T.; of recombinant human stratum corneum 211:586-589(1995). degradation of intercellular cohesive layer of the skin in the continuous
VSPC TRIGA Q71QI5 Q71Q10 Q71Q10 Q9PTL3 Q9YGJ9 CTR2 ANOGA Q9X53 Q7SZE1 CTR1 ANOGA GBUTK2 VSP1 TRIJE VSP1 TRIJE	ALIGNMENTS	PRT; nence u ptation:21)	œ; Craniata; Catarrhin	OF 23-5 kman A., terizati ific hum	426 (1994). damandis B.P., mapping and tryptic enzymer. EMBL/GenBank.	6/S0378-1119((rgonza-Barrett ; analysis of tl me 19913 regi	(A., Edlund M., Edho of stratum corneum of ithchy dermatitis."	
257 2 257 2 257 2 257 2 257 2 257 2 257 2 257 2 257 2 258 2 25		STANDARD; tel. 34, Creat tel. 34, Last tel. 45, Last recursor (EC	ms=PRSS6, lan). la; Chordat a; Primate		<pre>J. Biol. Chem. 269:19420-19426(1994). [2] [2] [2] INDERINATION N.A. TISSUB=Keratinocytes; Yousef G.M., Scorilas A., Diamandis B.P.; "Molecular characterization, mapping and tissue human stratum corneum chymotryptic enzyme gene. Submitted (DEC-1999) to the EMBL/GenBank/DDBJ of the EMBL/GenBa</pre>	[3] SEQUENCE FROM N.A. SEGUENCE FROM N.A. PUDMEd=11054574; DOI=10.1016/S0378-1119(00)00382-6 Gan L., Lee I., Smith R., Argonza-Barrett R., Lei i Moss P., Paeper B., Wang K.; "Sequencing and expression analysis of the serine j cluster located in chromosome 19q13 region."; Gene 257:119-130(2000)	OM N.A. Backman A., Ny A. P., Egelrud T.; overexpression of tel for chronic it DEC-2000) to the	CHARACTERIZATION. CHARACTERIZATION. MEDLINE=95314630; PubMed=7794273; Skytt A., Stroemqvist M., Egelrud "Primary substrate specificity of chymotryptic enzyme."; Chymotryptic enzyme."; Biochem. Biophys. Res., Commun. 21: Biochem. Biophys. Res., commun. 21: Structures in the cornified 1:
2 37 78 4 4 37 78 6 6 6 9 37 78 8 8 37 78 8 8 9 78 78 8 9 78 9 78 9 9 78 9 9 78 9 9 78 9 9 78 9 9 78 9 9 78 9 9 9 78 9 9 9 9	LT 1 HUMAN	KLK7 HUMAN P49862; 01-OCT-1996 (F 01-OCT-1996 (F 25-OCT-2004 (F Kallikrein 7 F	enzyme) (hSCCE) Name=KLK7; Syronyms=PRSS6, Homo aspiens (Human). Eukaryotes; Metazoa; Chorda Mammalia; Eutheria; Primat. NCBI_TAXID=9606;	[1] SEQUENCE FROM N.A., TISSUB-SKin; MEDLINE=94108225; P. Hansson L., Stroemq Egelrud T., Stroemq "Cloning, expression "Cloning, expression chymotryptic enzyme	J. B101. Chem [2] SEQUENCE FROM TISSUE=Keratin Yousef G.M., MOlecular Chhuman stratum Submitted (DEM Submitted	[3] SEQUENCE FROM PubMed=110545 Gan L., Lee I Moss P., Paep "Sequencing a "Sequencing a cluster locat Gene 257:119-	[4] SQUENCE FROM N.A. Hansson L., Backman A., Ny Wallbrandt P., Egelrud T., Epidermal overexpression mice; a model for chronic Submitted (DEC-2000) to th	[5] CHARACTERIZATION. MEDLINE=95314630; Pu Skytt A., Stroemqvis "Primary substrate s chymotryptic enzyme. pliochem. Biophys. Re -!- FUNCTION: May ca
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Altschul S.E., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.E., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.E., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Krywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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"Generation and initial analysis of more than 15,000 full-length human
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                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:MBK23.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                              MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
L. Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032005; AAH32005.1; -.
EMBL; BC032005; JEZX.
R. GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:peptidase activity; IEA.
R. GO; GO:0006239; F:peptidase activity; IEA.
R. GO; GO:0004295; F:peptidase activity; IEA.
R. GO; GO:0004295; F:peptidase GI.
R. InterPro; JRR001314; Peptidase SI.
InterPro; JRR001314; Peptidase SI.
InterPro; JRR001314; Peptidase SI.
R. Fam; PR00089; Trypsin; I.
R. PRINTS; PR00089; Trypsin; I.
R. PRNNTS; PR00020; Trypsin; I.
R. PROSITE; PS00134; TRYPSIN DOM; I.
R. PROSITE; PS00134; TRYPSIN DOM; I.
R. PROSITE; PS00135; TRYPSIN HIS; UNKNOWN_I.
R. PROSITE; PS00135; TRYPSIN HIS; UNKNOWN_I.
R. PROSITE; PS00135; TRYPSIN PROFESSE.
R. PHYDROLAGES; PECTERSE; I.
R. PROSITE; PS00135; TRYPSIN PROFESSE.
R. PROFESSE.

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  Stratum corneum chymotryptic enzyme, preproprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.
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                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissue=skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   residues with aromatic side chains in the PI position. SCCE cleaves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-Phe-|-Tyr-26, and 26-Tyr-|-Thr-27, Could play a role in the activation of precursors to inflammatory cytokines.

TISSUE SPECIFICITY: Abundantly expressed in the skin and is expressed by keratinocytes in the epidermis. Very low levels are also seen in the brain and kidney.

SIMILARITY: Belongs to the peptidase SI family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
shedding of cells from the skin surface. Specific for amino acid
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(By similarity).
(By similarity).
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2D68B6B15A76A668 CRC64;
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Last annotation update)
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Kallikrein 7.
Charge relay system (ECharge relay system (ECharge relay system (By similarity.
By similarity.
Allinked (GlCNAC...)
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EMBL; AF166330; AAD49718.1; -.
EMBL; AF245227; AAG33360.1; -.
EMBL; AF332583; AAK69624.1; -.
PIR; A53968; A53968.
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58 VLVNERWVL 66
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                                                                                                                                                                                                                                 subfamily.
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QBN5N9;
01-OCT-2002 (
01-OCT-2002 (
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Matches
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaines P.J., Sampson C.M., Rushlow K.E., Stiegler G.L.; "Cloning of a family of serine protease genes from the cat flea Ctenocephalides felis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ctenocephalides felis (Cat flea).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Siphonaptera; Pulicidae; Pulicinae;
Ctenocephalides.
                                                                                                                                                                                                                                                                                                                                                          Spilliaert R.; "Atlantic Cod Trypsin Y - Member of a Novel Trypsin Group."; Mar. Biotechnol. 1:598-607(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to peptidase family S1.
EMBL; AJ459311; CAD30563.1; -.
HSSP; P00746; 1FDP.
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249 AA; 27400 MW; 8FB98462CEDBEFC9 CRC64;
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GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:chypidase activity. IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:000508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1.
InterPro; IPR009033; Peptidase S1A.
InterPro; IPR009003; Peptidase S1A.
PF00089; Trypsin; 1.
  01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Trypsinogen Y precursor (Fragment).
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Last annotation update)
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-!- SIMILARITY: Belongs to peptidase family S1
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66.7%; Pred. No. 31;
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SMART; SM00020; TRYPSIN D.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                       Name=trpY gene;
Gadus morhua (Atlantic cod)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     >249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Pyloric caecum;
Gudmundsdottir A.;
                                                                                                                                                                                                                                                                                                    TISSUE=Pyloric caecum;
PubMed=10612685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||:|::|||
50 VLINDQWVL 58
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
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                                                                                                                                                                                                                   NCBI_TaxID=8049;
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SEQUENCE
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                                                                                                  SEQUENCE FROM N.A.
MEDINDE=97471969; PubMed=9330910;
MEDINDE=97471969; PubMed=9330910;
Sato S., Fabata S.,
Miyajima N., Tabata S.,
"Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty physically assigned DIA Res. 4:215-230(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Oviduct;
Lavery K.S., Gabler C., Killian G.J.;
Submitred (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ271156; CAC00531.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                            455 AA; 52305 MW; 763F5D5278D22F13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 AA; 11239 MW; FFFEGAESAB43CED9 CRC64;
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GO, GO:0008233; F:peptidase activity; IEA.
GO, GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR0091254; Peptidase S1.
InterPro; IPR0090013; Pept_Ser_Cys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 2;
Pred. No. 38;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam, PF00089; Trypsin, 1.
PROSITE, PS50240; TRYPSIN DOM, 1.
Hydrolase; Protease, Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8JFQ7;
01-OCT-2002 (TrEMBLrel. 22, Created)
                                                                                                                                                                                                                                                                                                                     EMBL; AB005233; BAB11469.1; -.
InterPro; IPR001810; F-box.
Pfam; PF00646; F-box; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100
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104 IINERWVL 111
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus (Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                  NCBI_TaxID=3702;
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SEQUENCE
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235 AA.
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                                       Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 8-87 AND 95-246.
               06668;
25-0CT-2004 (TrEMBLrel. 28,
25-0CT-2004 (TrEMBLrel. 28,
25-0CT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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PRELIMINARY;
                                                                                            Trypsinogen (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 VLINKOWVL 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VLVNERWVL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                        NCBI_TaxID=31033;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rissum=Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sugita A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON TER
SEQUENCE
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P00752;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2004 (TrEMBLrel. 26, Last aemotation update)
101-MAR-2004 (TrEMBLrel. 26, Last amotation update)
Thrombin-like enzyme defibrase (Fragment).
Agkistrodon caliginosus (Korean viper) (Gloydius ussuriensis).
Agkistrodon caliginosus (Korean viper) (Gloydius ussuriensis).
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
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0
                                                                                                                                                                                                                                                                                                                                                        80.9%; Score 38; DB 2; Length 223; 75.0%; Pred. No. 43; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.9%; Score 38; DB 2; Length 234; 87.5%; Pred. No. 45; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Snake venom gland;
Sun D.-J., Yang T.-S.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY2042421, AAP20637.1; --
                             GO; GO:000426; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0006289; F:trypsin activity; IEA.
GO; GO:0006589; F:proteolysis and peptidolysis; IEA.
InterPro; IPR001254; Peptidase S1A.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR00903; Peptidase S1A.
InterPro; IPR00903; Peptidase S1A.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Trypsin; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006208; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR009003; Peptidase S1.
SMART; SM00020; Trypsin; 1.
PROSITE; PS00240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN SIN; UNKNOWN 1.
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SEQUENCE 234 AA; 25351 MW; 0124C1485525F560 CRC64;
                                                                                                                                                                                                                                                                                                                       223 AA; 24844 MW; C34EBE9455DD7DE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 AA.
                                                                                                                                                                                                                                                                                   Hydrolase, Protease, Serine protease.
NON TER 1
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EMBL; AF053916; AAD21836.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 87.5%,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 ILNERWYL 42
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Best Local Similarity
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                   P00761; 1EPT
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                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Tschesche H., Mair G., Godec G., Fiedler F., Ehret W., Hirschauer C., Lemon M., Fritz H., Schmidt-Kastner G., Kutzbach C.; The primary structure of porcine glandular kallikreins."; Adv. Exp. Med. Biol. 120:245-260(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Generation of alpha- and beta-kallikreins from porcine pancreatic prokallikrein by the action of trypsin."; Chem. Pharm. Bull. 36:4891-4899(1988).
                                                            Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Actinopterygii, Teleostei, Buteleostei, Neoteleostei, Acatchomorpha, Acatchopterygii, Percomorpha, Tetraodontiformes;

Tetradontoidea, Tetraodontidae, Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
28-FRB-2003 (Rel. 41, Last sequence update)
25-CCT-2004 (Rel. 45, Last amoutation update)
Glandular kallikrein precursor (EC 3.4.21.35) (Tissue kallikrein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The primary structure of the kallikrein from porcine pancreas.";
Thesis (1976), University of Munich, Germany.
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MEDLINE-89230643; PubMed=3246048;
Kamada M., Aoki K., Ikekita M., Kizuki K., Moriya H., Kamo M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.9%; Score 38; DB 2; Length 235; 66.7%; Pred. No. 46; tive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                            Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
-! SINILARITY: Belongs to peptidase family S1.
EMBL, AX661446; AAU06121.1; -.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR009003; Peptidase_SA.
InterPro; IPR009003; Peptidase_SA.
PEdm; PF000089; Trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 AA; 26025 MW; 489D3617C943CC5A CRC64;
Last sequence update)
Last annotation update)
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Tomiya N., Yamaguchi T., Awaya J., Kurono M., Endo S., Arata Y.,
Takahashi N., Ishihara H., Mori M., Tejina S.;
Takahashi N., Ishihara H., Mori M., Tejina S.;
Structural analyses of asparagine-linked oligosaccharides of porcine pancreatic kallikrein.";
Biochemistry 27:7146-7154(1988).
-!- FUNCTION: Glandular kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release Lys-bradykinin.
-!- CATALYTIC ACTIVITY: Preferential cleavage of Arg-|-Xaa bonds in small molecule substrates. Highly selective action to release kallidin (1ysyl-bradykinin) from kininogen involves hydrolysis of Met-|-Xaa or Leu-|-Xaa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Refined 2-A X-ray crystal structure of porcine pancreatic kallikrein A, a specific trypain-like serine proteinase. Crystallization, structure determination, crystallographic refinement, structure and its comparison with bovine trypsin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen Z., Bode W.;
"Refined 2.5 A X-ray crystal structure of the complex formed by
"Refined 2.5 A X-ray crystal structure of the complex inhibitor.
Crystallization, Patterson search, structure determination,
refinement, structure and comparison with its components and with the
bovine trypsin-pancreatic trypsin inhibitor complex.";
J. Mol. Biol. 164:283-311(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH HIRUSTASIN. MEDLINE=97184690; PubMed=9032072; DOI=10.1016/S0969-2126(97)00183-4; Mittl P.R.B., di Marco S., Fendrich G., Pohlig G., Heim J., Sommerhoff C., Fritz H., Priestle J.P., Gruetter M.G.; An mew structural class of serine protesse inhibitors revealed by the structure of the hirustasin-kallikrein complex.";
            MEDLINE=90336040; PubMed=2379280;
Kamada M., Ikekita M., Kurahashi T., Aoki K., Kizuki K., Moriya H., Sweeley C.C., Kamo M., Taugita A.;
Generation of a different type of beta-kallikrein from porcine pancreatic alpha-kallikrein by the action of chymotrypsin --
observation of proteolytic processing occurring around 'kallikrein autolysis loop' region.";
                                                                                                                                                                                                                                                              "Investigation of the sequence of amino acid residues 127 to 174 the kallikrein from porcine pancreas."; Thesis (1978), University of Munich, Germany.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Monomer. SIMILARITY: Belongs to the peptidase S1 family. Kallikrein subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2 ANGSTROMS), AND REVISIONS.
MEDLINE-83189107; PubMed=6551452;
Bode W., Chen Z., Bartels K., Kutzbach C., Schmidt-Kastner G.,
Bartunik H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF COMPLEX WITH BOVINE PANCREATIC TRYPSIN INHIBITOR.
MEDLINE-83189108; PubMed=6188842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitil P.R.E., di Marco S., Fendrich G., Pohlig G., Heim J., Sommerhoff C., Fritz H., Priestle J.P., Gruetter M.G.; Structure 5:585-585(1997).
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-82194877; PubMed-7043199;
Fiedlar F., Fink E., Tschesche H., Fritz H.;
"Porcine glandular kallikreine.";
Meth. Enzymol. 80:493-532(1981).
                                                                                                                                                            Chem. Pharm. Bull. 38:1053-1057(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=89062455; PubMed=3196708;
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                                                                                                                                                                                                       SEQUENCE OF 128-175.
SEQUENCE OF 84-98.
                                                                                                                                                                                                                            TISSUE=Pancreas;
                                                                                                                                                                                                                                             Ehret W.;
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PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_HIS; 1.
3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase;
                                                                                                                                                                  N-linked (GlcNAc. . .) (Potential).
N-linked (GlcNAc. . .) (Potential).
CAUTION: Native porcine kallikrein is a monomer. Chains of pancreatic beta-kallikrein are heterogeneous artifacts of
                                                                                                                    Glandular kallikrein.
Kallikrein (autolysis) loop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27170 MW; 5991CEDE406A19A1 CRC64;
                                                                                                                                                                             Charge relay system.
Charge relay system.
Charge relay system.
        proteolytic degradation during isolation.
PDB; 1HIA; X-ray; A/X=8-87, B/Y=95-246.
PDB; 2KAI; X-ray; A/X=8-87, B=95-246.
PDB; 2PKA; X-ray; A/X=8-87, B-95-246.
MEROPS; S01.160; -.
                                          InterPro; IPR009003; Pept Ser_Cys.
InterPro; IPR001224; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PP00089; Trypsin; 1.
                                                                                                                      246
1104
158
158
204
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239
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103
198
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222
226
231
235
246 AA;
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SEQUENCE
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DISULFID
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CARBOHYD
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STRAIN=BALB/c; TISSUE=Brain;
MEDLINE=9825202; PubMed=9556608; DOI=10.1074/jbc.273.18.11189;
Shimizu C., Yoshida S., Shamachi T., Kato K., Momota Y., Matsumoto K., Shiosaka T., Midorikawa R., Kamachi T., Kawabe A., Shiosaka S.;
"Characterization of recombinant and brain neuropsin, a plasticity-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yoshida S., Hirata A., Inoue N., Shiosaka S.; "Cloning and assignment of mouse neuropsin gene, Prss19 to chromosome
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BALB/c; TISSUE=Hippocampus; MEDINE=9548817; PubMed=763137; Chen Z.-L., Yoshida S., Kato K., Momota Y., Suzuki J., Tanaka T., Ito J., Nishino H., Aimoto S., Kiyama H., Shiosaka S.; "Expression and activity-dependent changes of a novel limbic-serine processe gene in the hippocampus."; J. Neurosci. 15:5088-5097 (1995).
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                80.9%; Score 38; DB 1; Length 246; 77.8%; Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                               15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8).
Mamme=Klk8, Synonyme=Nrpn, Prss19;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 related serine protease.";
J. Biol. Chem. 273:11189-11196(1998).
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA sequences."
Query Match
Best Local Similarity 77.5.
                                                                                                                                                                                                                 STANDARD;
                                                                                                             |||| :|||
36 VLVNPKWVL 44
                                                                                   1 VLVNERWVL 9
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                                                                                                                                                                                                                 NRPN MOUSE
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NRPN_MOUSE
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                                                       "Crystal structure of neuropsin, a nippocampar process."; kindling epileptogenesis."; J. Biol. Chem. 274:4220-4224(1999).
-:- FUNCTION: Suggested to be involved in kindling epileptogenesis and hippocampal plasticity. Has a strong proteolytic activity against
                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: Expressed specifically in the limbic system of mouse brain and is localized at highest concentration in pyramidal neurons of the hippocampal CA1-3 subfields.

MASS SPECTROMETRY: WW=26613; WETHOD=MALDI; RANGE=29-260;
                                                                                                                                                                           -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-.
-!- ENZYME REGULATION: Strongly inhibited by diisopropyl
fluorophosphate, leupeptin and (4-amidinophenyl)methanesulfonyl 1-
MEDLINE-99134351; PubMed-9933620; DOI=10.1074/jbc.274.7.4220; Kishi T., Kato M., Shimizu T., Kato K., Matsumoto K., Yoshida S., Shiosaka S., Hakoshima T. "Crystal structure of neuropsin, a hippocampal protease involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Charge relay system (By similarity). Charge relay system (By similarity). Charge relay system (By similarity).
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PRINTS; PR00722; CHYMOTRYBSIN.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
3D-structure; Direct protein sequencing; Glycoprotein; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-linked (GlcNAc. . .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                            NOTE=Ref.4.
MASS SPECTROMETRY: MW=26229; METHOD=MALDI; RANGE=33-260;
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EMBL; BC055895; AAH55895.1; -.
PDB; INPM; X-ray; A/B=33-256.
MEROPS; S01.244; -.
MICAPTO; IPR000303; Pept Ser Cys.
InterPro; IPR001254; Peptidase_51.
InterPro; IPR001314; Peptidase_51.
                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Secreted.
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ACT SITE
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Valenzuela J.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Charge relay system (By similarity).
Charge relay system (By similarity).
Charge relay system (By similarity).
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-linked (GlcNAc. . .) (Potential). 58DF4F0602A0B7F5 CRC64;
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Neoptera; Endopterygota; Diptera; Nematocera; Psychodoidea;
Psychodidae; Phlebotomus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase; Serine protease; Signal; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 1; Length 260;
Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases EMBL; AY128106; AAM96938.1; -. HSSP; P18291; 1F18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR009003; Pept Ser Cys.
Pfam; PF00089; Trypsin; 1.
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Last annotation update)
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By similarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neuropsin.
                                                                                                                                             EMBL; AJ005641; CAA06643.1; --
HSSP; Q61955; INPM.
MEROPS; S01.244; --
INTERPRO; IRRO0103; Pept Ser Cys.
INTERPRO; IPRO01035; Peptidase_S1.
INTERPRO; IPRO01314; Peptidase_S1.
INTERPRO; IPRO01314; Peptidase_S1A.
PRUNTS; PRO0122; CHYMOTRYPSIN,
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PSS01240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN—IS; 1.
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PROSITE; PS50240; TRYPSIN DOM; 1.
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llarity 77.8%;
Conservative
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260 AA;
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nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein;
SIGNAL
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ACT_SITE
ACT_SITE
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CARBOHYD
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CHAIN
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          ACCOCCOOCO ON THE PROPERTY OF 
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MEDLINE-98389725; PubMed=9722524; DOI=10.1074/jbc.273.36.23004;

MEDLINE-98389725; PubMed=9722524; DOI=10.1074/jbc.273.36.23004;

Davies B.J., Pickard B.S., Steel M., Morris R.G.M., Lathe R.;

"Serine proteases in rodent hippocampus.";

"Serine proteases in rodent hippocampus.";

"Islol. Chem. 273:23004-23011 (1998).

"Islol. Chem. 273:23004-23011 (1998).

"Islol. Suggested to be involved in kindling epileptogenesis and hippocampal plasticity. Has a strong proteolytic activity against thorometin (By similarity).

"Islola Carlory: Preferential cleavage: Arg., Lys-.

"ISSUE SPECIFICITY: Restricted to hippocampus.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                088780;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Neuropsin precursor (EC 3.4.21.-) (NP) (Kallikrein 8) (Brain serine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28523 MW; BE5F6F6BE37CD60E CRC64;
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61 VLVGDRWVL 69
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1; Mismatches
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        6; Conservative
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                                                                                                                                                                                          PRELIMINARY;
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219 VLINERW 225
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                                            1 VLVNERW 7
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Q9SNY9
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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                                                                                                        Length 262;
                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The sequence of C. elegans cosmid C32E8.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilson R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
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PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
PROSITE; PS00135; TRYPSIN SER; UNKNOWN 1.
Hydrolage; Proceage; Serine proceage.
SEQUENCE 262 AA; 28863 WW; 31F11012206A65D4 CRC64;
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SEQUENCE 313 AA; 35608 MW; 4372ED66478E434A CRC64;
                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUNA-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein C32E8.6.
Name-C32E8.6; ORFNamee=C32E8.6;
Caenorhabditis elegans.
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Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                  313 AA.
                                                                                                      Score 38; DB
Pred. No. 51;
2; Mismatches
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GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
PICAPPC; IPRO00873; AMP-bind.
PEM; PF00501; AMP-binding; I.
PRINTS; PR00154; AMPBINDING.
PROSITE; PS00455; AMP_BINDING; I.
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MEDLINE=99069613; PubMed=9851916;
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85.7%;
                                                                                                    h 80.9%;
Similarity 75.0%;
6; Conservative ;
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HSSP; P08659; 1LCI.
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57 ILNERWYL 64
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Matches 6; Conserv
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                                                                                                      Query Match
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"Genes encoding for branched-chain amino acid aminotransferase are
differentially expressed in plants.";
Plant Physiol. Biochem. 39:855-860(2001).

EMBL, AF193846; AAR07192.1;
HSSP; P00510; 111K.

GO; GO:0004084; F.branched-chain-amino-acid transaminase acti. . .; IEA.
GO; GO:00016740; F.transferase activity; IEA.
GO; GO:0010715; P.metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
VOEB_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
lamiids, Solanales, Solanaceae, Solanum.
VCBI_TaxID=4113;
   Gaps
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"Genes encoding for branched-chain amino acid aminotransferase are
differentially expressed in plants.";
Plant Physiol. Biochem. 39:855-860(2001).
EMBL; AF193845; AFR77191.1;
HSSP; O15382; 1KT8.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Branched-chain amino acid aminotransfersee (EC 2.6.1.42).
Indels
                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Branched-chain amino acid aminotransferase (EC 2.6.1.42).
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InterPro; IPR005786; B_amino_transII.
Pfam; PF01063; Aminotran 4; 1.
TIGRPAMs; TIGR01123; ilvE II; 1.
PROSITE; PS00770; AA TRANSFER CLASS 4; 1.
Aminotransferase; Transferase.
                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                    PRT;
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GO; GO:0004084; F:branched-chain-amino-acid transaminase acti. . .; IEA. GO; GO:0016740; F:transferase activity; IEA. GO; GO:0016740; F:transferase activity; IEA. GO; GO:0009081; P:branched chain family amino acid metabolism; IEA. GO; GO:0008152; P:metabolism; IEA. InterPro; IPR00153; P:metabolism; IEA. InterPro; IPR001534; Aminotrans IV. InterPro; IPR00153; Aminotrans IV. 1. FFam; PF01063; Aminotran 4; I. TIGRFAMS; TIGR01123; ilv8 II. 1. Aminotransferase; Transferase;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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80.9%; Score 38; DB 2; Length 418;
Best Local Similarity 75.0%; Pred. No. 84;
Matches 6; Conservative 1; Mismatches 1; Indels
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188 VLANERWI 195
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TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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RESULT 2
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Sequence 34, Appl
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                                                                                                                                                                                                                                                                                                                         lssued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-518-243-34
US-09-518-243-34
US-08-944-4813-33
US-08-557-146-12
US-09-624-6004-4
US-09-644-6004-4
US-08-557-146-2
US-08-557-146-2
US-08-57-146-2
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US-08-57-146-2
US-08-57-146-2
US-08-57-146-2
US-08-918-24-146-2
US-08-918-24-16
US-09-18-243-40
US-09-918-243-40
US-09-918-243-40
US-09-918-243-40
US-09-918-243-40
US-09-918-243-40
US-09-918-243-40
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US-08-482-130C-75
US-08-484-211C-75
                                                                                                                                                                                                  513545 segs, 74649064 residues
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                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                     OM protein - protein search, using sw model
                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                US-09-905-083A-34
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Match Length DB
                                                                                                                                          1 VLVNERWVL 9
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Perfect score:
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                                                                            Run on:
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No.
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NS-09-502-600-34

Sequence 34, Application US/09502600A

Sequence 34, Application US/09502600A

Parent No. 6204-304

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer

TITLE OF INVENTION: Ovarian Cancer

FILE REPERENCE: D6223CIP-C

CURRENT FILING DATE: 2000-02-11

CURRENT APPLICATION NUMBER: US/09/502,600A

PRIOR FILING DATE: 03-14-1998

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 34

LENGTH: 9
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| Sequence 34, Application US/09918243
| Patent NO. 6627403
| GENERAL INFORMATION:
| APPLICANT: Cannon, Martin J.
| APPLICANT: Cannon, Martin J.
| APPLICANT: Santin, Alessandro:
| TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer:
| FILE REFERENCE: D623GTP/C/D/CIP
| CURRENT APPLICATION NUMBER: US/09/918,243
| CURRENT RILING DATE: 2001-07-30
| PRIOR FILING DATE: 2001-07-13
| NUMBER OF SEQ ID NOS: 136
| SEQ ID NO 34
| LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Residues 58-66 of the SCCE protein US-09-502-600-34
US-08-906-769-75
US-08-906-616-75
US-08-816-616-75
US-08-818-75
US-08-639-075A-75
US-09-012-692-75
US-09-012-692-75
US-08-916-613-75
US-08-818-75
US-08-818-75
US-08-818-75
US-08-817-795-17
US-08-817-795-17
US-08-817-795-17
US-08-817-795-17
US-08-817-795-17
US-08-817-795-17
US-08-817-795-17
US-08-906-768-17
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us-09-905-083a-34.rai

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Sequence 12, Application US/08557146
; Sequence 12, Application US/08557146
; Patent No. 5834290
; GENERAL INFORMATION:
; APPLICANT: Bealtud, Torbjorn
APPLICANT: Bealtud, Torbjorn
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
; TITLE OF INVENTION: Bnzyme (SCCE)
; UNUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case, Patent Department
STREET: New York
; STATE: New York
; COUNTY: New York
; COUNTY: 1155 Avenue of the Americas
; TIP: 10036-2787
; COMPUTER READABLE FORM:
; AMBIUM TYPE: Floppy disk
; CAMPUTER PRADABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3; Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 47; DB 3 100.0%; Pred. No. 0.6;
                  SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: BECKEY, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183
TELECHONE: 847/935-1729
TELECHONE: 847/936-2623
                                                                                                                                                                                                                                                                                                                                                          TELEX:
INFORMATION FOR SEQ ID NO: 33.
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
STRANDEDNESS: single
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US-08-944-483-33
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 225 amino acids TYPE: amino acids
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Best Local Similarity 100.
Matches 9; Conservative
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  OPERATING SYSTEM:
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                                                                                        FILING DATE:
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                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09261416A
Sequence 7, Application US/09261416A
Fatent No. 6291663
GENERAL INPORMATION:
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: TADG-12: A No. 6291663el Transmembrane Serine Protease
TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
FILE REFERENCE: D6192
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 7
LENGTH: 154
TYPE: PRT
CORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: COHENTS, TRACEY L.
APPLICANT: COLENTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRANADOS, BUWARD N.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STEWART, KENT D.
APPLICANT: STEWEN D.
APPLICANT: STEWEN D.
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES TITLE OF INVENTION: OF THE PROSTATE
WINMER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                           100.0%; Score 47; DB 4; Length 9; 100.0%; Pred. No. 4.1e+05; ative 0; Mismatches 0; Indels
              NAME/KEY: CHAIN
CHER INFORMATION: Residues 58-66 of the SCCE protein US-09-918-243-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-944-483-33; Sequence 33, Application US/08944483; Patent No. 6232456; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
                                                                                      Ouery Match
Best Local Similarity luv.
9; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VLVNERWVL 9
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                                                                                                                                                                                                                                                                                                                                            US-09-261-416-7
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                  RESULT 3
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100.0%; Score 47;
100.0%; Pred. No. C
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                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: polypeptide
                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                  single
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COTHER INFORMATION: SCCE
US-09-644-600-4
                                                                                                                                                                                                                                                                                                                                                                                                 30 VLVNERWVL 38
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 9; Conserv
       CLASSIFICATION:
                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                Sequence 4, Application US/09027337B

Patent No. 5972616

GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TANG-15: An Extracellular Serine Protease Overexpressed in TITLE OF INVENTION: Breast and Ovarian Carcinomas
FILE REFERENCE: D604
CURRENT APPLICATION NUMBER: US/09/027,337B

UNDMER OF SEQ ID NOS: 13
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Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 9; Conservative 0; Mismatches O. Thanh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 47; DB 2; Length 225; Best Local Similarity 100.0%; Pred. No. 0.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
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FILING DATE: 16-SEP-1998
TOPOLOGY: linear
MOLECULE TYPE: polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                   30 VLVNERWVL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 VLVNERWYL 38
                                                                                                                                            1 VLVNERWVL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Unknown
PEATURE:
                       ; MOLECULE TYR
US-08-557-146-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 225
                                                                                                                                                                                                                                                 US-09-027-337-4
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i Sequence 4, Application US/09644600

i Batent No. 6451500

j GENERAL INFORMATION:

APPLICANT: O'BLIEN, Timothy J.

TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease

TITLE OF INVENTION: TA
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Sequence 4. Application US/09654600A

Patent No. 6649741

GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi

TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
TITLE REFERENCE: D6064CIP/D

CURRENT APPLICATION NUMBER: US/09/654,600A

CURRENT FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 225;
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100.0%; Pred. No. 0.6;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
NAME: Sterner, Richard J.
REGISTRATION UNMERR: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPOME: (212) 819-8783
TELEPAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acids
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Sequence 3, Application US/08824874

09/027,337

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Gaps
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APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 47; DB 2; Length 253; illarity 100.0%; Pred. No. 0.68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                      ADDRESSEE: White & Case, Patent Department STREET: 1155 Avenue of the Americas CITY: New York
Patent No. 5962300
GENERAL INFORMATION:
APPLICANT: Hilman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STRATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy
NAME: Billings, Lucy
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-154-344-2
; Sequence 2, Application US/09154344
Patent No. 5981256
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: GenBank
CLONE: 532504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: line
                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-824-874-3
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JEACHER DESCRIPTION OF SECTIFICATION OF SEGURATION OF S
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                                                                                                                                                                                                                                                                                                        DB 4; Length 225;
                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 47;
Best Local Similarity 100.0%; Pred. No. (
Matches 9; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
     PRIOR FILING DATE: 1999-10-20
1998-02-20
NUMBER OF SEQ ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 253 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-557-146-2
                                                                                                                                                                                                                   CTHER INFORMATION: SCCE US-09-654-600A-4
                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 VLVNERWVL 38
                                                                                                                                                                                                                                                                                                                                                                                                           1 VLVNERWVL 9
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                                                                                       SEQ ID NO 4
LENGTH: 225
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                                                                                                                                                                                                FEATURE:
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ZIP: 10036-2787 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMpatible

New York Y: U.S.A.

COUNTRY:

58 VLVNERWVL 66

RESULT 11 US-08-824-874-3

STATE:

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Gaps

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Query Match 100.0%; Score 47; DB 3; Length 253; Best Local Similarity 100.0%; Pred. No. 0.68; Matches 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09210084

Patent No. 6197511

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTR.

ZIP: 94304
COMPTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: IBM Compatible
DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 253 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                          LENGTH: 253 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-930-188-2
                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                  58 VLVNERWVL 66
                                                                                                                                                                                                                                                                  1 VLVNERWVL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY: GenB
CLONE: 532504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-09-764-762-3
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; Patent No. 6093397
; GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
APPLICANT: Johnstone, Edward M.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND TITLE OF INVENTION: RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 47; DB 2; Length 253; 100.0%; Pred. No. 0.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
SOFTWARE: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/00/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 819-8783
TELEPAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,0822
                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
                                                                                         UMBER: US/09/154,344
16-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Indiana
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NIMBER: X9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 317-276-3861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 VLVNERWVL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VLVNERWVL 9
                                                                                                                        FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-154-344-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
US-08-930-188-2
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0; Gaps

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Sequence 3, Application US/09764762
Patent No. 647259
GENERAL INFORMATION:
JETUICANT: Hillanen, Jennifer L.
JITUE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES:
CORRESPONDENCE SISS:
CORRESPONDENCE SISS:
STREET: 1314 Porter Drive
CITY: Pala Alto
CITY: Pala Alto
CONPUTER: Diskette
COMPUTER: Dis
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 Query Match
 100.0%;
 Score 47;
 DB 4;
 Length 253;

 Best Local Similarity 100.0%;
 Pred. No. 0.68;

 Matches 9;
 Conservative 0;
 Mismatches 0;
 Indels 0;
 Gaps

 Qy 1 VLVNERWVL 9 | 1 | | | | | | | |
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 Db SR VLVNERWVL 66
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> Search completed: July 13, 2005, 17:34:26 Job time : 19.4444 secs

Sequence

Sequence 36, Appli Sequence 2, Appli Sequence 6, Appli Sequence 48, Appl Sequence 48, Appl Sequence 48, Appl Sequence 639, Appl Sequence 95, Appl Sequence 95, Appl Sequence 1, Appli Sequence 60, Appl Sequence 60, Appl Sequence 50, Appl Sequence 50, Appl Sequence 60, Appl Sequence 60, Appl Sequence 60, Appl Sequence 61, Appl

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database

```
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
TITLE CARTINAT: Santin, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
FILE REFERENCE: D6223CIP/C/D/CIP
CURRENT APPLICATION WUMBER: US/09/918,243
CURRENT FILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 34
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 58-66 of the SCCE protein
US-09-918-243-34
| US-10-262-511-94
| US-09-888-615-94
| US-09-764-762-3
| US-10-71-214-48
| US-10-71-214-48
| US-10-71-214-48
| US-10-71-214-48
| US-10-264-283-90
| US-10-10-264-283-90
| US-10-10-64-765-63
| US-10-10-64-765-63
| US-10-948-394-38
| US-09-918-243-40
| US-10-918-243-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 47; DB 9; I
llarity 100.0%; Pred. No. 1.6e+06;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-461-787-8
US-10-072-012-609
US-10-072-012-610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 34, Application US/09918243
Patent No. US20020142317A1
GENERAL INFORMATION:
     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLVNERWVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
    US-09-918-243-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
    Query Match
Best Local S
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Matches
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Sequence 34, Appl
Sequence 34, Appl
Sequence 100, App
Sequence 96, Appl
Sequence 96, Appl
Sequence 97, Appl
Sequence 104, Appl
Sequence 104, Appl
Sequence 104, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                          July 13, 2005, 17:29:45; Search time 64.8889 Seconds (without alignments) 53.584 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                               | Cgn2_6/ptodata1/pubpaa/USO7_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/pubpaa/USO7_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/pubpaa/USO6_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/pubpaa/USO6_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/pubpaa/USO7_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/pubpaa/USO7_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/pubpaa/USO8_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/pubpaa/USO8_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/pubpaa/USO9_PUBCOMB.ppp:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-905-083-34
US-10-312-34
US-10-831-075-34
US-10-262-511-100
US-10-262-511-98
US-09-789-210-33
US-09-789-210-33
US-10-262-511-104
US-10-262-511-104
US-10-262-511-104
                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                   1726220 segs, 386332138 residues
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                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match.100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications AA:*
                                                                     - protein search, using sw model
                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Gaps

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RESULT 2

Result

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FILE REFERENCE: D6223CIP/C/D/CIP3
CURRENT APPLICATION NUMBER: US/10/831,075
CURRENT FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 10/372,521
NUMBER OF SEQ ID NOS: 140
SEQ ID NO 34
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/377,917
PRIOR APPLICATION NUMBER: 60/377,917
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR PELLING DATE: 2002-05-17
PRIOR FILING DATE: 2002-06-19
PRIOR FILING DATE: 2002-06-19
PRIOR FILING DATE: 2002-06-19
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Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
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Malyankar, Uriel M.
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Zerhusen, Bryan D.
Anderson, David W.
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                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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| Publication No. US20030223973A1
| Publication No. US20030223973A1
| GENERAL INFORMATION:
| APPLICANT: O'Brien, Timothy J. |
| APPLICANT: Santin, Alessandro |
| TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer |
| TITLE OF INVENTION WHERE: US/10/372,521
| CURRENT APPLICATION NUMBER: US/10/372,521
| CURRENT FILING DATE: 2003-02-21
| PRIOR PRICATION NUMBER: US 09/918,243
| PRIOR FILING DATE: 2001-07-30
| NUMBER OF SEQ ID NOS: 136
| LENGTH: 9
                    Sequence 34, Application US/09905083

Betent No. US20020146708A1

BETENT No. US20020146708A1

BETENT NO. US20020146708A1

APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer File Reference: D6223CIP/C/Div CURRENT APPLICATION NUMBER: US/09/905,083

FURENT APPLICATION NUMBER: US 09/502,600

PRIOR FILING DATE: 2000-02-11

PRIOR FILING DATE: 2000-02-11

SEQ ID NO 34

LENGTH: 9
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; Publication No. US20040224891A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
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NAME/KEY: CHAIN

OTHER INFORMATION: Residues 58-66 of the SCCE protein US-09-905-083-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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US-10-372-521-34
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APPLICANT: Carterron, Elina
APPLICANT: Carterron, Elina
APPLICANT: di, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Miller, Charles E.
APPLICANT: Ratefall, Luca
APPLICANT: Scone, David J.
APPLICANT: Shimket's Richard A.
APPLICANT: Shimket's Richard A.
APPLICANT: Cared, Mark E.
APPLICANT: Lacah, Mark E.
APPLICANT: Berghs, Constance
APPLICANT: PAGE, MICHEL E.
APPLICANT: PAGE, MICHEL
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FEATURE:

NAME/KEY: CHAIN

OTHER INFORMATION: Residues 58-66 of the SCCE protein US-10-831-075-34
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0;
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Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Rewda, Ramesh
APPLICANT: Kekuda, Ramesh
APPLICANT: Li, Li
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PRIOR APPLICATION NUMBER: 60/328,029
PRIOR PILING DATE: 2002-10-09
PRIOR PELING DATE: 2002-10-09
PRIOR PELICATION NUMBER: 60/381,038
PRIOR FILING DATE: 2002-05-16
PRIOR FILING DATE: 2002-05-16
PRIOR PLICATION NUMBER: 60/373,260
PRIOR PLICATION NUMBER: 60/373,260
PRIOR FILING DATE: 2002-04-17
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
PRIOR PLING                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
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Best Local Similarity 100.0%; Pred. No. 5;
Matches 9; Conservative 0; Mismatches
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PRIOR FILING DATE: 2001-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
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Malyankar, Uriel M.
Ort, Tatiana
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APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
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Anderson, David W.
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Agee, Michele L.
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Miller, Char
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; ORGANISM: Homo sapiens
US-10-262-511-98
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                                     PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2002-04-17
PRIOR PILING DATE: 2002-04-17
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2001-10-05
PRIOR FILING DATE: 2001-10-05
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: Curassequist version 0.1
LENGTH: 97
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APPLICANT: Leach, Martin D.
APPLICANT: Agee, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
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CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR APPLICATION NUMBER: 60/373,917
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR APPLICATION NUMBER: 60/381,642
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Publication No. US20040038223A1
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Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
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Malyankar, Uriel M.
Ort, Tatiana
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Anderson, David W.
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Miller, Charles E.
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Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
                FILING DATE: 2002-05-16
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APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
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Best Local Similarity 100.
Matches 9; Conservative
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Li, Li
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; ORGANISM: Homo sapiens
US-10-262-511-100
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Gaps

Gaps

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APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
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                                          TELERAX: 847/938-2623

INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
TENGTH: 224 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-789-210-33
                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/262,511

CURRENT FILING DATE: 2003-05-28

PRIOR APPLICATION NUMBER: 60/326,483

PRIOR FILING DATE: 2001-10-02

PRIOR APPLICATION NUMBER: 60/373,815

PRIOR FILING DATE: 2002-04-19

PRIOR FILING DATE: 2001-10-09

PRIOR PLILNG DATE: 2001-10-09

PRIOR APPLICATION NUMBER: 60/381,642

PRIOR FILING DATE: 2002-06-17

PRIOR APPLICATION NUMBER: 60/381,62

PRIOR APPLICATION NUMBER: 60/381,039

PRIOR APPLICATION NUMBER: 60/381,039

PRIOR APPLICATION NUMBER: 60/381,039

PRIOR APPLICATION NUMBER: 60/381,038
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  TELECOMMUNICATION INFORMATION:
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Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
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Miller, Charles E.
Rastelli, Luca
Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
Shimkets, Richard A.
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Gorman, Linda
Zerhusen, Bryan D.
Anderson, David W.
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Leach, Martin D.
Agee, Michele L.
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Malyankar, Uriel M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
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Catterton, Elina
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Best Local Similarity 100.
Matches 9; Conservative
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GENERAL INFORMATION:
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APPLICANT:
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US-09-789-210-33

JS-09-789-210-33

Sequence 33, Application US/09789210

Publication No. US20040241646A1

GENERAL INFORMATION:

APPLICANT: COLBITTS, TRACEY L.

FRIEDMAN, PAULA N.

GRANADOS, EDWARD N.

KLASS, MICHAEL R.

KLASS, MICHAEL R.

STEWART, KENT D.

STEWART, KENT D.

STROUPE, STEWARD D.

TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS

AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES

OF THE PROSTATE
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             PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
PRIOR PILING DATE: 2002-05-17
PRIOR PILING DATE: 2002-10-09
PRIOR PILING DATE: 2002-10-09
PRIOR PILING DATE: 2002-10-09
PRIOR PAPLICATION NUMBER: 60/381,038
PRIOR PILING DATE: 2001-0-09
PRIOR PILING DATE: 2001-0-09
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2001-0-05
PRIOR PILING DATE: 2001-10-05
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
SOFTWARE: FASTEM: DOS
SOFTWARE: 20-Feb-2001
CLASSIFICATION NUMBER: US/09/789,210
FILING DATE: 20-Feb-2001
CLASSIFICATION NUMBER: 08/944,483
APPLICATION NUMBER: 08/944,483
FILING DATE: 4UNKNOWN>
APPLICATION NUMBER: 08/944,483
FILING DATE: 4UNKNOWN>
ANTORNEY/AGENT INFORMATION:
NAME: BECKER, CHERYI L.
REFERENCE/DOCKET NUMBER: 35,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 47; DB 1
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 9; Conservative 0; Mismatches
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CORRESPONDENCE ADDRESS:
ADDRESSE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
FILING DATE: 2001-10-09
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US-10-262-511-96
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APPLICANT: Sothenberg, Martin D.
APPLICANT: Beach, Martin D.
APPLICANT: Beach, Martin D.
APPLICANT: Beach, Martin D.
APPLICANT: Berge, Constance
FILE SPERENCE: 1402-462C
CURRENT APPLICATION NUMBER: 60/326,483
PRIOR PAPLICATION NUMBER: 60/326,483
PRIOR PAPLICATION NUMBER: 60/373,815
PRIOR PAPLICATION NUMBER: 60/373,815
PRIOR PELING DATE: 2001-10-02
PRIOR PELING DATE: 2001-10-09
PRIOR PELING DATE: 2002-04-19
PRIOR PELING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR PELING DATE: 2002-05-17
PRIOR PELING DATE: 2002-05-17
PRIOR PELING DATE: 2002-05-17
PRIOR PELING DATE: 2002-05-16
PRIOR FILING DATE: 2002-05-16
PRIOR PELING DATE: 2002-05-16
PRIOR PELING DATE: 2002-05-16
PRIOR PELING DATE: 2002-05-16
PRIOR PELING DATE: 2002-05-17
PRIOR PELING DATE: 2002-04-17
PRIOR PELING DATE: 2002-05-17
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PRIOR PELING DATE: 2002-04-17
PRIOR PELING DATE: 2002-04-17
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SCOTTWARE: CuraSeqList version 0.1
SEQ ID NO 102
LENGTH: 247
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Suo, Xiaojia (Sasha)
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Ort, Tatiana
Gorman, Linda
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Miller, Charles E.
Rastelli, Luca
Stone, David J.
                    Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
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Anderson, David W.
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Catterton, Elina
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Shenoy, Suresh G.
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APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
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US-10-262-511-102
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Best Local Similarity
The 9; Conserve
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                 PRIOR FILING DATE: 2001-10-09
PRIOR PLING DATE: 2002-04-17
PRIOR PLING DATE: 2002-04-17
PRIOR PLING DATE: 2002-04-17
PRIOR PLING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/377,435
PRIOR APPLICATION NUMBER: 60/327,435
PRIOR PLING DATE: 2001-10-05
PRIOR PLING DATE: 2001-10-05
SOFTHARB: CLTASEQUIST VERSION 0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10600187

| Sequence 4, Application US/10600187
| Publication No. US20040086910A1
| GENERAL INFORMATION:
| APPLICANT: O'Brien, Timothy J. |
| APPLICANT: Tanimoto. Hirotoshi |
| TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease |
| TITLE OF INVENTION: Overexpressed in Carcinomas |
| FILE REFERENCE: D6064CIP/D |
| CURRENT APPLICATION NUMBER: US/10/600,187 |
| CURRENT FILING DATE: 2003-06-20 |
| PRIOR PILING DATE: 2000-09-01 |
| PRIOR APPLICATION NUMBER: 09/421,213 |
| 09/027,337 |
| 1998-02-20 |
| NUMBER OF SEQ ID NOS: 98 |
| NUMBER OF SEQ ID NOS: 98
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APPLICANT: Smithson, Glennda; APPLICANT: Millet, Isabelle; APPLICANT: Reyman, John A.; APPLICANT: Kekuda, Ramesh; APPLICANT: Uu, Jingfang; APPLICANT: Li, Li
APPLICATION NUMBER: 60/328,056
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Best Local Similarity luv.
9, Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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US-10-600-187-4
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                      TYPE: PRT GAGANISM: Homo sapiens US-10-262-511-104
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Indels

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Ju, Jingfang
Li, Li
Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
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Gorman, Linda
Zerhusen, Bryan D.
Anderson, David W.
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Malyankar, Uriel M.
                    Millet, Isabelle
Peyman, John A.
Kekuda, Ramesh
Smithson, Glennda
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Best Local Similarity 100.
Matches 9; Conservative
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; ORGANISM: Homo sapiens
US-10-262-511-94
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APPLICANT: Miller, Charles E.
APPLICANT: Stone, David J.
APPLICANT: Stone, David J.
APPLICANT: Stone, David J.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shenberg, Mark E.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
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NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraSeqList version 0.1
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CURRENT APPLICATION NUMBER: 05/10/262,511

CURRENT FILING DATE: 2003-05-28

PRIOR FILING DATE: 2003-05-28

PRIOR FILING DATE: 2001-10-02

PRIOR FILING DATE: 2002-04-19

PRIOR FILING DATE: 2002-04-19

PRIOR FILING DATE: 2002-04-19

PRIOR FILING DATE: 2002-04-19

PRIOR FILING DATE: 2002-05-17

PRIOR APPLICATION NUMBER: 60/381,642

PRIOR APPLICATION NUMBER: 60/381,038

PRIOR FILING DATE: 2002-05-16

PRIOR FILING DATE: 2002-0-16

PRIOR FILING DATE: 2002-0-16

PRIOR FILING DATE: 2002-0-16

PRIOR FILING DATE: 2001-0-09

PRIOR FILING DATE: 2002-04-17

PRIOR FILING DATE: 2002-04-19

PRIOR FILING DATE: 2002-04-19

PRIOR FILING DATE: 2001-00-05

PRIOR FILING DATE: 2001-10-05

PRIOR FILING DATE: 2001-10-05

PRIOR FILING DATE: 2001-10-05
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US-10-262-511-94
is Sequence 94, Application US/10262511
is Publication No. US20040038223A1
j GENERAL INFORMATION:
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                                                                                            Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
Malyankar, Uriel M.
Ort, Tatiana
Gorman, Linda
                                                                     Suo, Xiaojia (Sasha)
                                                                                                                                                                                                                                                                       Zerhusen, Bryan D.
Anderson, David W.
                                                                                                                                                                                                                                                                                                             Zhong, Mei
Catterton, Elina
Kekuda, Ramesh
               Ju, Jingfang
Li, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-92
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55 VLVNERWVL 63
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                                                                  APPLICANT:
APPLICANT:
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APPLICANT: Anderson, David W.
APPLICANT: Cartetron, Blina
APPLICANT: Miller, Charles E.
APPLICANT: Bastalli, Luca
APPLICANT: Brond, Martin D.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shenoy, Mark E.
APPLICANT: Berghs. Conceance
Martin D.
APPLICANT: Marker E.
APPLICANT: Marker E.
APPLICANT: Martin D.
APPLICANT: Mar
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US-09-888-615-98
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
CORRATING SYSTEM: DOS
SOFTWARE: FastESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,762
FILING DATE: I6-Jan-2001
CLASSIFICATION: < UNINDOWN.
PRIOR APPLICATION NATA:
CLASSIFICATION: < UNINDOWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYCE Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/210,084
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                       APPLICANT: FLOWMAN, GREGORI,
APPLICANT: CARNEBEEL, SEAN
APPLICANT: CARNEBEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: SUDANSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFRERECE: 036602/1214
CURRENT PELLING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR APPLICATION NUMBER: 02/214,047
PRIOR APPLICATION NUMBER: 02/214,047
SOFTWARE: PATENTING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PATENTING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PATENTING DATE: 200-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PATENTING DATE: 200-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PATENTING DATE: 201
SEQ ID NO 98
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 3, Application US/09764762; Patent No. US20020068841A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
Sequence 98, Application US/09888615
Patent No. US20020064856A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: CA
COUNTRY: USA
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US-09-764-762-3
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Peptide #
Peptide #
Human bra
Human liv
Human pep

Protein e

Human sec Human nov

Aae08238 H
Adr68794 H
Abd23551
Ads21222
Abb43858
Abb43858
Abg46617
Aam94771
Aam94617
Aay89030
Abb51130
Abo45387
Abo6884
Abo69387
Abo08884
Abo69376
Ade09276
Ade09276
Ade09276
Ade09276
Ade09276

Polypepti

Bechum

Human Novel

Protein a

Human pol Polypepti Novel pro Human the

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The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypain enzyme (SCCB). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                           Human stratum corneum chymotrypsin enzyme peptide #5 (residues 6-14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diagnosing cancer comprises detecting stratum corneum chymotrypsin
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                                                                       AAM64837
ABG59233
ABG46617
AAW98431
AAX36291
AAW89030
ABB51130
ABB51130
                                                                                                                                                                                                                  ABO00884
ADE09276
ADS12009
                                                                                                                                                                                         AB026867
                                                                                                                                                                                                       AAC08397
                                                  ABB43858
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                                                                                                                                                                                                                                                                                                                                                AAE08240 standard; peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-FEB-2001; 2001WO-US003977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-FEB-2000; 2000US-00502600
                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
88
864
223
223
47
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WO200159158-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O'brien TJ;
AAE08240;
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Human NOV
Human NOV
Human NOV
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Human SCC
Human SCC
Amino aci
Protein d
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Ovarian c
Human hea
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Human tum
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Human HSC
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Human gas
Human gas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                  July 13, 2005, 16:12:23; Search time 76.6667 Seconds (without alignments) 45.402 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
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                                                                                                                                                                                                                                                    .. 2105692
           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                              2105692 seqs, 386760381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                             - protein search, using sw model
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ADA05732
ADN62896
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ABB84421
ABB84406
AAU8740
ABU07471
ABR58471
ADR58471
ADR68833
ADN39180
ADU6815
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ADR72880
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AAB63582
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Gapop 10.0 , Gapext 0.5
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geneseqp2000s:*
geneseqp2001s:*
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geneseqp2003as:*
geneseqp2003bs:*
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seq length: 200000000
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Maximum DB
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                                                                                                                                                                                                                               Searched:
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Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.
                                                            Novel human diagnostic protein #23369.
                                    (first entry)
                                                                                                                                             WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                             biodiversity.
                                                                                                                        Homo sapiens.
                                     18-FEB-2002
                                                                                                                                                                      11-OCT-2001
             ABG23378;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel method for vaccinating an individual against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating an individual with a SCCE peptide, which elicits an immune response in the individual with a SCCE peptide, which elicits an immune response in chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating an individual against SCCE, particularly an individual having, suspected or at risk of getting ovarian, lung, prostate, pancreatic or colon cancer. The oligonucleotide is useful for treating a neoplastic state in an individual, such as ovarian, breast, lung, colon, prostate, or pancreatic cancer, and other cancers in which SCCE is overexpressed. The peptides are also useful in the monitoring and development of immunotherapies for ovarian and other malignancies. The present sequence represents a peptide fragment of serine protease SCCE (stratum corneum chymotrytic enzyme).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for vaccinating an individual against SCCE, and in monitoring and developing immunotherapies for ovarian and other malignancies.
                                                                                                                                                                                             Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:35.
               Gaps
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                                                                                                                                                                                                                   serine protease; stratum corneum chymotrytic enzyme; SCCE; immune response; ovarian cancer; lung cancer; prostate cancer;
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             Indels
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Pred. No. 1.8e+06; 
; Mismatches 0;
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                                                                                                                     ADR68796 standard; peptide; 9 AA.
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100.08;
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                                                                                                                                                                                                                                                                                                                                                                 21-FEB-2003; 2003US-00372521
                                                                                                                                                                     02-DEC-2004 (first entry)
            9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       (UYAR-) UNIV ARKANSAS
                                                  ||||||||||||| 9
                                    1 LLPLQILLL 9
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Best Local Similarity
Matches 9; Conserv
 Best Local Similarity
                                                                                                                                                                                                                                                                                           WO2004075723-A2.
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                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                  10-SEP-2004
                                                                                                                                              ADR68796;
             Matches
                                                                                             RESULT 2
ADR68796
ID ADR6
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I is useful in gene therapy techniques to restore normal cutivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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hilarity 100.0%; Pred. No. 12;
Conservative 0; Mismatches
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                                                                 31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                 Tang YT;
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Best Local Similarity
9; Conserve
                                                                                                                                                                                                                                                 Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                       WPI; 2001-639362/73
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                                                                                                                                                                            (HYSE-) HYSEQ INC
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ID ADA
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ABG23378 standard; protein; 136 AA.

RESULT 3 ABG23378 ID ABG2

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The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more
                                                                       immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, cancer or dyslipidemia, and in chromosome mapping, tissue typing
                                                            human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
                                                                                                                          immune disorder; haematopoietic disorder; dyslipidaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smithson G, Millet I, Peyman, Smithson G, Millet I, Peyman, Patturajan M, Spytek KA, Edinger SR, L. Gorman L, Zerhusen BD, Anderson DW, Zhous I Ort T, Gorman L, Zerhusen BD, Anderson DW, Pena CEA, S. Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, S. Jiw, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 170; 586pp; English.
                                    Human NOV18c protein SEQ ID NO:96
                                                                                                                                                                                                                                               2001US-0326483P.
2001US-0327435P.
2001US-0327449P.
2001US-0327449P.
2001US-0328029P.
2001US-0328044P.
2001US-0328044P.
2001US-0328044P.
2001US-033044P.
2001US-0330144P.
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2001US-0349575P.
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2002US-0373817P.
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2002US-0381038P.
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2002US-0381642P.
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            06-NOV-2003 (first entry)
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N-PSDB; ADA05735.
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                                                                                                                                                                        WO2003029424-A2.
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17-OCT-2001;
18-OCT-2001;
22-OCT-2001;
24-OCT-2001;
                                                                                                                                                  Homo sapiens
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29-OCT-2001;
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16-MAY-2002;
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05-OCT-2001;
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17-MAY-2002;
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containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the mucleic acid molecule dascribed above; (5) acell comprising the mucleic acid molecule above binds to the polypeptide or nucleic acid molecule in a presence or amount of the above polypeptide or nucleic acid molecule in a gample; (8) methods for determining the presence of or nucleic acid molecule in a cample; (8) methods for determining the presence of suppeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (13) methods of treating the athology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide in a mamunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian in antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a syndrome associated with a human disease. The polypeptide or the nucleic acid can able used as hybridisation condisorers such as diabetes or obesity, infections, cachexia, cancer, advances such as diabetes or obesity, infections, cachexia, cancer, advanced energy in chromosome mapping, tissue typing, preventive medicine and bypobes, in chromosome mapping, tissue typing, preventive and various content in the process. The present sequence represents a human NOVX from the process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer. associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 40; DB
100.0%; Pred. No. 18;
Live 0; Mismatches
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; 2001US-0327435P.
; 2001US-0327449P.
; 2001US-0327917P.
; 2001US-0328029P.
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Matches 9; Conserv
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05-OCT-2001;
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obesity, or

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Dipippo

A, Shenoy SG; Berghs C, Di

CEA,

Ju J, Li L, Guo X; an K, Malyankar UM; Zhong M, Catterton E;

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probleming with the cells own genes and preventing their expression. Nova probe under an diagnostic assays to detect and quantitate the presence of probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NoVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators and antagonists) of the expression and activity of NoVX. The anti-NoVX polypeptide antibodies, agonists and antagonists may also be used to modulate NoVX polypeptide expression and activity of NoVX polypeptides. The anti-NoVX polypeptide antibodies may also be used to modulate NoVX polypeptide antibodies may also be used as diagnose and treat: metabolic disorders, diabetes, obesity, infectious disorders, Alzheimer's Disease, parkinson's Disorder, immune disorders, has antibacterial with obssity, the metabolic syndrome X and disturbances associated with obssity, the metabolic syndrome X and casticus and various dyslipidaemias, metabolic maxing disorders associated with chronic diseases and various cancer. They may also be used as antibacterial agents. The present sequence of a human NOVX protein.
                              NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and polynucleotides may be used to treat disorders associated with decreased expression or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX
                invention relates to isolated NOVX polypeptides and polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 40; DB 8; Length 198; 100.0%; Pred. No. 18; 0; Mismatches 0; Indels
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2001US-0327449P.
2001US-0327917P.
2001US-0328029P.
2001US-0328044P.
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Best Local Similarity 100.
Matches 9; Conservative
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05-0CT-2001; 2
09-0CT-2001; 2
09-0CT-2001; 2
09-0CT-2001; 2
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Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastlelli L, Stone DJ, Pena CEA, Shenoy SG;
Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                    2001US-0330142P.

2001US-0330309P.

2001US-0339266P.

2001US-0343629P.

2001US-0346357P.
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2002US-0374977P.
2002US-0381037P.
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2002US-0381042P.
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EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MILLER C E.
RASTELLI L.
PENAR D J.
PENA C E A.
SHENOY S G.
SHINNERS R A.
ROTHENBERS M E.
LEACH M D.
AGER M L.
BERGHS C I.
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GANGOLLI E A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GUO X.
PATTURAJAN M.
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ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIEGER D K.
SPADERNA S K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MILLET I.
PEYMAN J A.
KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-213931/20.
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CATTERTON E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMITHSON G.
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                                                    17-OCT-2001; 2
18-OCT-2001; 2
22-OCT-2001; 2
24-OCT-2001; 2
29-OCT-2001; 2
01-NOV-2001; 2
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22-APR-2002;
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(RIEG/)
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(/LIMS)

PEYM/)

KEKU/

(LILL/)

(ELLE/)

(MALY/

SPYT/

(PATT/

(ZERH/ (ZHON/)

ANDE/ CATT/ (JIWM)

GORM/

(MILL/) (RAST/) (STON/)

Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.

(ROTH/) (LEAC/) (AGEE/)

(BERG/

DIPI/

(SHEN/)

PENA/

EISE/)

Claim 1; SEQ ID NO 96; 395pp; English

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Gaps

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2001US-0330309P.
2001US-0341058P.
2001US-0339266P.
2001US-0343629P.
                                   2001US-0349575P.
2001US-0346357P.
                                                        2002US-0373817P.
                                                             2002US-0373826P.
                                                                   2002US-0373884P.
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2001US-0328849P
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             18-OCT-2001;
22-OCT-2001;
24-OCT-2001;
29-OCT-2001;
01-NOV-2001;
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16-MAY-2002;
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                                                                       22-APR-2002;
                                                             19-APR-2002
                                                                                            17-MAY-2002
                                                                                        16-MAY-2002
                                                                                                      29-MAY-2002
                                                                                                                 01-OCT-2002
                                                                                                  28-MAY-2002
                                                                                                            25-JUN-2002
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(CURA-) CURAGEN CORP.

Dipippo VA; Catterton E; Guo X; yman JA, Kekuda R, Ju J, Li L, Guo X Edinger SR, Ellerman K, Malyankar UM; Berghs C, Di Zhong M, Smithson G, Millet I, Peyman JA, NELLELTMAN K, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shimkets RA, Rothenberg ME, Leach MD, Agee ML, B. Shimkets RA, Rothenberg ME, Leach MD, Agee ML, B.

WPI; 2003-381626/36. N-PSDB; ADA05731.

New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics

Claim 1; Page 169-170; 586pp; English.

The present into acstribes NOVA process.

(e.g. NOVI). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically by chinds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to comprise apathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating contributions and antiliparemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a condition and modulator of and antiliparemic activities, and can be used in gene therapy. The colypeptide is useful in manufacturing a medicament for treating a colyperine associated with a human disease. The polypeptide or produced manual and present may be used in gene therapy. The colypeptide is useful in manufacturing a medicament for treating a colyperine may be used in gene therapy. acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various The present invention describes NOVX proteins, where X can be 1 to

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                                                                                                                                                                                                                                                                                                                                        anorexia; cancer, cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
                                                                                                                                                                                                                                                                                                                            numan; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
                                                                                                              Gaps
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                                                                                    6; Length 250;
                                                                                                              0; Indels
                                                                                   Query Match 100.0%; Score 40; DB Best Local Similarity 100.0%; Pred. No. 23; Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                           ADN62896 standard; protein; 250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-OCT-2001; 20010S-0327435P.
05-OCT-2001; 20010S-0327435P.
09-OCT-2001; 20010S-0328044P.
09-OCT-2001; 20010S-0328044P.
09-OCT-2001; 20010S-0328044P.
12-OCT-2001; 20010S-0328044P.
15-OCT-2001; 20010S-0328044P.
15-OCT-2001; 20010S-03380309P.
24-OCT-2001; 20010S-0339266P.
24-OCT-2001; 20010S-0343629P.
25-OCT-2001; 20010S-0343629P.
25-OCT-2001; 20010S-0343629P.
25-OCT-2001; 20010S-0343629P.
19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373815P.
19-APR-2002; 2002US-0373815P.
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2002US-0381642P.
2002US-0383656P.
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2002US-0381037P.
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MILLET I.
PEYMAN J A.
                                                                                                                                      1 LLPLQILLL
                                     present invention.
                                                                                                                                                                                                                                                                                                                                                                              wasting disorder.
                                                              Sequence 250 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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16-MAY-2002;
                                                                                                                                                                                                                                                                                                     Human NOV18a
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MILLER C E.
RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKET'S R A.
ROTHENBERG M E
LEACH M D.
                                      GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
                               MALYANKAR U M.
               PATTURAJAN M.
                                                                                                         EISEN A.
GANGOLLI E A.
                                                                                                                    SPADERNA S K.
                   SPYTEK K A.
EDINGER S R.
                                                                                                     DIPIPPO V A.
                                                      CATTERTON E.
                                                                                                                                                        WPI; 2004-213931/20.
                           ELLERMAN K.
KEKUDA R.
                                                                                                                 RIEGER D
                                                                                                                                                            N-PSDB; ADN62895.
                                                   ZHONG M.
           GUO X.
                                                          GI W.
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(KEKU/)
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(ANDE/)
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           (GUOX)
                           ELLE/
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Disclosure; Page 97; 137pp; English.
                                                                                                                                 AAR67888 standard; protein; 253 AA.
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                                                                                                                                                                                                                                     (revised)
(first entry)
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irpiolitii 11
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09-AUG-1995
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                                                                                                                                                                                    AAR67888;
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Best Local S
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AAW05383
                                                                              RESULT 8
                                                                                                           AAR67888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to isolated NOVX polypeptides and polynucleotides.

NOVX polypeptides and polynucleotides are used to prevent; diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and cativity of NOVX by supplementing the patient our production or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX binding with the cells own genes and preventing their expression. NOVX binding with the cells own genes and preventing their expression. NOVX polypeptides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of setorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX. The anti-NOVX polypeptide antibodies, agonists and antagonists may also be used as antigens in the anti-NOVX polypeptides may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polymelectides may be used in this way to prevent, and the various disseas, nectabolic disorders, diabetes, obesity, infectious dissease, anorexia, cancer, cancer associated acheeving may be used and disorders, and the various dyslipidaemias, metabolic disorders, and the various dyslipidaemias, metabolic disorders, and the various dyslipidaemias, metabolic disorders, and the warious diseases and various associated with observe the metabolic syndrome x and care associated with chronic diseases and various associated with observe the metabolic diseases and various cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dipippo VA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, Patturajan M, Spyrek KA, Edinger SR, Ellerman K, Malyankar UW, Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Aniller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and talated vectors, transformed cells and polypeptides, useful for treating skin disorders, e.g. acne or psoriasis, and for identification of specific inhibitors.
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                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis; callosities; keratosis pilaris; ichthyoses; eczema.
They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human stratum corneum chymotrophic recombinant enzyme (SCCE).
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                                                                                                                                          8; Length 250;
                                                                                                                                                                                                 0; Indels
                                                                                                                                          100.0%; Score 40; DB 100.0%; Pred. No. 23;
                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                      Similarity 100.
9; Conservative
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                                                                                                                                                                                                                                                                1 LLPLOILLL
                                                                                    Sequence 250 AA;
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Best Local
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This invention describes a novel non-human transgenic mammal or mammalian sequence comprising at least a significant part of a nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant; occupant in skin. The product of the invention is useful as a model for its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or testing of a comment or a paramaceutical formulation, and for the development of a diagnostic method. It can also be useful for screening or identifying a composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or composition effective for the prevention or treatment of an abnormal or composition effective for the prevention or treatment of an abnormal or composition effective for the prevention or treatment of an opposition and paramaceum diseases scale compound or composition effective for the prevention or treatment of an opposition and paramaceum and inherited skin diseases

Compound or composition effective for the prevention or treatment of an opposition and hyperkeracosis, epidermal inflammation, dermal inflammation, bruttus, atopic dermatitis, eczema, acne and inherited skin diseases

Compound or composition effective for the prevention or treatment of an anodel for further studies of itch mechanisms and the testing of potential compounds and compositions for relieve of various skin diseases
                                                                                                                                                                                                                                                                                                                                                           Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protease; krin cancer; hyperkeretosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human stratum corneum chymotryptic enzyme, SCCE
human kallikrein 7 (KLK7), used in the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           where itch is a component. This sequence represents the N-terminal fragment of the human stratum corneum chymotryptic enzyme, SCCB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synonymous with numan kallikrein / (KbK7), us
transgenic mammals described in the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 6; Page 37; 74pp; English
                                                     08-FEB-2002; 2002WO-IB001300.
                                                                                                     09-FEB-2001; 2001CA-02332655.
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                                                                                                                                                                                                                                                              Egelrud T, Hansson
                                                                                                                                                                                                                                                                                                                 WPI; 2002-643380/69
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Matches 9; Conserv
                                                                                                                                                                                (EGEL/) EGELRUD T. (HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synonymous with
  15-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB84406;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human amyloid precursor protein protease (AAW05383) is involved in the processing or clearance of amyloid precursor protein to form beta-amyloid peptide. Its amino acid sequence was deduced from a cDNA clone (AAT39783) obtd. from a human lung library. Recombinant protease can be produced in transformed or transfected prokaryotic (partic. E. coli) or eukaryotic appartic. N-120 host cells. It is used to develop products for the design and testing of cpds. useful for treating or preventing conditions associated with beta-amyloid peptide, esp. Alzheimer's disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated human amyloid precursor protein protease - used to develop prods. for the treatment or diagnosis of associated conditions, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                        Amyloid precursor protein protease; Alzheimer's disease; diagnosis;
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                                                                                                                                                     Human amyloid precursor protein protease.
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AAW05383 standard; protein; 253 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-US004294,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-00416257
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Best Local Similarity 100...
                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dixon EP, Johnstone EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ELIL ) LILLY & CO ELI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT39783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 253 AA;
                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                   WO9631122-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                      02-APR-1996;
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                                                                                                     31-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                      10-OCT-1996.
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Homo sapiens

WO200262135-A2

Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, or stratum corneum chymotryptic enzyme (SCCE) or its variant, or product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or testing of a commodition at a pharmaceutical formulation, and for the development of a diagnostic method. It can also be used as a model for screening or identifying a composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of the inflammatory skin diseases selected from diseases consisting of epidermal hyperkeratosis, accema, acne and inherited skin diseases with epidermal hyperkeratosis. The mammal of the invention is also useful as a model for further studies of itch mechanisms and the testing of potential compounds and compositions for relieve of various skin diseases where itch is a component This sequence represents the human stratum corneum chymotryptic enzyme, SCCE which is a serine protease synonymous with human kallikrain 7 (KLKT) and is used in the development of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; protease; cancer; immune-related disorder; cardiovascular disease; neuronal-associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain; mood disorder; hypertension; psychotic disorder; neurological disorder; dyskinesia;
                                                                                                                                                                                                                                                Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 40; DB 5; Length 253; 100.0%; Pred. No. 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of novel human protease #39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                          Claim 10; Page 58-59; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU82740 standard; protein; 253 AA
                                                        08-FEB-2002; 2002WO-IB001300
                                                                                    09-PEB-2001; 2001CA-02332655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-2002 (first entry)
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                                                                                                                                                                           Egelrud T, Hansson L;
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                                                                                                                                                                                                      WPI; 2002-643380/69.
                                                                                                                               (EGEL/) EGELRUD T. (HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3est Local Similarity
                                                                                                                                                                                                                     N-PSDB; ABQ76226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 253 AA;
WO200262135-A2.
                            15-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU82740;
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The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. restenosis and coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. diabetes, plan, sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypotension, hypotension, psychotic disorders, neurological disorders (e.g. Alzheiner's disease, Parkinson's disease) and dyskinesias. The nucleic acids and polypeptides are also useful for treating viral infections such as ocular disease (e.g. virus (HIV), and non-viral infections such as ocular disease (e.g. glaucoma) and macular degeneration. AAU82702-AAU82760 represent the novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
viral infection; human immunodeficiency virus; HIV; non-viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sudarsanam S, Manning G, Caenepeel S;
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                                        ocular disease; cytostatic; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human proteases of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Fig 2N; 313pp; English.
                                                                                                                                                                                                                                                                                                                        26-JUN-2001; 2001WO-US020171.
                                                                                                                                                                                                                                                                                                                                                                                             26-JUN-2000; 2000US-0214047P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABK31782.
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                                                                                                                                                                              40200200860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Charydczak G;
                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plowman G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU07440;
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molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer grading; cancer assessing; cancer monitoring.

VO200281638-A2

17-OCT-2002.

domo sapiens

Prostate cancer; gene expression; differential regulation;

Protein differentially regulated in prostate cancer #74.

(first entry)

28-JAN-2003

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2003-058520/05.
                                          N-PSDB; ABX10343
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Sun Z,
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0
                                                            100.0%; Score 40; DB 6; Length 253; 100.0%; Pred. No. 23; 0; Mismatches 0; Indels
regulated in prostate cancer
                                                                             Local Similarity 100.
nes 9; Conservative
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LLPLQILLL 14

ABU07471 standard; protein; 253 AA. ABU07471; ABU07471 ID ABUC XX AC ABUC

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Conservative

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Query Match

100.0%; Score 40; DB 6; Length 253; 100.0%; Pred. No. 23;

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The invention describes genes (1) which are differentially regulated in prostate cancer. (2) Is useful for diagnosing a prostate cancer in a semple comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises to prostate cancer. (1) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves cancer certains which are differentially-regulated in prostate cancer. (7) Is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer. (2) Is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells, which involves contacting a polypeptide differentially-regulated in prostate cancer. (2) is useful as molecular markers, as expension detecting, the test agent to modulate a biological activity of the polypeptide, and concert cells with a test agent modulates the biological activity. (1) is useful as molecular markers, as enty targets, and for detecting, diagnoshing, staging, grading, assessing, monitoring, prognosticating, conditions especially relating to prostate cancer. (1) and its expression conditions especially relating to prostate cancer. (1) and its expression products are used in the diagnostic test to assay for presence of cancer e.g., in tissue sections, in blopps, assay for presence of cancer e.g., in the polypeptide and thus conditions especially be used for expressing the polypeptide and thus conditions especially be used for expressing the polypeptide and thus conditions are used in the diagnostic test prostate cancer. The identification of specific penes, and groups of genes, expressed in pathways which are useful in diagnostic, therapeutic, and the in prostate cancer permine the definition of a pathways which are useful in prostate cancer permine the pre
                                                                                                                                                                                                                                                                                                                                                              Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 293-294; 416pp; English
                                                                                                                                                                                          (ORIG-) ORIGENE TECHNOLOGIES INC.
                                                                      08-APR-2002; 2002WO-US010824
                                                                                                                   06-APR-2001; 2001US-0281731P.
                      17-0CT-2002
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Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.

(ORIG-) ORIGENE TECHNOLOGIES INC. 06-APR-2001; 2001US-0281731P. 06-APR-2001; 2001US-0281732P. 08-APR-2002; 2002WO-US010824.

WPI; 2003-058520/05

Jay G;

Sun Z,

N-PSDB; ABX10375.

Claim 1; Page 351; 416pp; English.

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The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prosecte tissue, which involves determining the number of target genes which are differentially—regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (I) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves concerned the expression levels in a sample comprising prostate tissue of target genes which are differentially—regulated in prostate cancer. (C intervention in a subject having a prostate cancer, which involves contacting a polypeptide differentially—regulated activity of a polypeptide differentially—regulated activity of a polypeptide differentially—regulated cancer cells which involves contacting a polypeptide differentially—regulated in prostate cancer cells with a test agent under conditions effective for the test agent to modulate a biological activity (I) is useful as molecular markers, as drug targets, and for detecting, determining whether the test agent modulates the biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, determining predisposition to disease and conditions especially relating to prostate cancer. (I) and its expression conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic, then atture of genetic of cancer of cancer. (I) is useful for assessing cancer e.g., to determine the type of cancer. (I) a useful for assessing cancer e.g., to determine the type of cancer. (I) suspended by (I) can be used as target for therapy or drug discovery. (I) can also be used for expressing the polypeptide and groups of genes, expressed in pathways in the suspended and disease pathways and the delineation of targets in these pathways which are useful in disapnostic, therefore the polypeptide and disease pathways and the delineate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pathways which are useful in diagnostic, therapeutic, and clinical applications. This is the amino acid sequence of a protein diferentially regulated in prostate cancer
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The invention relates to a novel isolated polynucleotide. The polynucleotides of the invention have cytostatic activity, and may have a use in gene therapy, and in a vaccine. The composition and methods are useful in diagnosing and/or treating cancer, particularly ovarian cancer. The composition may also be used as a vaccine to prevent cancer. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide and polypeptide useful for diagnosing and/or treating cancer, particularly ovarian cancer, and as a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human stratum corneum chymotryptic enzyme - ovarian cancer clone 01676P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cytostatic; gene therapy; vaccine; cancer; ovarian cancer.
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                                                                                                                                                                                                                                    ABR58471 standard; protein; 253 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-OCT-2002; 2002WO-US031467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-OCT-2001; 2001US-0327135P. 30-MAY-2002; 2002US-0384531P.
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WPI; 2003-372001/35.
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                                                                                                                                                                                                                                                                                                                   ABR58471;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                          OM protein - protein search, using sw model
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July 13, 2005, 16:54:03; Search time 13.5556 Seconds (without alignments) 63.882 Million cell updates/sec BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-905-083A-35 1 LLPLQILLL 9 Scoring table: Perfect score: Sequence: Run on: Title:

283416 segs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	serine proteinase	cation transport P	hypothetical prote	conserved hypothet	tax-responsive ele	hepatocarcinogenes	Q	conglutinin precur	conglutinin - bovi	hypothetical prote	probable permease	hypothetical prote	ᆽ	hypothetical prote	cytochrome aa3 con	hypothetical prote	cholera toxin tran	transcription acti	amyloid precursor-	hypothetical prote	transport protein	lipopolysaccharide	chloramphenicol re	probable transport	probable transport	31	m	stromelysin 3 (EC	Na+/H+-exchanging
ID	A53968	D97163	A71875	B64638	JC7300	JC4857	833603	JN0450	145878	T17215	H82994	T12520	T50904	H75201	H84314	E70890	E82257	A25970	A46362	E75440	AF1535	JQ0708	B43750	B85535	F90684	A57468	JC6197	439	AI2088
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Score	40	36	35	35	34	34	34	34	34	34	34	34	34	33	33	33	33	33	33	32	32	32	32	32	32	32	32	32	32
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T29010 A31759 S23756	AB3214 T43766 G65039 A54984	JE0322 C84914 H86811 A41720	AB334 AB334 A98157 AH3130 T26360
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RESULT 1 A53968 serine pro N,Alternat C,Species: C,Date: 07	AS3968 serine proteinase SCCE precursor - human serine proteinase stratum corneum chymotryptic enzyme C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Drecies: 09-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
R; Hansson, J. Biol. C A; Title: C	R.Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T. J. Biol. Chem. 269, 19420-19426, 1994 A.Fitle: Cloning, expression, and Characterization of stratum corneum chymotryptic enzyme
A; kererenc A; Accessic A; Status:	A;Retelence Atlane: Absyco; Mullistanouzzi Frill:0034/05 A;Accession: A53968 A;Status: preliminary
A; Molecule A; Residues: A; Cross-ref	A;Molecule type: mkNA A;Residues: 1-253 «HAN» A;Coneting: UniPROT:P49862; GB:L33404; NID:g521214; PIDN:AAC37551.1; PID:g532504
A;Generica A;Gene: GI A;Cross-re A;Map posi	A;Gene: GDB:PRSS6; SCCE A,Cene: GDB:377730 A;Map position: 7q35-7q35
C; Superfan F; 30-245/L	C;Superfamily: trypsin; trypsin homology P;30-245/Domain: trypsin homology <try></try>
Query Match Best Local Matches	Query Match Best Local Similarity 100.0%; Pred. No. 2; Bast Local Similarity 100.0%; Pred. No. 2; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
È	1 LIPLOILLE 9
qq	6 LIPLOILLI 14
RESULT 2	

Cation transport P-type ATPase CAC2137 [imported] - Clostridium acetobutylicum (Species: Clostridium) 14-Sep-2001 #text_change 09-Jul-2004 (Species: Clostridium) 16: Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, R; Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R. J. Bacteriol. 183, 4823-4838, 2001 A;Reference number: A96900; MUD:21359325; PMID:21359325 A;Reference number: Aperimental source: Clostridium acetobutylicum ATCC824 A;Reperimental source: Clostridium acetobutylicum ATCC824 A;Genetics: A;Genetics:

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C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
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nes 8; Conservative
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A; Residues: 1-266 < MAS>
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C; Species: Helicobacter pylori
C; Species: Helicobacter pylori
C; Species: Helicobacter pylori
C; Species: Helicobacter pylori
C; Species: Helicobacter pylori
C; Statession: B64638
R; Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J. M.; Cotton, M.D.; Weldman, J.M.; Frijii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A; Athchors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A; Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Variety: merrain J999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004 C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004 C; Accession: A71875 F; AAlm, A. J. Ling, L. S. L.; Moir, D. T.; King, B. L.; Brown, E. D.; Doig, P. C.; Smith, D. R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S. D.; Jiang, Q.; Taylor, D. E.; Vovis, G. F.; Nature 397, 176-180, 1999 A; Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A; Reference number: A71800; MUID:99120557; PMID:9923682
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A;Residues: 1-493 <ARN>
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C;Genetics:
A;Start codon: GTG
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88.9%; Pred. No. 37;
ive 0; Mismatches 1; Indels
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90.0%; Score 36; DB 77.8%; Pred. No. 40; iive 2; Mismatches
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C;Accession: JC7300
R;Masaki, T.; Noguchi, H.; Kobayashi, M.; Yoshida, M.; Takamatsu, K.
DNA Res. 7, 187-193, 2000
A;Title: Isolation and characterization of the gene encoding mouse tax-responsive element
A;Reference number: JC7300
A;Accession: JC7300
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A;Residues: 1-267 <KIS>
K,Cross-references: UNIPROT:09R1S4
C;Comment: This is a basic-leucine zipper type transcription factor involved in hepatocel
C;Genetics:
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C;Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 17-Mar-1999
C;Accession: S33603
R;Lim, B.L.; Lu, J; Reid, K.B.M.
Immunology 78, 159-165, 1993
A;Title: Structural similarity between bovine conglutinin and bovine lung surfactant prot A;Reference number: S33603; MUID:93170856; PMID:8436402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004
C;Accession: JG4857
R;Kishimoto, T.; Kokura, K.; Kumagai, Y.; Makino, Y.; Tamura, T.
B;chlen Biophys. Res. Commun. 224, 746-751, 1996
A;Title: HTF: A b-zip transcription factor that is closely related to the human XBP/TREB:
A;Reference number: JG4857
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C;Superfamily: X box-binding protein 1; fos/jun DNA-binding domain homology
C;Keywords: leucine zipper; transcription factor
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C,Superfamily: X box-binding protein 1; fos/jun DNA-binding domain homology
C,Keywords: leucine zipper; transcription factor
F,58-98/Domain: fos/jun DNA-binding domain homology <FUD>
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A;Molecule type: mRNA
A;Residues: 1-369 < LINA
C;Superfamily: pulmonary surfactant protein D; C-type lectin homology
F;248-367/Domain: C-type lectin homology <LCH>
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88.9%; Pred. No. 32;
Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.0%; Score 34; DB 2; Length 266; 88.9%; Pred. No. 32;
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                                                                                                                                                                                                                                                                                          A; Cross-references: UNIPROT: Q9ESS3; DDBJ: AB036745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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A)Contents: annotation
R;Liou, L.S.; Sastry, R.; Hartshorn, K.L.; Lee, Y.M.; Okarma, T.B.; Tauber, A.I.; Sastry,
J. Immunol. 153, 173-180, 1994
A;Title: Bovine conglutinin gene exon structure reveals its evolutionary relationship to
A;Reference number: 146010; WUID:94267222; PMID:8207234
A;Accession: I46010
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;75.371/Product: conglutinin.N #status predicted <MA2>
F;248-369/Domain: C-type lectin homology <LCH>
F;248-369/Domain: C-type lectin homology <LCH>
F;63,87,99,135,141,159,162,198,210/Binding site: carbohydrate (Lys) (covalent) #status pr
F;63,87,99,135,141,159,162,198,210/Modified site: 5-hydroxylysine (Lys) #status experimer
F;78,96,108,111,129,132,147,153,171,195/Modified site: 4-hydroxyproline (Pro) #status exp
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C;Decies: 19-Dec.1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
C;Accession: 145878
R;Liou, L.S.; Sastry, R.; Hartshorn, K.L.; Lee, Y.M.; Okarma, T.B.; Tauber, A.I.; Sastry, Gene 141, 277-281, 1994
A;Title: Bovine conglutinin (BC) mRNA expressed in liver: cloning and characterization of A;Reference number: 145878, MUID:94215917; PMID:8163202
                                                                                                                                                                                                                                                                                                                                                                         A;Cross references: EMBL:U06860; NID:9507183; PIDN:AAB60624.1; PID:9514256
C;Comment: This protein mediates the agglutination of erythrocytes with antibody and comment: This protein is a Ca2+-dependent serum lectin specific for N-acetylglucosamine
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A,Cross-references: UNIPROT:P23805, GB:L18871, NID:g495012, PIDN:AAA20126.1, PID:g495013
C,Superfamily: pulmonary surfactant protein D, C-type lectin homology
F,248-369/Domain: C-type lectin homology <LCH>
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C;Species: Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17215
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
Bubmitted to the Protein Sequence Database, September 1999
A;Reference number: 218723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Introns: 67/1; 106/1; 142/1; 178/1; 217/1; 245/1
C;Superfamily: pulmonary surfactant protein D; C-type lectin homology
C;Keywords: calcium binding; glycoprotein; hydroxylysine; hydroxyproline
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-371/Product: conglutinin #status predicted <MAT>
F;46-214/Region: collagen-like
F;75-371/Product: conglutinin-N #status predicted <MA2>
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Pred. No. 44;
1; Mismatches 1; Indels
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A;Reference number: $34054; MUID:93319501; PMID:8328957
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A;Molecule type: mRNA
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77.8%;
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-371 <LIO>
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Biochem. J. 293, 15-19, 1993
A;Title: Research Communication. Localization of the receptor-binding site in the colled
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ar. J. Blochem. 215, 793-799, 1993
Tr. J. Blochem. 215, 793-799, 1993
Tr. J. Blochem. 215, 793-799, 1993
Freference number: 835044, MUID:93358905; PMID:8354286
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R; Kawasaki, N.; Itoh, N.; Kawasaki, T.
Bocchem. Biophys. Res. Commun. 198, 597-604, 1994
A;Title: Gene organization and 5'-flanking region sequence of conglutinin: A C-type mamm A; Reference number: JC2396; MUID:94128104; PMID:8297370
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A;Residues: 21-209,'S',211-371 <LEE>
R;Rawasaki, N.; Yokota, Y.; Kawasaki, T.
Arch. Biochem. BLophys. 305, 533-540, 1993
A;Title: Differentiation of conglutination activity and sugar-binding activity of conglu A;Reference number: S36879; MUID:93384312; PMID:8373191
A;Accession: S36879
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A,Molecule type: mRNA
A,Residues: 1-371 <8702>
A,Cross-references: UNIPROT:P23805; DDBJ:D14085; NID:g285643; PIDN:BAA03170.1; PID:g2856
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A, Residues: 1-371 <KA2>
A, Residues: 1-371 <KA2>
A, Note: The authors translated the codon GAT for residues 250 and 270 as Glu
R; Lu, J; Laursen, S.B.; Thiel, S.; Jensenius, J.C.; Reid, K.B.M.
Biochem. J. 292, 157-162, 1993
A, Title: The CDNA cloning of conglutinin and identification of liver as a primary site
A, Reference number: S33235; MUID:93277452; PMID:7684896
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R; Lee, Y.M.; Leiby, K.R.; Allar, J.; Paris, K.; Lerch, B.; Okarma, T.B.
Biol. Chem. 266, 2715-2723, 1991
A; Title: Primary structure of bovine conglutinin, a member of the C-type animal lectin A; Reference number: A23740; MUID: 91131556; PMID: 1993651
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A;Title: The carbohydrate specificity of conglutinin and its homology to proteins in
A;Reference number: A29416; MUID:87184551; PMID:3566740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JN0450; JC2396; $\overline{S}$33235; A23740; $\overline{S}$5674; I46010; A29416; $\overline{S}$34054
R;Suzuki, Y: Yin, Y.P.; Makino, M.; Kurimura, T.; Wakamiya, N.
Biochem. Biophys. Res. Commun. 191, 335-342, 1993
A;Title: Cloning and sequencing of a 3D-342, 1993
A;Title: Cloning and sequencing of a 2DNA coding for bovine conglutinin.
A;Reference number: JN0450; MUID:93213261; PMID:8460993
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A;Residues: 21-54;75-86, X', 88-89, X', 91, X', 93-94;208-209, X', 211-227 <KAW>
A;Experimental source: serum
R;Lu, J: Wiedemann, H: Holmskov, U.; Thiel, S.; Timpl, R.; Reid, K.B.M.
Eur. J. Biochem. 215, 793-799, 1993
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A;Residues: 1-172,'H',174-217,'A',219-271,'V',273-371 <LUU>
A;Cross-references: EMBL:X71774; NID:g395267; PIDN:CAA50665.1; PID:g395268
                                           Gaps
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ed. No. 44;
Mismatches
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A;Residues: 75-86, 'X', 88-89, 'X', 91,'I' <LUA>
A;Restidues: 75-86, 'X', 88-89, 'X', 91,'I' <LUA>
A;Experimental source: lung
A;Young, N.M.; Leon, M.B.
Biochem. Biophys. Res. Commun. 143, 645-651,
77.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: C3b-binding protein N;Contains: conglutinin-N
                                       7; Conservative
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LLPLSVLLL 11
                                                                                                          1 LLPLQILLL 9
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                 conglutinin precursor
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My protoporphyrin methyl transferase [imported] - Rubrivivax gelatinosus

My protoporphyrin methyl transferase [imported] - Rubrivivax gelatinosus

My protoporphyrin methyl transferase

My protoporphyrin methyl transferase

My protoporphyrin methyl transferase

My protoporphyrin transferase

My protoported

My protoporphyrin

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein PAB0088 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: H75201
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc A;Accession: H75201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: bchH
C;Superfamily: Rhodobacter capsulatus magnesium-protoporphyrin O-methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-1236 <NAG>
A;Cross-references: UNIPROT:Q9JPA4; EMBL:AB034704; PIDN:BAA94057.1
A;Experimental source: strain IL144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1236;
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Pred. No. 1.4e+02;
0; Mismatches 1;
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Pred. No. 27;
3; Mismatches
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88.9%;
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66.7%;
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      1044 LPLQLLLL 1051
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A,Molecule type: DNA
A,Residues: 1-146 <KAW>
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathota, A;Reference number: A82950; MUID:2043737; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable permease of ABC iron transporter PA5216 [imported] - Pseudomonas aeruginosa (st
C,Species: Pseudomonas aeruginosa
C,Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: UNIPROT:Q9HTX4; GB:AE004934; GB:AE004091; NID:g9951515; PIDN:AAG0860
Experimental source: strain PAO1
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C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
C;Accession: T12520
R;Wambutt, R:, Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A;Reference number: 217524
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                                 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-429 <POU-
A;Cross_references: EMBL;AL117404
A;Experimental source: adult testis; clone DKFZp434H2235
C;Genetics:
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A;Molecule tyteliminary
A;Residues: 1-1092 «WAM>
A;Residues: 1-1092 «WAM>
A;Crossreferences: EMBL:AL080133
A;Experimental source: adult testis; clone DKFZp434G173
C;Genetics:
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1; Mismatches
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Pred. No. 63;
1; Mismatches
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C, Genetics:
A, Gene: PA5216
C, Superfamily: sfuB protein
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381 LPLQLLLL 388
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-539 <STO>
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A; Accession: T17215
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A; Reference number: A84160; MUID:20504483; PMID:11016950
A; Accession: H84314
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-277 <STO>
A; Cross-references: UNIPROT:Q9HPI3; GB:AE004437; NID:g10581096; PIDN:AAG19884.1; GSPDB:G
C; Genetics: Cco
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Ajvene: CCp Query Match Best Local Similarity 75.0%; Pred. No. 52; Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	_		
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			Gaps
Ajvene: Ccp Query Match 82.5%; Score 33; DB 2; Length 277; Best Local Similarity 75.0%; Pred. No. 52; Matches 6; Conservative 2; Mismatches 0; Indels			ö
Ajvene: CCp Query Match 82.5%; Score 33; DB 2; Best Local Similarity 75.0%; Pred. No. 52; Matches 6; Conservative 2; Mismatches		Length 277;	0; Indels
Ajvene: CCp Query Match Best Local Similarity 75.0%; Matches 6; Conservative		Score 33; DB 2; Pred. No. 52;	2; Mismatches
Ajvene: ccp Query Match Best Local Similarity Matches 6; Conser		82.5%;	vative
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Search completed: July 13, 2005, 17:31:30 Job time : 14.5556 secs

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Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A., Bgelrud T., "Cloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase."; J. Biol. Chem. 269:19420-19426(1994).
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P49862 homo sapien
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                                                                                                                                                                                                                                                                                                                                               Perfect score:
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                                                                                                                          OM protein
                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
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                                                                                                                                                                                        Run on:
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Q7xi51 oryza sativ Q6u881 spodoptera P53246 bos taurus Q863a1 bos taurus Q8mhz9 bos taurus Q8mhz9 bos taurus Q8mhz9 bos taurus Q8nhz9 homo sapien Q8a81 pseudomonas Q9htx4 pseudomonas Q82i14 streptomyce Q86yp9 homo sapien Q7vb38 prochloroco Q6mzp0 homo sapien			e) late)	Craniata; Vertebrata; Buteleostomi; Catarrhini; Hominidae; Homo.	databases. CRC64;	Length 66;); Indels 0; Gaps 0;			pdate) update) (Stratum corneum chymotryptic		Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.		Wallbrandt P., Carlstein A.,
2 Q7XIS1 2 Q6USB1 1 PSPD BOVIN 2 Q86XB1 2 CL46 BOVIN 2 Q8NTGB 2 Q8RTGB 2 Q9RTX4 2 Q8RCI6 2 Q8CI6 2 Q8CI6 2 Q8CI6 2 Q8CYB 2 Q7VB3B 2 Q7VB3B	ALIGNMENTS	PRT; 66 AA.	28, Created) 28, Last sequence update) 28, Last annotation update) ant 3.		mandis E.P.; EMBL/GenBank/DDBJ - 82E1C392BC822FDB	0%; Score 40; DB 2; 0%; Pred. No. 2.6; 0; Mismatches 0		PRT; 253 AA.	ted) sequence u annotation 3.4.21)	, scce;		EQUENCE OF 23-53.	; kman A.,
885.0 885.0		PRELIMINARY;	(TrEMBLrel. (TrEMBLrel. (TrEMBLrel. splice vari	Metazoa; Chordata; utheria; Primates; 9606;	I.P., 04) to AT66047 7171	100.0%; Similarity 100.0%; 9; Conservative	LLPLQILLL 9 LLPLQILLL 14	STANDARD;	(Rel. 34, (Rel. 34, (Rel. 45, precursor	enzyme) (hSCCE). Name=KLK7; Synonyms=PRSS6, Homo ganiens (Human).	Metazoa; Chordata; utheria; Primates; 9606;	[1] SEQUENCE FROM N.A., AND SEQUENCE TISSUB-Skin;	MEDLINE=94308225; PubMed=8034709 Hansson L., Stroemqvist M., Baec
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		8 O H &	4444	8888			<i>&</i> 8	RE	A DT DT DT DT DT	B S S	8888	RP RP	E EX

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Kallikrein 7.
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9; Conservative
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253 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=KLK7;
                              ACT_SITE
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      CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chymotryptic enzyme.9 Commun. 211:586-589(1995).

First FUNCTION: May catalyze the degradation of intercellular cohesive structures in the catalyze the degradation of intercellular cohesive structures in the conflict layer of the skin in the continuous shedding of cells from the skin surface. Specific for amino acid residues with aromatic side chains in the Pl position. SCE cleaves insulin B chain at 6-Leu-| -Cys-7, 16-Tyr-| -Leu-17, 25-Phe-|-Tyr-26, and 26-Tyr-|-Thr-27. Could play a role in the activation of precursors to inflammatory cytokines.

-!- TISSUE SPECIFICITY: Abundantly expressed in the skin and is expressed by keratinocytes in the epidermis. Very low levels are also seen in the brain and kidney.

-!- SIMILARITY: Belongs to the peptidase SI family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00722; CHYMOTRYBSIN.
SMART; SM00020; Tryp SPc; 1.
PR0SITE; PS0240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Direct protein sequencing; Glycoprotein; Hydrolase; Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hansson L., Backman A., Ny A., Edlund M., Edholm E., Tornell J., Wallbrandt P., Egelrud T.;
"Epidermal overexpression of stratum corneum chymotryptic enzyme in mice; a model for chronic ithchy dermatitis ";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE=95314630; PubMed=7794273;
Skytt A., Stroemqvist M., Egelrud T.;
"Primary substrate specificity of recombinant human stratum corneum
                           Yousef G.M., Scorilas A., Diamandis E.P.; "Molecular characterization, mapping and tissue expression of the human stratum corneum chymotryptic enzyme gene."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6; Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Ross P., Paeper B., Wang K., Resquencing and expression analysis of the serine protease gene cluster_located in chromosome 19q13 region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 604438; -. GO: 6008236; F: Berine-type peptidase activity; TAS. GO: 60: 000854; P: Peddermal differentiation; TAS. InterPro; IPR009003; Pept Ser Cys. InterPro; IPR001254; Peptidase_S1. InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Activation peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, L33404; AAC37551.1; -. BMBL, PR166330, AAD49718.1; -. EMBL, AF24527; AAG33360.1; -. EMBL, AF332583; AAK69624.1; -. PIR, A53968; A53968, AS3968, ASSP, P00760; LEX. MEROPS; S01.300; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00089; Trypsin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC:6368; KLK7.
H-InvDB; HIX0015373; -.
                                                                                                                                                                                                                                                                                                                                                            Gene 257:119-130(2000).
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   IISSUE=Keratinocytes;
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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CHARACTERIZATION.
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SIGNAL 1
PROPEP 23
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MEDINE-ESKIN;

XX MEDINE-ESKIN;

XX Exausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Xx Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Xx Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Xx Altschul S.F., Zeeberg B. B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Xx Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Xx Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Xx Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Xx Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Xx Stapleton M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Xx Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Xx Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Xx Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Xx Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

Xx Hilalon D.K., Muray D.W., Sodergren E.J., Lu X., Gibbs R.A.,

Xx Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Xx Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Xx Hardesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Xx Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Xx Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
        (By similarity)
(By similarity)
(By similarity)
                                                                                                                                                                                                                                                                                                                                                                       .) (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 40; DB 1; Length 253; 100.0%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. -!- SIMILARITY: Belongs to peptidase family S1. EMBL; BC032005; AAH32005.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                 2D68B6B15A76A668 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC032005; AH32005.1; F. F. BC032005; LANDER, BC032005; AH32005.1; F. GO; GO: 0004263; F:chymotrypsin activity; IEA. GO; GO: 0004293; F:peptidase activity; IEA. GO; GO: 0004295; F:trypsin activity; IEA. GO; GO: 0006508; P:proteolysis and peptidolysis; IEA. InterPro; IPR001354; Peptidase S1. InterPro; IPR001314; Peptidase S1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Stratum corneum chymotryptic enzyme, preproprotein.
Charge relay system (I Charge relay system (I Charge relay system (I By similarity.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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N-linked (Glo
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=CZECH II; TISSUE=Mammary tumor;

MEDINRE-228825; PubMed=1247932; DOI=10.1073/pnas.242603899;

MISCHINE-228825; PubMed=1247932; DOI=10.1073/pnas.242603899;

A straubberg R.L., Feingold E.A., Grouse J.H., Derge J.G.,

A lacknil S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhate N.K.,

A lacknil S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhate N.K.,

A plachul R.F., Jordan H., Moore T., Max S. I., Wang J., Haich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A plachen M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., McKernan K.J., Malek J.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muray D.W., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton B., Ketteman M., Madan A., Robrigues S., Sanchez A.,

Nhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schhein J.E.,

T "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%; Score 38; DB 2; Length 104; 88.9%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FEB-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the FKBP-type PPIase family.
EMBL; BC022900; AAH22900.1; -.
HSSP; P18203; 1FKL.
MGD; MGI:1913370; FKbp11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM, PF00254; FKBP C; 1.
PROSITE; PS50059; FKBP PPIASE; 1.
SEQUENCE 104 AA; 11085 MW; 0534D57467566914 CRC64;
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Last annotation update)
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                     104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO: 0005615; C:extracellular space; TAS. GO; GO: 0016021; C:integral to membrane; TAS. InterPro; IPR001179; FKBP_PPIase.
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STRAIN-CZECH II; TISSUE-Mammary tumor;
                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                     PRT;
                                                                                                                                                                              QBR5D6;
01-UNN-2002 (TrEMBLrel. 21,
01-UNN-2002 (TrEMBLrel. 21,
01-MRN-2004 (TrEMBLrel. 26,
Pkbpl1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL_2004 (TrEMBLrel. 27, 05-JUL_2004 (TrEMBLrel. 27, 05-JUL_2004 (TrEMBLrel. 27, Pkbpll protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                     PRELIMINARY;
   7 LLPLQLLLL 15
                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
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es 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                Name=Fkbp11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
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Q6PKE2
ID Q6PK
AC Q6PK
DT 05-J
DT 05-J
DT 05-J
                                                                                          RESULT 5
                                                                                                                         Q8R5D6
                                                                                                                                                                                    STRAINE-EVB/N: TISSUE-Salivary gland;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Lischul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

A Lischul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

DA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Noilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahe S.J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

K. Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,

A Gones S.J., Marra M.A.;

Park M. Manna A.,

A Modriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield M. B.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield M. B.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield M. B.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield M. B.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield M. B.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield M. B.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield M. B.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield M. B.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield M. B.,

A Rodriguez A.C., Grimwood J., Schm
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                 100.0%; Score 40; DB 2; Length 253; 100.0%; Pred. No. 10; ive 0; Mismatches 0; Indels
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Pred. No. 7.2;
1; Mismatches 0; Indels
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Strauberg R.;
Strauberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC021345; AAH21345.1; -.
MGJ; MGI:191370; Fkbpl1.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
RRDIENCE 73 AA; 7819 MW; 93E8F53399BF3C11 CRC64;
                           01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Salivary gland;
InterPro; IPR009003; Pept_Ser_Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.0%;
88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                               Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LLPLQILLL 14
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08 VCA9
10 VGA9
10 VG
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Gaps

.. 0

0; Indels

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CHAIN
  STRAIN=FVB/N, TISSUE=Nammary tumor;

STRAIN=FVB/N, TISSUE=Nammary tumor;

MEDLINE=238825; PubMed=1247932; DOI=10.1073/pnas.242603899;

A Straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Rischul S.F., Zeeberg B., Buetow K.H., Schnefer C.F., Bhark N.K.,

A Rischul S.F., Zeeberg B., Buetow K.H., Schnefer C.F., Bhark N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina F.B., Tooshiyuki S., Carninci P., Prange C.,

R Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

B Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Willalon D.K., Murny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfaus G.G.,

Minting M., Madan A., Young A.C., Shevchenko Y., Boutfaus G.G.,

B Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Genezation and initial analysis of more than 15,000 full-length human
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05-JUL-2004 (Rel. 44, Last annotation update)
FK506 binding protein 11 precursor (EC 5.2.1.8) (Peptidyl-prolyl cistrans isomerase) (PPIase) (Rotamase) (19 kDa FK506-binding protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=Embryo; MEDLING189/nature01266; MEDLINE=22354683; PubMed=1246681; DOI=10.1038/nature01266; Okazaki Y., Furuno M., Kawukawa T., Adachi J., Bono H., Kondo S., Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T. Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FKBP-19).
Name-Fkbp11;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAINEFUB/N; TISSUE-Mammary tumor;
Strainsberg R.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, BC002311, AAH02311.11, ...
GO, GO:0005615, C:extracellular space; TAS.
GO, GO:0016021, C:integral to membrane; TAS.
InterPro; IRR001179; FKBP PPIase.
PROSITE; PSS0059; FKBP PPIASE; 1.
SEQUENCE 138 AA; 15105 MW; C138BBB0EFDDF59D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Q9D1M7; Q9CRE4;
28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 88.9
Matches 8, Conservative
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Mus musculus (Mouse).
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                                                                     NCBI_TaxID=10090;
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ID FK11 M
FK11 MOUSE

IDT 28-FEB

DT 28-FEB

DE FKSO6
IDE (FKSO6
IDE (FKSOE

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Dallek J. A., Endel D., Brucher C. F., Fortzer A., Prazer K.S., Acasteclind T. Cartbollid M. Gissic. (Caddik A., Fordson I.J., Jarvis E.D., R. Garsteclind T. Cartbollid M. Gissic. (Caddik A., Fordson I.J., Jarvis E.D., R. Kanal A., Kawaji H. Kanasawa Y., Kachisterki R. M., King B.L., Sonsylow A. Kunchin H. M. Gissic. (C. Gadik A., Kang B.L., Ramai A., Kawaji H., Kanasawa Y., Kachisterki R. M., King B.L., B. M. Milatis L., Walkendin H.J., McCansel L., Milhamal R., Mandia E., Makendin H.J., McCansel L., Milhamal R., Mandia E., Makendin H.J., McCansel L., Milhamal R., Mandia E., Mandia E., Makendin H.J., McCansel L., Milhamal R., Mandia E., Man
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GG; GO:000576; C:extracellular; ISS.
GG; GO:0017106; F:activin inhibitor activity; ISS.
GG; GO:0005125; F:cytokine activity; ISS.
GG; GO:0005179; F:portein binding; ISS.
GG; GO:0005179; F:portein binding; ISS.
GG; GO:000718; F:portein binding; ISS.
GG; GO:000718; F:cell growth and/or maintenance; ISS.
GG; GO:000718; P:cell growth and/or maintenance; ISS.
GG; GO:000718; P:cell growth and/or maintenance; ISS.
GG; GO:000718; P:cell surface receptor linked signal transdu. .; ISS.
GG; GO:000718; P:cell-cell signaling; ISS.
GG; GO:000728; P:cell-cell signaling; ISS.
GG; GO:00042841; P:hemoglobin biosynthesis; ISS.
GG; GO:00045841; P:hemoglobin biosynthesis; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vulpecula).";
J. Mol. Endocrinol. 21:141-152(1998).

J. Mol. Endocrinol. 21:141-152(1998).

J. Folycriow: Inhibins and activins inhibit and activate, respectively, the secretion of follitropin by the pituitary gland. Inhibins/activins are involved in regulating a number of diverse functions such as hypochalamic and pituitary hormone secretion, gonadal hormone secretion, escretion, erythroid differentiation, insulin secretion, nerve cell survival, embryonic axial development or bone growth, depending on their subunit composition. Inhibins appear to oppose the functions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99027340; PubMed=9801457; Vammontfort D., Fidler A.B., Heath D.A., Lawrence S.B., Tisdall D.J., Greenwood P.J., McNatty K.; Greenwood P.J., McNatty K.; Greenwood P.J., mcDNA sequence analysis, gene expression and protein localisation of the inhibin alpha subunit of Australian brushtail possum (Trichosurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: Dimeric, linked by one or more disulfide bonds. Inhibin is a dimer of alpha and beta-A. Inhibin B is a dimer of alpha and
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trichosurus vulpecula (Brush-tailed possum).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

Mammalia, Metatheria, Diprotodontia, Phalangeridae, Trichosurus.
                                                                                                                                                                          ;
57 144 PPIase, FKBP-type.
53 53 S -> F (in Ref. 1; BAB11559).
198 198 S -> R (in Ref. 1; BAB11559).
201 AA; 22137 MW; 94D955C57264BBB2 CRC64;
                                                                                                                    95.0%; Score 38; DB 1; Length 201; 88.9%; Pred. No. 20; ative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the TGF-beta family.
                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                               361 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF033340; AAC63945.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibin alpha chain precursor.
                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                     7 LLPLQLLLL 15
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                                                                                                                                                                                                                     1 LLPLQILLL
                                                                                                                                         Local Similarity
Les 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activins.
                                                                                                                                                                                                                                                                                                                                                                                            IHA_TRIVU
077755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=INHA;
                      CONFLICT
CONFLICT
SEQUENCE
                                                                                                                       Query Match
  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
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GO; GO:0045578; P:negative regulation of B-cell differentiation; ISS.

GO; GO:0045786; P:negative regulation of cell cycle; ISS.
GO; GO:0046881; P:negative regulation of follicle-etimulating. .; ISS.
GO; GO:0045077; P:negative regulation of interferon-gamma bio. .; ISS.
GO; GO:0045079; P:negative regulation of macrophage different. .; ISS.
GO; GO:0045650; P:negative regulation of phosphorylation; ISS.
RO; GO:001393; P:neurogenesis; ISS.
RO; GO:001394; P:neurogenesis; ISS.
RO; GO:001541; P:voarian follicle development; ISS.
RO; GO:0046881; P:positive regulation of follicle-stimulating. .; ISS.
RICEPTO; IPRO01399; TGFb.
REM: PF00019; TGF beta; 1.
REM: PRO0157; TGFb; 1.
REMART; SM00204; TGFB; 1.
REMART; SM00204; TGFB; 1.
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By similarity.
Inhibin alpha chain.
By similarity.
By similarity.
By similarity.
N-linked (GlCNAc...) (Potential).
N-linked (GlCNAc...) (Potential).
N-linked (GlCNAc...) (Potential).
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Eremothecium.
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STRAIN=ATCC 10895;
Voegeli S.E., Dietrich F.S., Brachat S., Lerch A., Gaffney T.,
Philippsen P.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE016815; AAS50586.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB 1; Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.5%; Score 37; DB 2; Length 552; 77.8%; Pred. No. 87; arive 2; Mismatches 0; Indels
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62707 MW; 62A8842023DEEA04 CRC64;
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6-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                              Hormone; Signal
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InterPro; IPR005599; Alg9 trans.
InterPro; IPR001202; WW REBS WWP.
Pfam; PF03901; Glyco transf 22; IPROSITE; PS01159; WW DOMAIN 1; UN
                                                                                                                                                                                                                                                                                                                                                                   250; TGF BETA 1; 1.
Growth Factor; Hor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38945 MW;
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8; Conservative
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              31ycoprotein;
SIGNAL
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7 LPLOILL 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium.
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Q97H76
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"Identification of a nucleocapsid protein (VP35) gene of shrimp white
spot syndrome virus and characterization of the motif important for
targeting VP35 to the nuclei of transfected insect cells.";
                                                                                                                                                                                                                                                   MEDLINE=20517548; PubMed=11062040; DOI=10.1006/viro.2000.0597; Tsai M.F., Tzeng H.F., Leu J.H., Chou C.M., Huang C.J., Yu H.T., Tzeng H.F., Leu J.H., Chou C.M., Huang C.J., Lin J.Y., Kou G.H., Lo C.F.; Identification and characterization of a shrimp white spot syndrome virus WSSV) gene that encodes a novel chimeric polypeptide of cellular-type thymidine kinase and thymidylate kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-21844071; PubMed=11853398; DOI=10.1006/viro.2001.1273;
Chen L.L., Leu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,
Lo C.F., Kou G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
                                                                                             White spot syndrome virus (WSSV).
Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.
                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=21548311; PubWed=11689662;
DOI=10.1128/JVI.75.23.11811-11820.2001;
Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
"Complete genome sequence of the shrimp white spot bacilliform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium yoelii yoelii.
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 2; Length 79;
Pred. No. 20;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
LO C.-F., Kou G.-H.;
Lo C.-F., Kou G.-H.;
Submitted COT-2033, AAL33136.1;
EMBL, AF33400570; AAL89055.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 AA; 9287 MW; 800910C7FFA0EC7E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-WAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                               79 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             637 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=17XNL;
PubMed=12368865; DOI=10.1038/nature01099;
                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                  Virol. 75:11811-11820(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.0%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MtN3/saliva family, putative.
                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                            Virology 293:44-53(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 LLPLQLILL 42
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                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                       NCBI_TaxID=92652;
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                                                                                       WBv132 (WSSV187)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=PY01249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                          08VB59:
                               Q8VB59
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                                                                                                                                                                                                         virus.
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        RESULT 10
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                   28VB59
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Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoalib A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J., Carucci D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,
Daly M.J., Bennett G.N., Koonin B.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing
J. Bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
BRIS., ABOO714; ARK80095.1;
BRIS., PO91163; D97163.
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R GO; GO:0015622; F:ATP binding; IEA.

R GO; GO:0015622; F:ATP binding; IEA.

R GO; GO:0016620; F:ATP ase activity; oxupled to transmembrane m. . .;

R GO; GO:0016820; F:hydrolase activity; IEA.

R GO; GO:0016812; F:hydrolase activity; acting on acid anhydrid. . .;

R GO; GO:0016812; P:metabolism; IEA.

R GO; GO:001592; P:metabolism; IEA.

R GO; GO:001592; P:metabolism; IEA.

R GO; GO:0015932; P:metabolism; IEA.

R InterPro; IPR001757; ATPase E1-E2.

R InterPro; IPR001757; ATPase E1-E2.

R InterPro; IPR001855; B:E2 ATPase IV.

R InterPro; IPR001855; H-ATPase IV.

R InterPro; IPR001893; D:H-ATPASE IV.

R InterPro; IPR001895; H-ATPASE IV.

R Pfam; PF00189; Cation_ATPASE IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                               parasite Plasmodium yoelli yoelli.";
Nature 419:512-519(2002)
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBU whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.0%; Score 36; DB 2; Length 637; 100.0%; Pred. No. 1.6e+02; cive 0; Mismatches 0; Indels
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EMBL; AABL01000328; EAA20540.1; -.
GO; GO:0016020; C:membrane; IEA.
InterPro; IPR04316; MIN3 slv.
Pfam; PF03083; MtN3 slv; Z.
SEQUENCE 637 AA; 70992 MW; BCS06320B2AEIFES CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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MEDLINE=21359325; PubMed=11466286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2001 (TrEMBLrel. 18, Created)
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Best Local Similarity 100...

Best Local Similarity
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Best Loca Matches

SERBERE

RESULT 13 Q6NB96

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EMBL; AF482910; AAM20485.1; -.

R GO; GO:00165783; C:endoplasmic reticulum; IEA.

GO; GO:0016509; C:endoplasmic reticulum; IEA.

R GO; GO:0016563; C:nucleus; IEA.

R GO; GO:000566; F:iron ion binding; IEA.

R GO; GO:0016491; F:oxidoreductase activity; IEA.

R GO; GO:0000468; F:transcription factor activity; IEA.

R GO; GO:00003700; F:transcription factor activity; IEA.

R GO; GO:000633; P:fatty acid biosynthesis; IEA.

R GO; GO:0006633; P:fatty acid biosynthesis; IEA.

R GO; GO:0006634; F:transcription of transcription, DNA-dependent; IEA.

R InterPro; IPR001525; Desaturase.

R InterPro; IPR001356; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L MOIL BIOIL EVOL. 15:35-49(1998).

C -! - CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

R MOIL BIOIL EVOL. 15:35-49(1998).

R EMBL; U338081; AABST168.1; --

R GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.

GO; GO:000491; F:NADH dehydrogenase (ubiquinone) activity; IEA.

R GO; GO:000491; F:NADH dehydrogenase cupiety; IEA.

R GO; GO:0006120; P:MICochondrial electron transport, NADH to u. .;

R InterPro; IPR00159; NADHUB Oxred4.

R InterPro; IPR00150; Oxidored q1.

R InterPro; IPR00150; Oxidored q2.

R InterPro; Oxidored q5.

R Pfam; PP01059; Oxidored q5.

R PRINTS; PR01437; NUOXDRDIASE4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Arvicolinae;
Clethrionomys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.5%; Score 35; DB 2; Length 183; 87.5%; Pred. No. 73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 AA; 21196 MW; 728DA94FAFCD14FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 AA; 23967 MW; 8AF1788697AED6A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O21527;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
NADH dehydrogenase subunit 4 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clethrionomys gapperi (Southern red-backed vole).
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PRINTS; PR00075; FACDDSATRASE.
PRINTS; PR00024; HOMEOBOX.
                               Genetics 162:1737-1752(2002).
EMBL; AF482910; AAM28485.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183
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Best Local Similarity
Matches 7; Conserv
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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STRAIN=CGA009 / ATCC BAA-98;
PubMed=14704707; DOI=10.1038/nbt923;
Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L., Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R., Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C., Harrison F.H., Gibson J., Harwood C.S.;
Complete genome sequence of the metabolically versatile photosynthetic bacterium Rhodopseudomonas palustris.";
Mat. Biotechnol. 22:55-61(2004).
EMBL; BX572595; CAE26376.1; ---
Complete proceome; Hypothetical protein.
SEQUENCE 181 AA; 19632 MW; CDB44D8210E565D1 CRC64;
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Helicoverpa assulta (Oriental tobacco budworm).
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Heliothinae; Helicoverpa.
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Knipple D.C., Rosenfield C.L., Nielsen R., You K.M., Jeong S.E.;
"Evolution of the integral membrane desaturase gene family in moths
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Bradyrhizobiaceae; Rhodopseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 2; Length 181;
Pred. No. 72;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                        Score 36; DB 2; Length 845.
Pred. No. 2.16+02;
                                                                                                                                                                                                            845 AA; 93779 MW; 401293AA1FF9D757 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                 TIGRFAMS; TIGRO1494; ATPASE_P-type; 3.
PROSITE; PS00154; ATPASE_L1_E2; UNKNOWN_1.
Complete proteome.
SEQUENCE 845 AA; 93779 MW; 401293AA1FP9
                                                                                                                                                                                                                                                                                                                                2; Mismatches
Pfam; PF00122; E1-E2_ATPase; 1.
                                                                                                                                                                                                                                                                 90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.5%;
87.5%;
                                                        PRINTS; PR00119; CATATPASE.
PRINTS; PR00120; HATPASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OrderedLocusNames=RPA0932;
                                                                                                                                                                                                                                                                                                 Local Similarity 77.8
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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05-JUL-2004
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DC Neopt
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Thu Jul 14 09:53:58 2005

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Search completed: July 13, 2005, 17:29:24 Job time : 64.2222 secs

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ALIGNMENTS
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Best Local Similarity 100.
Matches 9; Conservative
2787
2787
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                                               LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-918-243-35
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Sequence 3, Appli
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Sequence 3, Appli
Sequence 2, Appli
Sequence 31, Appl
Sequence 131, Appl
Sequence 1033, Appl
Sequence 1075, Ap
Sequence 1075, Ap
Sequence 12970, Ap
Sequence 12970, Ap
Sequence 12075, Apple
Sequence 6, Appli
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Sequence 36, Appl
Sequence 17, Appl
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                                                                   July 13, 2005, 16:58:04; Search time 19.4444 Seconds (without alignments) 34.552 Million cell updates/sec
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Sequence 3, Ap
Sequence 3, Ap
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-918-243-35
US-08-557-146-2
US-08-824-874-3
US-08-9154-34-2
US-08-930-188-2
US-09-764-76-3
US-09-764-76-3
US-09-764-76-3
US-09-90-016-7716
US-09-918-22-03
US-09-918-22-03
US-09-30-016-7716
US-09-30-016-7716
US-09-205-258-1083
US-09-205-258-1083
US-09-205-258-109
US-09-319-157A-19
US-08-339-157A-19
US-08-339-157A-19
US-08-918-039-157A-19
US-08-918-039-157A-19
US-08-918-039-157A-19
US-08-918-039-157A-19
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3-08-007-999B-3
3-08-689-276A-3
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                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                              1 LLPLQILLL 9
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Match Length
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52836, A
21399, A
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38, Appl
36, Appl
9507, Ap
2, Appli
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; Batent No. 6627403
; Batent No. 6627403
; GENERAL INFORMATION:
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;
; FILE REFERENCE: B6223CIP/C/D/CIP
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US
; FRIOR APPLICATION NUMBER: US
; RADOR SEQ ID NOS: 136
; SEQ ID NO 35

LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                      WESCULE OF 25.4 Application US/09502600A

Sequence 35, Application US/09502600A

Sequence 35, Application US/09502600A

Sequence 35, Application US/09502600A

Sequence 35, Application US/09502600A

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer

FILE REFERENCE: D6223CIP-C

CURRENT APPLICATION NUMBER: US/09/502,600A

PRIOR PILING DATE: 03-14-1998

SEQ ID NO 35

SEQ ID NO 35
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; OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-09-502-600-35
US-09-358-0558-15
US-09-358-0558-15
US-09-993-238-15
US-09-918-243-36
US-09-918-243-36
US-09-918-243-28
US-09-270-76-52836
US-09-270-76-52836
US-09-248-796A-21399
US-08-713-556F-38
US-09-489-039A-9507
US-09-489-039A-9507
US-08-477-254A-2
US-08-477-254A-2
US-08-477-254A-2
US-08-477-254A-2
US-08-478-277-18-2
US-08-478-277-18-2
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,344
FILING DATE: 16-SEP-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
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  CORRESPONDENCE ADDRESS
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Best Local Similarity
Matches 9; Conserv
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STATE: New York
COUNTRY: U.S.A.
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CLONE: 532504
                                                                                                                     94304
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Sequence 2, Application US/08557146

Patent No. 5834290

GENERAL INFORMATION:

APPLICANT: Bealrud, Torbjorn

APPLICANT: Hansson, Lennart

TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic

TITLE OF INVENTION: Enzyme (SCCE)

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: White & Case, Patent Department

STREET: 1155 Avenue of the Americas

CITY: New York

STREET: New York

COUNTRY: U.S.A.

ZIP: 10036-2787

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBP C compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)

CLASSIFICATION NUMBER: US/08/557,146

FILING DATE: 14-DEC-1995
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                                                                                                Query Match 100.0%; Score 40; DB 4; Length 9; Best Local Similarity 100.0%; Pred. No. 4.1e+05; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                ) NAME/KEY: CHAIN
) OTHER INFORMATION: Residues 6-14 of the SCCE protein
US-09-918-243-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 40; DB
100.0%; Pred. No. 4.2
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08824874
Patent No. 5962300
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hill Preeti
TITLE OF INVENTION:
UMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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FEATURE:
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Gaps
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Recombinant Stratum Corneum Chymotryptic
Enzyme (SCCE)
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COUNTRY:
ZIP: 10036-2787

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPDY disk
COMPUTER: IBM PC compatible
COMPUTER: PACTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PACTENTIN Release #1.0, Version #1.25 (BPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-154-344-2

Sequence 2, Application US/09154344

Patent No. 598126

GENERAL INFORMATION:

APPLICANT: Egelrud, Torbjorn

APPLICANT: Hansson, Lennart

ITLE OF INVENTION: Recombinant Stratum Corneum

TITLE OF INVENTION: Brayme (SCCE)

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: ADDRESS:

STREET: 1155 Avenue of the Americas
                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: Filed Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: BF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 anino acids
ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: USA
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  100.0%; Score 40; DB 3; Length 253; 100.0%; Pred. No. 4.2;
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                                          0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                     US-09-210-084-3
; Sequence 3, Application US/09210084
; Patent No. 6197511
; GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL KALLIKREIN
; TITLE OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE:
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; Patent No. 6472195
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Matches 9; Conservative
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY: GenB
CLONE: 532504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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US-09-764-762-3
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APPLICANT: Dixon, Eric P.
APPLICANT: Johnstone, Edward M.
APPLICANT: Little, Shella P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND
TITLE OF INVENTION: RELATED NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 40; DB 2; Length 253; 100.0%; Pred. No. 4.2;
                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,188
                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                            1103326-181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTAMTION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: x9239
TELEPHONE: 317-277-1090
TELEPHONE: 317-277-1090
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Eli Lilly and Company
STREFT: Lilly Corporate Center
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08930188 Patent No. 6093397
                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFRENCE/POCKET NUMBER: 1103
TELECOMMUNICATION:
TELEPHONE: (212) 819-8783
                                                                                                                                                                TELEPHONE: (212) 819-8783
TELEPAX: (212) 819-8783
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                : 253 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LLPLQILLL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                               US-09-154-344-2
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Query Match
Best Local Similarity 100.0%; Pred. No. «
Matches 9; Conservative 0; Mismatche
                                                                                                                NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9239
TELECOMMUNICATION INFORMATION:
TELEFAX: 317-277-1090
INFORMATION FOR SEQ ID NO: 2:
SEGUIENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7716, Application US/09949016
Patent No. 6812339
                               APPLICATION NUMBER: US 06
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein PCT-US96-04294-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 LLPLQILLL 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-949-016-7716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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APPLICANT: Dixon, Bric P.
APPLICANT: Johnstone, Edward M.
APPLICANT: Little, Shella P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND TITLE OF INVENTION: RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 253;
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                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPTUTER: IBM COMPatible
COMPTUTER: IBM COMPATIBLE
SOFTWARE: FASISED for Windows Version 2.0
CURRIN APPLICATION NUMBER: US/09/764,762
FILING DATE: 16-Jan-2001
CLASSIFICATION NUMBER: 09/210,084
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: 09/210,084
FILING DATE: CURROWN>
REPERENCAMION AND AND ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 96-0552 US
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
SEQ
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ZIP: 46285
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
^^TPTWARE: PatentIn Release #1.0, Version #1.30
^^TTWARE: PatentIn Release #1.0, Version #1.30
                     ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLONE: 532504
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application PC/TUS9604294
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 253 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
CORRESPONDENCE ADDRESS:
                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLPLQILLL 14
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASISEQ for Windows Version 4.0
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Patent No. 6294344
GENERAL INFORMATION:
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: Ovarian Cancer
FILE REFERENCE: D62232IP-C
CURRENT FILING DATE: 2000-02-11
CURRENT APPLICATION NUMBER: US/09/502,600A
                                                             0; Gaps
DB 5; Length 253;
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                                                             0; Indels
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                                                             Mismatches
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us-09-905-083a-35.rai

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EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
                                                                                                                                                  FILING DATE: 1997-06-06
APPLICATION UNMBER: 60/048,895
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,884
                                                                                                                                                                                                                                                                 FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,894
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APPLICATION NUMBER: 60/048,964
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PPLICATION NUMBER: 60/048,901
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APPLICATION NUMBER: 60/048,916
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APPLICATION NUMBER: 60/048,949
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APPLICATION NUMBER: 60/048,883
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EARLIER APPLICATION NUMBER: 60/094,657
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APPLICATION NUMBER: 60/048,971
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APPLICATION NUMBER: 60/048,974
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NUMBER OF SEQ ID NOS: 1227
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1083
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APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alesandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
FILE REFERENCE: D6223CIP(C/D/CIP)
CURRENT APPLICATION NUMBER: US/09/918,243
CURRENT APPLICATION NUMBER: US/09/918,243
PRIOR PILING DATE: 2001-07-30
PRIOR PILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 33
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                    90.0%; Score 36; DB 3; Length 9; 100.0%; Pred. No. 4.1e+05; Live 0; Mismatches 0; Indels
                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
CHER INCOMMATION: Residues 5-13 of the SCCE protein
US-09-502-600-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-09-918-243-33
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Patent No. 6525174
GENERAL INFORMATION:
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REPRENCE: PZ007P1
CURRENT PILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-06-04
EARLIER PILING DATE: 1998-06-04
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,881
EARLIER PILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 09/039,211
PRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 136
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 33, Application US/09918243; Patent No. 6627403; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: O'Brien, Timothy J.
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 8; Conservative
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ORGANISM: Homo sapiens
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60/048,893

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FILING DATE: 1998-07-15
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                                                                       NAME/KEY: SITE
1 LOCATION: (8)
2 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-1083
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APPLICANT: Mueller, Ken
APPLICANT: Mueller, Ken
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
APPLICANT: The Government of the Universe of America
APPLICANT: The Government of the Universe of America
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: SF, a No. 6558910el Family of Taste Receptors
FILE REFERENCE: 0120/97E08 US/09/393,634
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver. 2
EBNGTH.
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66.7%; Pred. No. 68;
iive 3; Mismatches 0; Indels
                                                                                                                                                                       4; Length 73;
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APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER PILING DATE: 1998-06-04
EARLIER FILING DATE: 1998-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
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Pred. No. 15;
1; Mismatches
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NAME/KEY: MOD RES
LOCATION: (143)
OTHER INFORMATION: Xaa = any amino acid
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; Sequence 37, Application US/09393634
: Patent No. 6558910
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LMPIQILLM 50
                 TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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25 LPLQLLLL 32
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Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
Matches 6; Conserv
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US-09-205-258-1079
LENGTH: 73
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                                                       FEATURE
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R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,373
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,875
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,374
R RILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,374
R APPLICATION NUMBER: 60/048,917
R FILING DATE: 1997-06-06
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R PILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,974
R FILING DATE: 1997-06-06
R PELING DATE: 1997-06-06
R PELING DATE: 1997-06-06
R PILING DATE: 1997-06-06
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FILING DATE: 1997-12-18
APPLICATION NUMBER: 60/092,921
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APPLICATION NUMBER: 60/048,964
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,915
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APPLICATION NUMBER: 60/049,019
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APPLICATION NUMBER: 60/048,898
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APPLICATION NUMBER: 60/048,962
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APPLICATION NUMBER: 60/048,963
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APPLICATION NUMBER: 60/048,877
APPLICATION NUMBER: 60/049,020
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,971
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FILING DATE: 1997-06-06
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PPLICATION NUMBER: 60/048,901
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APPLICATION NUMBER: 60/048,892
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APPLICATION NUMBER: 60/048,970
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NPPLICATION NUMBER: 60/048,916
                                                    APPLICATION NUMBER: 60/048,876
                                                                                                      APPLICATION NUMBER: 60/048,895
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                                                                             1997-06-06
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TYPE: PRT
ORCANISM: 424
ORCANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
OCTION: (152)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (314)
FEATURE:
NAME/KEY: SITE
COCATION: (315)
FEATURE:
NAME/KEY: SITE
OCCATION: (316)
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EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 1079
LENGTH: 424
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376 LPLQLLL 383
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
                              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1726220 segs, 386332138 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                              US-09-905-083A-35
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		•			SUMMARIES	
Result No.	Score	Query Match	* Query Match Length DB	DB	ID	Description
	40	100.0	6	. 6	US-09-918-243-35	Sequence 35, Appl
7	40	100.0	თ	6	US-09-905-083-35	Sequence 35, Appl
e	40	100.0	σ.	15	US-10-372-521-35	Sequence 35, Appl
4	40	100.0	6	16	US-10-831-075-35	Sequence 35, Appl
ß	40	100.0	198	15	US-10-262-511-96	Sequence 96, Appl
9	40	100.0	250	15	US-10-262-511-92	Sequence 92, Appl
7	40	100.0		6	US-09-888-615-98	~
80	40	100.0		σ	US-09-764-762-3	Sequence 3, Appli
σ	40	100.0		14	US-10-071-214-2	Sequence 2, Appli
10	40	100.0		14	US-10-071-214-48	Sequence 48, Appl
11	40	100.0		14	US-10-264-283-90	Sequence 90, Appl

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Gaps

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Query Match 100.0%; Score 40; DB 9; Length 9; Best Local Similarity 100.0%; Pred. No. 1.6e+06; Matches 9; Conservative 0; Mismatches 0; Indels

1 LLPLQILLL LLPLQILLL

ò g RESULT 2

S	S	00.0 253 119 00.0	US-10-295-027-498 US-10-13-999-48 Sequence 48, Appl US-10-643-795A-95 US-10-643-795A-95 US-10-643-795A-95 US-10-643-795A-95 US-10-948-518-95 US-10-348-318-95 US-10-348-318-33 US-10-343-33 US-09-905-083-33 US-10-425-115-233 US-09-905-083-33 US-10-435-39-207950 US-10-435-39-207950 US-10-435-39-207950 US-10-435-39-207950 US-10-435-39-207950 US-10-435-39-207950 US-10-435-39-207950 US-10-435-39-207950 US-10-335-377-6097 US-10-435-377-6097 US-10-335-977-6097 US-10-335-977-6097 US-10-335-977-6097 US-10-335-977-6100 US-10-335-977-6101 US-10-335-977-6101 US-10-335-977-6101 US-10-425-115-24490 US-10-425-115-24490 US-10-425-115-24490 US-10-425-115-24490 US-10-425-115-24490 US-10-425-115-24490 US-10-33-977-6103 US-10-425-115-218429 US-10-33-977-6103 US-10-425-115-218429 US-10-33-977-6103 US-10-435-977-6103 US-10	, 5 p 60 41
	100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 99.0 99	1 1 40 100 0 40 100 0 40 100 0 40 100 0 40 100 0 40 100 0 40 100 0 40 100 0 40 100 0 40 100 0 6 40	28555333 2855333 2855333 2855333 285533 28553 28	S C C L L C C L L C C C L L C C C L L C C C L C

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Gaps

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APPLICANT: Berghs, Constance TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
                                                                                                                                                                                                                                                                                                                                            Length 9;
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                                                                                                                                                                                                                                                    NAME/KEY: CHAIN
OTHER INFORMATION: Residues 6-14 of the SCCE protein
                                                                                                                                                                                                                                                                                                                                            100.0%; Score 40; DB 16;
100.0%; Pred. No. 1.6e+06;
tive 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2001-10-09
PRIOR PELICATION NUMBER: 60/381,642
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR APPLICATION NUMBER: 60/380,029
PRIOR PRILING DATE: 2002-10-09
PRIOR PLILNG DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/381,039
PRIOR PLILNG DATE: 2002-10-09
FILE REFERENCE: D6223CIP/C/D/CIP3
CURRENT APPLICATION NUMBER: US/10/831,075
CURRENT FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 10/372,521
NUMBER OF SEQ ID NOS: 140
SEQ ID NO 35
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 96, Application US/10262511 Publication No. US20040038223A1 GENERAL INFORMATION: APPLICANT: Smithson, Glennda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ju, Jingfang
Li, Li
Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
Malyankar, Uriel M.
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Shenoy, Suresh G.
Shimkets, Richard A.
Rothenberg, Mark E.
Leach, Martin D.
Agee, Michele L.
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Miller, Charles E.
Rastelli, Luca
Stone, David J.
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Anderson, David W.
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Peyman, John A.
Kekuda, Ramesh
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Catterton, Elina
                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100,
Matches 9; Conservative
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Gorman, Linda
                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT:
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APPLICANT:
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      Sequence 35, Application US/09905083

Sequence 35, Application US/09905083

Patent No. US20020146708A1

GENERAL INFORMATION:

APPLICANT: O' Exien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer

FILE REFERENCE: D6223CIP/C/Div

CURRENT APPLICATION NUMBER: US/09/905,083

CURRENT FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 09/502,600

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 35

LEMOTH: 9

LEMOTH: 9
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| Publication No. US20030223973A1
| GENERAL INFORMATION. |
| APPLICANT: Cannon, Martin J. |
| APPLICANT: Cannon, Martin J. |
| APPLICANT: Santin, Alesandro |
| TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer |
| FILE REFERENCE: D6223CIP/C/D/CIP2 |
| CURRENT FILING DATE: 2003-02-21 |
| PRIOR APPLICATION NUMBER: US 09/918,243 |
| PRIOR FILING DATE: 2001-07-30 |
| NUMBER OF SEQ ID NOS: 136 |
| SEQ ID NO 35 |
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Publication Wo. US20040224891A1
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 40; DB 9; Length 9; 100.0%; Pred. No. 1.6e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Residues 6-14 of the SCCE protein US-10-372-521-35
                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CHAIN
OTHER INFORMATION: Residues 6-14 of the SCCE protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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      US-09-905-083-35
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                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Matches 9; Conservative
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CORGANISM: Homo sapiens
US-09-888-615-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
CORGANISM: Homo sapiens
US-10-262-511-92
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US-09-764-762-3
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       PRIOR APPLICATION NUMBER: 60/328,056

PRIOR FILING DATE: 2001-10-09

PRIOR FILING DATE: 2002-04-17

PRIOR FILING DATE: 2002-04-17

PRIOR FILING DATE: 2002-04-17

PRIOR FILING DATE: 2002-04-19

PRIOR PLICATION NUMBER: 60/373,826

PRIOR PLICATION NUMBER: 60/373,826

PRIOR FILING DATE: 2001-04-19

PRIOR FILING DATE: 2001-10-05

PRIOR FILING DATE: 2001-10-06

PRIOR FILING D
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APPLICANT: Shinkets, Richard A.
APPLICANT: Leach, Martin D.
APPLICANT: Leach, Martin D.
APPLICANT: Leach, Michele L.
APPLICANT: Ages, Michele L.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME TITLE REFERENCE: 21402-462.
FILE REFERENCE: 21402-462.
FRIOR RELING DATE: 2003-05-28
FRIOR FILING DATE: 2001-10-02
FRIOR FILING DATE: 2001-10-02
FRIOR FILING DATE: 2002-04-19
FRIOR FILING DATE: 2001-0-09
FRIOR FILING DATE: 2001-0-09
FRIOR FILING DATE: 2001-0-09
FRIOR FILING DATE: 2001-0-09
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Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
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Malyankar, Uriel M
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Anderson, David W.
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Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
FILING DATE: 2002-05-16
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APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ju, Jingfang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Tatiana
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Miller, Char
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-511-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LLPLQILLL 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LLPLQILLL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-10-09
PRIOR PLILNG DATE: 2002-10-09
PRIOR PLICATION NUMBER: 60/381,038
PRIOR PLILING DATE: 2002-05-16
PRIOR PLILING DATE: 2001-10-09
PRIOR PLILING DATE: 2001-10-09
PRIOR PLILING DATE: 2002-04-19
PRIOR PLILING DATE: 2002-04-19
PRIOR PLILING DATE: 2002-04-19
PRIOR PLILING DATE: 2001-10-05
PRIOR PLING DATE: 2001-10-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Sequence 98, Application US/0988615
Sequence 98, Application US/0988615
Sequence 98, Application US/0988615
SEGUENCE 1 INFORMATION:
APPLICANT: PLOWMAN, GREGORY
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REPERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 98
LENGTH: 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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US-10-071-214-48

Sequence 48, Application US/10071214

Sequence 48, Application WS/10071214

Publication No. US20030066099A1

GENERAL INFORMATION:

APPLICANT: HANSSON, Lennart

APPLICANT: HANSSON, Lennart

APPLICANT: BEFERRUD, TOTABJON

TILLE REFERENCE: HANSSON-3A

CURRENT APPLICATION NUMBER: US/10/071,214

CURRENT APPLICATION NUMBER: US/67,422

PRIOR APPLICATION NUMBER: US 60/267,422

PRIOR APPLICATION NUMBER: US 60/267,422

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

NUMBER OF SEQ ID NOS: 50

SOFTWARE PATENTING NATE: 2010-02-09

SOFTWARE PATENTING DATE: 2010-02-09

SOFTWARE PATENTING DATE: 2010-02-09

SOFTWARE PATENTING DATE: 2010-02-09

SOFTWARE PATENTING DATE: 2010-02-09

LENGTH: 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) OTHER INFORMATION: Deduced amino acid sequence from the C-terminal part of SCCE from US-10-071-214-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.590
CURRENT APPLICATION NUMBER: US/10/264,283
CURRENT FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 111
SOFTWARE: COTIXA INVENTION Disclosure Database
SEQ ID NO 90
LENGTH: 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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Publication No. US200301444941
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
US-10-264-283-90
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US-10-295-027-498
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US-10-264-283-90
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                                                             Db
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Sequence 2, Application US/10071214

Sequence 2, Application US/10071214

Sequence 2, Application US/10071214

Sequence 2, Application US/10071214

GENERAL INFORMATION:
TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN

TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN

FILE REFERENCE: HANSON-3A

CURRENT FILING DATE: 2002-02-11

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: US 60/267, 422

PRIOR APPLICATION NUMBER: DK PA 2001 00218

PRIOR APPLICATION UNMBER: DK PA 2001 00218

PRIOR APPLICATION UNMBER: DK PA 2001 00218

NUMBER OF SEQ ID NOS: 50

NUMBER OF SEQ ID NOS: 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 40; DB 9; Length 253; Best Local Similarity 100.0%; Pred. No. 34; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                      ZIP: 94304

COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette
    MEDIUM TYPE: Diskette
    OPERATING SYSTEM: DOS
    SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/764,762
FILING DATE: 16-Jan-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/210,084
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLONE: 532504
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                        ADDRESSEE: Incyte Pharmac STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY: GenBank
                                                                    CITY: Palo Alto
STATE: CA
                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-10-071-214-2
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Best Local Similarity
Matches 9; Conserv
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LENGTH: 253
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PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-04-12
PRIOR PILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 48
LENGTH: 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: FREDERIC J. DESAUVAGE
APPLICANT: FREDERIC J. DESAUVAGE
APPLICANT: RENNETH J. HILLAN
APPLICANT: PAUL POLAKIS
APPLICANT: PAUL POLAKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VICTORIA SMITH
SUSAN D. SPENCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THOMAS D. WU
ZEMIN ZHANG
                                                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: Homo sapiens
US-10-173-999-48
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CRGANISM: Homo sapiens
US-10-408-765A-639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LLPLQILLL 14
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Best Local Similarity
Matches 9; Conserv
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                           PAPPLICANT: Murtary, Richard
APPLICANT: Murtary, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Bos Biotechnology, Inc.
TITLE OF INVENTION: Methods of biagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Screening for Modulators of Cancer, TITLE OF INVENTION: Methods of Screening for Modulators of Cancer, CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR PLING DATE: 2001-11-15
PRIOR PLILING DATE: 2001-11-15
PRIOR PLILING DATE: 2001-11-15
PRIOR PLILING DATE: 2001-11-21
PRIOR PLILING DATE: 2001-11-21
PRIOR PLILING DATE: 2001-11-24
PRIOR PLILING DATE: 2001-11-24
PRIOR PLILING DATE: 2001-11-24
PRIOR PLILING DATE: 2002-01-10-8
PRIOR PLING DATE:
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APPLICANT: Mack, David H.
APPLICANT: Gish, Kurt C.
APPLICANT: Eds Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
TITLE OF INVENTION: Cancer
FILE REFERENCE: 018501-002420US
CURRENT APPLICATION NUMBER: US/10/173,999
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: US 60/299,234
PRIOR APPLICATION NUMBER: US 60/315,287
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
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US-10-173-999-48
; Sequence 48, Application US/10173999
; Publication No. US20040005563A1
                                                         APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
Publication No. US20030232350A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity luv.
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; ORGANISM: Homo sapiens
US-10-295-027-498
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                                                                                                                                                                                                                                                                                                                                                                             Sequence 639, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Sounitra S.
APPLICANT: Eaby, Eoin D.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary W.
APPLICANT: Glenn, Gary W.
APPLICANT: Glenn, Gary W.
APPLICANT: Glenn, Gary W.
APPLICANT: Warnock, DenrIFIED IN THE MITOCHONDRIAL PROTEOME
FILE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
FILE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660084.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FLING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Score 40; DB 15; Length 253; larity 100.0%; Pred. No. 34; Conservative 0; Mismarches n. Tadala.
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Best Local Similarity 100.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 0; Indels
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; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR FILING DATE: 2002-08-19
; PRIOR PELLING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US 60/419,008
; PRIOR PILING DATE: 2002-09-23
; PRIOR PELLING DATE: 2002-09-15
; PRIOR FILING DATE: 2002-01-15
; PRIOR FILING DATE: 2002-10-15
; PRIOR FILING DATE: 2002-11-15
; PRIOR FILING DATE: 2002-11-15
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 95
; LEMOTH: 253
; TYPE: PRT
; ORGANISM: HOME SADIEN
US-10-643-795A-95
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Search completed: July 13, 2005, 18:23:39 Job time : 66.8889 secs

1 LLPLQILLL 9

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July 13, 2005, 16:12:23 ; Search time 76.6667 Seconds
GenCore version.5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-905-083A-36

1 SLLLPLQIL 9 Perfect score: Sequence:

Scoring table:

2105692 seqs, 386760381 residues Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

geneseqp2003as:*geneseqp2003bs:* A_Geneseq_16Dec04: geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2002s:* geneseqp2001s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

Human NOV Human NOV Human NOV Human str Human amy Human SCC Human SCC Amino aci Protein d Protein d Ovarian c Human hea Human str Human str Bacterial Cancer/an Human ova Human HSC Human str Human str Human tum Antipsori Description Add 53378 Add 65736 Add 65732 Add 62896 Add 62896 Add 62896 Add 6472 Add 6472 Add 6472 Add 6472 Add 6484 Add 6484 Add 6484 Add 6483 Aae08241 ADA05736 ADN62900 ADA05732 AAR67888 AAW05383 ABB84421 ABB84406 ABU07471 ABR58471 ADB80484 ADJ68833 ADN39180 ADL06515 AAE08238 ADR68794 ADS21222 AAU82740 ABU07440 ADN62896 ADR72880 8 Length Query 100.0 100.0 100.0 Score

61 4 AAO12472 812 7 ABO65558 394 6 ABU71803 804 6 ABY71036 9 4 AAC08240 9 4 AAC08240 9 8 AAC08240 9 8 AAC08240 9 8 AAC08240 71 4 AAC19347 71 4 AAC19347 71 4 AAC193706 73 4 AAC193706 73 4 AAC193706 74 AAC193706 75 AAC2303 267 2 AAC2303 267 2 AAC2303 267 2 AAC2303 267 8 AD14109 282 AD161449		Adj71036 Human hea Abp70828 Murine C1 Aae08240 Human str Aae08320 Human str	Human Human Human		Aaw22303 Rat CRII. Ad127274 Amino aci Add30604 Plant yie Adi44109 Plant tra	
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ALIGNMENTS

RESULT 1

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Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia.
                                     Human stratum corneum chymotrypsin enzyme peptide #6 (residues 4-12).
AAE08241 standard; peptide; 9 AA.
                         (first entry)
                         01-NOV-2001
            AAE08241;
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WO200159158-A1. Homo sapiens

16-AUG-2001,

07-FEB-2001; 2001WO-US003977.

11-FEB-2000; 2000US-00502600

(UYAR-) UNIV ARKANSAS

O'brien TJ;

WPI; 2001-514676/56

Diagnosing cancer comprises detecting stratum corneum chymotrypsin

Claim 25; Page 103; 127pp; English.

The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide

Sequence 9 AA;

100.0%; Score 40; DB 4; Length 9;

Query Match

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us-09-905-083a-36.rag

Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder.

WO200175067-A2.

11-OCT-2001.

Novel human diagnostic protein #23369

(first entry)

18-FEB-2002

ABG23378;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel method for vaccinating an individual against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating an individual with a SCCE peptide, which elicits an immune response in the individual. A peptide of the invention acts as a stratum corneum chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating an individual against SCCE, particularly an individual having, suspected or at risk of getting ovarian, lung, prostate, pancreatic or colon cancer. The oligonucleotide is useful for treating a neoplastic state in an individual, such as ovarian, breast, lung, colon, prostate, or peptides are also useful in the monitoring and development of immunotherapies for ovarian and other malignancies. The present sequence represents a peptide fragment of serine protease SCCE (stratum corneum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for vaccinating an individual against SCCE, and in monitoring and developing immunotherapies for ovarian and other malignancies.
                                                                                                                                                                                                                                                                                        Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:36.
                                 Gaps
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                                                                                                                                                                                                                                                                                                                        serine protease; stratum corneum chymotrytic enzyme; SCCE;
immune response; ovarian cancer; lung cancer; prostate cancer;
pancreatic cancer; colon cancer.
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               Pred. No. 1.8e+06;
                                 Mismatches
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100.08; td ...
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Best Local Similarity 100.
Matches 9; Conservative
                               9; Conservative
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                                                                                        SLLLPLQIL 9
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               Best Local Similarity
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                               Matches
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ADR68797
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

oiodiversity.

31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167. 30-MAR-2001; 2001WO-US008631.

Tang YT;

Drmanac RT, Liu C, WPI; 2001-639362/73

N-PSDB; AAS87565.

(HYSE-) HYSEQ INC

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGK) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I is useful in gene therapy techniques to restore normal cutivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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ABG23378 standard; protein; 136 AA.

RESULT 3
ABG23378
ID ABG2

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New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
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                                                                human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antipakinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alaheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smithson G, Millet I, Peyman C.
Smithson G, Millet I, Peyman C.
Patturajan M, Spytek KA, Edinger SR, Elle Cort T, Gorman L, Zerhusen BD, Anderson DW, Zhong Ort T, Gorman L, Earhusen BD, Anderson DJ, Pena CEA, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Ji W, Miller CE, Rastelli L, Stone DJ, Agee ML, F L'AR RA, Rothenberg ME, Leach MD, Agee ML, F L'AR RA, Rothenberg ME, Leach MD, Agee ML, F L'AR RA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 170; 586pp; English.
                                       Human NOV18c protein SEQ ID NO:96
                                                                                                                                                                                                                                               02-OCT-2002; 2002WO-US031373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2002; 2002US-00262511
            06-NOV-2003 (first entry)
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N-PSDB; ADA05735.
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                                                                                                                                                                                          WO2003029424-A2.
                                                                                                                                                                                                                                                                                                                                                          09-0CT-2001;
12-0CT-2001;
15-0CT-2001;
17-0CT-2001;
18-0CT-2001;
22-0CT-2001;
24-0CT-2001;
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29-OCT-2001;
01-NOV-2001;
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05-OCT-2001;
05-OCT-2001;
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19-APR-2002;
19-APR-2002;
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09-OCT-2001;
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22-APR-2002;
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17-MAY-2002;
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2002US-0373815P. 2002US-0373817P. 2002US-0373826P.

2002US-0373260P.

2002US-0373884P. 2002US-0374977P. 2002US-0381037P.

2002US-0381042P. 2002US-0381642P. 2002US-0383656P.

2002US-0383831P 2002US-0391335P

2002US-0381038P

2001US - 0327449P 2001US - 0327917P 2001US - 0328044P 2001US - 0328056P 2001US - 032849P 2001US - 0328449P 2001US - 0330309P
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containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (6) an entibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above copypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for case in treating a pathology that is related to an aberrant expression or aberrant physiclogical interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (11) a method of cor preventing a pathology associated with the above polypeptide in a cor preventing a pathology associated with the above polypeptide in a cor preventing a pathology associated with the above polypeptide in a cor preventing a pathology associated with the above polypeptide in a cor preventing a pathology associated with the above polypeptide in a cor preventing a pathology associated with a method for producing the above polypeptide in a cor preventing a pathology associated with a method for producing the above polypeptide in a cor prevent in an animal activities, and can be used in gene therapy. The collaboration and antilipaemic activities, and can be used in gene therapy. The collaboration and antilipaemic activities, and can be used in gene therapy. The collaboration and antilipaemic activities, and can be used to prevent metabolic collaboration and antilipaemic and antilipaemic and antilaborate such as diabetes or obesity, infections, ca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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100.0%; Pred. No. 11;
tive 0; Mismatches
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Ju J, Li L, Guo X; nan K, Malyankar UM; Zhong M, Catterton E; na CEA, Shenoy SG;

1 CEA, Suc.

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Peyman JA, Kekuda R, Ju J, Li L, Guo X;
A, Edinger SK, Ellerman K, malyankar UM;
Anderson DW, Zhong M, Catterton E;
sili L, Stone DJ, Pena CEA, Shenoy SG;
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W, Miller CE, Raster.
W, Miller CE, Raster.
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                             2001US-0330309P.
2001US-0341058P.
2001US-0339266P.
2001US-0343629P.
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2002US-0373815P.
2002US-0373817P.
2002US-0373826P.
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Patturajan M, Spytek KA,
Ort T, Gorman L, Zerhuse
                                                                                                                                                                                                                                        PATTURAJAN M.
SPYTEK K A.
EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eisen A, Gangolli EA,
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RIEGER D K.
SPADERNA S K.
                                                                                                                                                                                                                                                                                    GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                                        PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
LEACH M D.
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BERGHS C.
DIPIPPO V A.
                                                                                                                                                                                           MILLET I.
PEYMAN J A.
KEKUDA R.
                                                                                                                                                                                                                                                                                                                                  MILLER C E.
RASTELLI L.
STONE D J.
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N-PSDB; ADN62899.
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      12-0CT-2001;
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17-0CT-2001;
18-0CT-2001;
22-0CT-2001;
24-0CT-2001;
24-0CT-2001;
29-0CT-2001;
01-NOV-2001;
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16-MAY-2002;
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Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.

Claim 1; SEQ ID NO 96; 395pp; English

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The invention relates to isolated NOVX polypeptides and polynucleotides.

NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and activity of NOVX polypeptides associated with decreased expression or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polypeptides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of crestorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators the production of antibodies and in assays to identify modulators anti-NOVX polypeptide antibodies may also be used as anti-NOVX polypeptide antibodies may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and entagonists may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX colypeptides and polypeptide antibodies may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious disorders, lamune disorders, disorders, allowed cachexia, neurodegenerative disorders associated with obesity, the metabolic syndrome X and the watting and seaso and various dancers.

The production of antibodies associated with obesity, the metabolic syndrome X and the watting and the various disorders. The man and the various diseases and various cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
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09-0CT-2001; 2
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2001US-0341058P.
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01-NOV-2001;
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The present into present in a describes Nova processes, where A can be a too 35 containers, the composition comprising a polypetide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a medulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating cor preduced mammal; and (14) a method for producing the above polypeptide. NovX sequences have antidiabetic, anorectic, antibacterial, virucide, amammal; and (14) a method for producing the above polypeptide in a mammal and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in mann disease. The polypeptide or the nucleic and antidiabetic and antidiabetic and the above polypeptide or the mucleic and antidiabetic and antidiabetic and the above polypeptide or the mucleic and antidiabetic and antidiabetic and the above polypeptide or the mucleic and antidiabetic an Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ortr T, Gorman L, Zerhusen BD, Anderson DW, Ehong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK; New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics. The present invention describes NOVX proteins, where X can be 1 to 55 acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson' disease, immune disorders, haematopoietic disorders and various Claim 1; Page 169-170; 586pp; English.

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                                                                                                                                                                                                                                                                              human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer, cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder;
      probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the present invention.
                                                                                               Gaps
dyslipidaemias. The nucleic acids can also be used as hybridisation
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                                                                                                                                                                                                                                                                                                               haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
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                                                                        100.0%; Score 40; DB 100.0%; Pred. No. 14;
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2002US-0391335P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001US-0327917P
                                                             Query Match
Best Local Similarity 100.00
Best Local Similarity 100.00
                                                                                                                                                                                                                                     01-JUL-2004 (first entry)
                                                                                                                   1 SLLLPLQIL 9
                                                                                                                                       SLLLPLOIL 9
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MILLET I.
PEYMAN J A.
                                                                                                                                                                                                                                                                                                                           wasting disorder.
                                                    Sequence 250 AA;
                                                                                                                                                                                                                                                                                                                                                                   US2004038223-A1.
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22-OCT-2001;
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09-OCT-2001;
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24-OCT-2001;
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19-APR-2002;
                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-APR-2002;
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                                                                                                                                                                                                                                                            Human NOV18a
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                                                                                                                                                                                                                 ADN62896;
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(MILL/)
(PEYM/)
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The invention relates to isolated NoVX polypeptides and polynucleotides.

NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and activity of NOVX polypeptides and polynucleotides may be used to treat disorders associated with decreased polynucleotides may be used to treat disorders associated with decreased production or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polynucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (agonists and antagonists) of the expression and activity of NOVX. The anti-NOVX polypeptide antibodies, agonists and antagonists may also be anti-NOVX polypeptide antibodies, agonists and antagonists may also be used to modulate NOVX polymclecide expression and activity of NOVX polypeptides. The anti-NOVX polypeptide antibodies may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polymclectides may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, disorders, disorders, and the various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dipippo VA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 92; 395pp; English.
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Patturajan M, Spytek KA,
Ort T, Gorman L, Zerhuse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MILLER C E.
STONE D J.
PENA C E A.
SHENOY S G.
SHENOY S G.
SHENOY S G.
LEACH M D.
LEACH M D.
BERGHS M L.
BERGHS C DIPIPPO V A.
                                                                                                                                                                                                                                             MALYANKAR U M.
                                                                                                                                                SPYTEK K A.
EDINGER S R.
ELLERMAN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EISEN A.
GANGOLLI E A.
                                                                                                                         PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                    ZERHUSEN B D.
ANDERSON D W.
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CATTERTON E.
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                                                                                                                                                                                                                                                                                                       GORMAN L.
KEKUDA R.
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                                                                                         GUO X
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(LEAC/)
(AGEE/)
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(EISE/)
(GANG/)
(RIEG/)
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                                                                                                                         (PATT/)
(SPYT/)
(EDIN/)
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                                                                                      (GDOX)
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                                                                                                                                                                                                                                                   MALY/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and skin care products, especially to treat and prevent acne, xeroderma, or other hyperkeratotic conditions (e.g. callosities or keratosis plansis), ichthyoses, psoriasis, eczema, etc. It is produced recombinantly following mammal, insect, plant, or microorganism transformation with plasmid pS507. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and telated vectors, transformed cells and polypeptides, useful for treating skin disorders, e.g. acne or psoriasis, and for identification of specific inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The enzyme encoded by this sequence is used in pharmaceutical, cosmetic
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                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                              Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis; callosities; keratosis pilaris; ichthyoses; eczema.
They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
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                                                                                                                                                                                                                                                                                                                      Human stratum corneum chymotrophic recombinant enzyme (SCCE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 40; DB 2; Length 253; 100.0%; Pred. No. 15; ive 0; Mismatches 0; Indels
                                                                  8; Length 250;
                                                                                            0; Indels
                                                                  14;
                                                                                             0; Mismatches
                                                                  100.0%; Score 40; 100.0%; Pred. No.
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                                                                                                                                                                                                                        AAR67888 standard; protein; 253 AA.
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                                                                                                                                                                                                                                                                             (revised)
(first entry)
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Best Local Similarity 100.
Matches 9; Conservative
                                                                               Similarity 100.
9; Conservative
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                                                                                                                          1 SULLPLOIL
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                                        Sequence 250 AA;
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                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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09-AUG-1995
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                                                                  Query Match
Best Local S:
Matches 9
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ន្តដូន
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RESULT 9 AAW05383

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This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, operably linked to a promoter that drives expression of heterologous sccor its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or testing of a cosmetic or a pharmaceutical formulation, and for the development of a dagnostic method. It can also be used as a model for a skin disease or skin cancer. The invention is also useful for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of a compound or composition effective for the prevention or treatment of a compound or composition effective for the prevention or treatment of a compound or composition effective for the prevention or treatment of a prunitus atopic dermalitie, eczema, anche and inflammation, dermal inflammation, of the invention is also useful as a model for further studies of itch mechanisms and the testing of potential compounds and compositions for relieve of warious skin diseases of the processitions for relieve of warious skin diseases consisting of the invention is also useful made the constant of the invention is also useful as a model for further studies of itch mechanisms and the testing of the private of the invention is the series.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human stratum corneum chymotryptic enzyme, SCCE human kallikrein 7 (KLK7), used in the development of the
                                                                                                                                                                                                                                                                                                                                                         Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; setine protease; transgenic mammal; skin; skin disease; skin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  where itch is a component. This sequence represents the N-terminal fragment of the human stratum corneum chymotryptic enzyme, SCCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Page 37; 74pp; English.
                                                  08-FEB-2002; 2002WO-IB001300
                                                                                                09-FEB-2001; 2001CA-02332655.
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                                                                                                                                                                                                                                                                                                            WPI; 2002-643380/69.
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                                                                                                                                                                           (EGEL/) EGELRUD T. (HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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15-AUG-2002
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Matches
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ABB84406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated human amyloid precursor protein protease - used to develop prods. for the treatment or diagnosis of associated conditions, esp. Alzheimer's disease.
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                                                                                                                                                                                                      Amyloid precursor protein protease; Alzheimer's disease; diagnosis;
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                                                                                                                                                   Human amyloid precursor protein protease.
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AAW05383 standard; protein; 253
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                                                                                                (first entry)
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       02-APR-1996;
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                                                                                                31-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                    10-OCT-1996.
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                                             AAW05383
                                                                                                                                                                                                                                 therapy.
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Gaps

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Indels

Homo sapiens

WO200262135-A2

Homo sapiens.

RESULT 10

ઠ 요 viral infection; human immunodeficiency virus; HIV; non-viral infection;

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This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, or its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or testing of a cosmetic or a pharmaceutical formulation, and for the development of a diagnostic method. It can also be used as a model for a skin disease or skin cancer. The invention is also useful for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of compound or composition effective for the prevention or treatment of the phorexeratosis, acanthosis, epidermal inflammation, dermal inflammation, pruritus, atopic dermatitis, eczema, acne and inherited skin diseases with epidermal hyperkeratosis. The mammal of the invention is also useful contrating and composition for relieve of various skin diseases of the mechanisms and the testing of potential compounds and compositions for relieve of various skin diseases of the mechanisms and the testing of potential compounds and compositions for relieve of various skin diseases of the mechanisms and the testing of the prevention or treatment of the prevention of the provence or prove
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 corneum chymotryptic enzyme, SCCE which is a serine protease synonymous with human kallikrein 7 (KLK7) and is used in the development of the transgenic mammals described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Page 58-59; 74pp; English
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                                                                                                      08-FEB-2002; 2002WO-IB001300
                                                                                                                                                        09-FEB-2001; 2001CA-02332655
09-FEB-2001; 2001DK-00000218
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                                                                                                                                                                                                                                                                                                                       Egelrud T, Hansson L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 SLLLPLOIL 12
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                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-643380/69.
                                                                                                                                                                                                                                         (EGEL/) EGELRUD T. (HANS/) HANSSON L.
                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABQ76226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 253 AA;
WO200262135-A2
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                                                    15-AUG-2002
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The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. restenosis and coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory disorders (e.g. restenosis and rhunits and psoriasis), central or peripheral nervous system thematoria arthritis and psoriasis), central or peripheral nervous system disorders, migraines, pain, sexual dysfunction, mood disorders, attention disorders, hypotension, hypertension, psychotic disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's disease) and dyskinesias. The nucleic acids and polypeptides are also useful for treating viral infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. disease) and danalar degeneration. AAU82702-AAU82760 represent the novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                       treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
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                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding novel human proteases, useful for useful for
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                                                                                                                                                                                                                                                                           Sudarsanam S, Manning G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                 ocular disease; cytostatic; enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human proteases of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Fig 2N; 313pp; English.
                                                                                                                                                                26-JUN-2001; 2001WO-US020171.
                                                                                                                                                                                                    26-JUN-2000; 2000US-0214047P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JAN-2003 (first entry)
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9; Conservative
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                                                                                                                                                                                                                                         (SUGE-) SUGEN INC
                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABK31782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 253 AA;
                                                                                       WO200200860-A2
                                                                                                                                                                                                                                                                                            Charydczak G;
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                                                                                                                            03-JAN-2002
                                                                                                                                                                                                                                                                             Plowman G,
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Best Local {
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WO200281638-A2.

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The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (I) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which are differentially-regulated in prostate cancer. CC detarget genes which are differentially-regulated in prostate cancer. Preferably, the expression levels in a sample comprising prostate cancer. CC is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells with a test agent under conditions effective for the test agent to modulate a biological activity of the test agent to modulate a biological activity of the test agent to modulate a biological activity of the test agent to modulate a biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, daynosing, staging, determining predisposition to diseases and conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer of cancer, its stage of development, the nature of genetic defect, etc. The polypeptide encoded by (I) can be used as target for therapy or drug diseases, its stage of development, the nature of genetic defect, etc. The polypeptide encoded by (I) can be used as target for therapy or drug diseases, and groups of genes, expressed in pathways in these partners of the polypeptide and development, the nature of genetic defect, etc. The polypeptide and development, the nature of genetic defection in the diagnostic cancer reg., to determine the propagated and development, the respective of cancer, its stage of development, the nature of genetic defect, etc. The polypeptide and dev
                                                                                                                                                                                                                                                                                                                                                                          genes which are differentially regulated in prostate cancer, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pathways which are useful in diagnostic, therapeutic, and clinical applications. This is the amino acid sequence of a protein diferentially
                                                                                                                                                                                                                                                                                                                                                                                               for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 293-294; 416pp; English.
                                                                                                                                                                                                (ORIG-) ORIGENE TECHNOLOGIES INC.
                                                                                                                     06-APR-2001; 2001US-0281731P.
                                                                      08-APR-2002; 2002WO-US010824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            applications. This is the am
regulated in prostate cancer
                                                                                                                                                                                                                                                                                                 WPI; 2003-058520/05.
                                                                                                                                                                                                                                                                                                                        N-PSDB; ABX10343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 253 AA;
                       17-OCT-2002
                                                                                                                                                                                                                                                  Sun Z,
                                                                                                                                                                                                                                                                                                                                                                            Novel
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                              Gaps
                              ;
100.0%; Score 40; DB 6; Length 253; 100.0%; Pred. No. 15; 0; Indels ive 0; Mismatches 0; Indels
                              9; Conservative
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                Local Similarity
 Query Match
                              Matches
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ABU07471; RESULT 14 ABU07471 ID ABU XX AC ABU

ABU07471 standard; protein; 253 AA.

(first entry) 28-JAN-2003

Protein differentially regulated in prostate cancer #74.

Prostate cancer; gene expression; differential regulation; molecular marker; drug target; cancer detection; cancer diagnosis; cancer staging; cancer grading; cancer assessing; cancer monitoring.

Homo sapiens.

NO200281638-A2

17-OCT-2002.

08-APR-2002; 2002WO-US010824.

06-APR-2001; 2001US-0281731P. 06-APR-2001; 2001US-0281732P.

(ORIG-) ORIGENE TECHNOLOGIES INC.

Jay G; Sun Z, WPI; 2003-058520/05. N-PSDB; ABX10375. Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.

Claim 1; Page 351; 416pp; English.

The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (I) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which are differentially-regulated in prostate cancer. (I) is also useful for identifying appostate cancer. Which involves contacting a prostate the modulate a biological activity of a polypeptide differentially-regulated in prostate cancer. (I) is also useful for identifying applypeptide differentially-regulated activity of a polypeptide differentially-regulated cancer cells which involves contacting a polypeptide differentially-regulated in prostate cancer cells with a test agent under conditions effective for the test agent to modulate a biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, determining predisposition to disease and conditions especially relating to prostate cancer. (I) and its expression conditions especially relating to prostate cancer. (I) and its expression conditions especially relating to prostate cancer. (I) and its expression conditions especially relating to prostate cancer. (I) and its useful conditions, in biopsy sample, in total RNA, in lymph, in blood etc. (I) is useful for assessing cancer e.g., to determine the type of cancer. (I) encancer (I) and its useful conditions of the polypeptide encoded by (I) can be used as target for therapy or drug discovery. (I) can also be used for expressing the polypeptide and groups of genes, expressed in pathways which are useful in diagnostic, therapeutics the polypeptide conditions to treat prostate cancer. The identificant is the useful an pathways which are useful in diagnostic, therapeutic, and clinical applications. This is the amino acid sequence of a protein diferentially regulated in prostate cancer

Sequence 253 AA;

Gaps ö 100.0%; Score 40; DB 6; Length 253; 100.0%; Pred. No. 15; 0; Mismatches 0; Indels Conservative Best Local Similarity Matches 9; Conserv Query Match

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The invention relates to a novel isolated polynucleotide. The polynucleotides of the invention have cytostatic activity, and may have a use in gene therapy, and in a vaccine. The composition and methods are useful in diagnosing and/or treating cancer, particularly ovarian cancer. The composition may also be used as a vaccine to prevent cancer. The present sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotide and polypeptide useful for diagnosing and/or treating cancer, particularly ovarian cancer, and as a vaccine.
                                                                                                                                                                                                 Human stratum corneum chymotryptic enzyme - ovarian cancer clone O1676P.
                                                                                                                                                                                                                            Human; cytostatic; gene therapy; vaccine; cancer; ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 40; DB 6; Length 253; Best Local Similarity 100.0%; Pred. No. 15; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 157-158; 169pp; English
                                                                                                      ABR58471 standard; protein; 253 AA.
                                                                                                                                                                                                                                                                                                                                                    02-OCT-2002; 2002WO-US031467.
                                                                                                                                                                                                                                                                                                                                                                                02-OCT-2001; 2001US-0327135P. 30-MAY-2002; 2002US-0384531P.
                                                                                                                                                                  07-JUL-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mannion J;
                 4 SLLLPLQIL 12
1 SLLLPLQIL 9
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                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                     ABR58471;
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Gaps

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Search completed: July 13, 2005, 17:19:54 Job time : 77.6667 secs

4 SLLLPLQIL 12

1 SLLLPLQIL 9

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

July 13, 2005, 16:54:03 ; Search time 13.5556 Seconds Run on:

(without alignments) 63.882 Million cell updates/sec

US-09-905-083A-36 40 Title:

1 SLLLPLQIL 9 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	ä	hypothetical prote	daunorubicin resis			1-acyl-sn-glycerol	tax-responsive ele	hepatocarcinogenes			probable transport	ExoT protein - Rhi	probable membrane	hypothetical prote	hypothetical prote	3-ph	probable permease	ABC transporter, m	hypothetical prote	antibiotic resista	hypothetical prote	SNF1-related prote	probable membrane	hypothetical prote	O-antigen transpor	probable competenc	myosin-heavy-chain	hypothetical prote	interleukin-2 prec
QI	A53968	H75201	AB3334	T02912	C97402	AC2620	JC7300	JC4857	B85327	C49349	B95976	S40176	S61692	G65039	C84914	T48649	A98157	AH3130	D83934	D69779	C91063	B90120	AC0834	A90083	A69149	AE0614	A46136	AC2445	145913
DB		7	7	~	~	~	~	~	N	7	7	~	N	~	7	N	N	~	~	~	~	7	7	~	Н	N	~	~	7
% Query Match Length	253	146	370	218	264	264	266	267	282	494	494	582	622	196	303	354	372	372	392	395	398	401	413	470	475	754	783	913	155
% Query Match	100.0	95.0	82.5	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0			٠		77.5			•		77.5	•	•	77.5	77.5		75.0
Score	4	38	33	32	32	32	32	32	32	32	32	32	32	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	30
Result No.	П	8	m	4	Ŋ	9	7	89	σ	10	11	12	13		15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

interleukin-2 - go interleukin-2 prec probable membrane	hypothetical prote probable phosphate NADH2 dehydrogenas	nypountical ploce call division prot cytochrome aa3 con probable high affi	r-call surface gly conserved hypothet surfactant protein	conglutinin precur conglutinin - bovi hypothetical 41.1K
S38662 S11488 E96979	T43766 T39622 T17092	G69/98 F83598 H84314 T43663	HLHUCB E82656 S33603	JN0450 I45878 S47704
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155 155 168	189 190 208	223 277 289	333 349 369	371 371 375
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ALIGNMENTS

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Cispecies: Homo sapiens (man)
Cibate: 07-Jul-1995 #text_change 09-Jul-2004
Cibate: 07-Jul-1995 #text_change 09-Jul-2004
Cibate: 07-Jul-1995 #tequence_revision 07-Jul-1995 #text_change 09-Jul-2004
Cibate: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
Cibatession: A53968
A; The Cooling, expression, and characterization of stratum corneum chymotryptic enzyme
A; Reference number: A53968; MUID:94308225; PMID:8034709
A; Reference number: A53968
A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-253 *HAN>
A; Cross-references: UNIPROT:P49862; GB:L33404; NID:g521214; PIDN:AAC37551.1; PID:g532504
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                           N;Alternate names: stratum corneum chymotryptic enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 40; DB 2; ilarity 100.0%; Pred. No. 1.6; Conservative 0; Mismatches 0.
serine proteinase SCCE precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                            C,Genetics:
A,Gene: GDB:PRSS6, SCCE
A,Crose.references: GDB:377730
A,Map position: 7435-7435
C,Superfamily: trypsin, trypsin homology
F,30-245/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
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RESULT 2

hypothetical protein PAB0088 - Pyrococcus abyssi (strain Orsay)
hypothetical protein PAB0088 - Pyrococcus abyssi
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: H75201
R;Anonymous, Genoscope abyssi genome sequence: insights into archaeal chromosome struc A;Reference number: A75001
A;Cession: H75201
A;Accession: H75

A;Gene: PAB0088 C;Superfamily: Pyrococcus abyssi hypothetical protein PAB0088

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Query Match

80.0%; Score 32; DB
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches
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Pred. No. 66;
2; Mismatches
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Best Local Similarity 75.0
Matches 6; Conservative
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19 ILLPLQLL 26
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19 ILLPLQLL 26
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Matches 6; Conserv
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A; Residues: 1-264 < KUR>
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A; Residues: 1-218 cBEV.
A; Experimental source: cultivar Columbia; BAC clone T13J8
A; Experimental source: cultivar Columbia; BAC clone T13J8
R; Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; J
Paz-Arres, J.; Weisshaar, B.
A; Title: Towards functional characterisation of the members of the R2R3-MYB gene from Ar
A; Reference number: Z14349; MUID: 9839469; PMID: 9839469
A; Acession: T51654
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable transcription factor MYB41 [similarity] - Arabidopsis thaliana (fragment) N;Alternate names: protein T13/08.220 C;Spectar Arabidopsis thaliana (mouse-ear cress) C;Date: 24-Mar-1999 #sequence revision 24-Mar-1999 #text_change 16-Aug-2004 C;Accession: T02912; T51654 C;Accession: T02912; T51654 T51654 C;Bevan, M; Pohl, T; Weizenegger, T; Hoheisel, J; Mewes, H.W.; Mayer, K.F.X.; Schuel submitted to the Protein Sequence Database, February 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-370 «KUR»
A;Cross-references: UNIPROT:Q8YHY9; UNIPROT:Q8FZX1; GB:AE008917; PIDN:AAL51837.1; PID:g1
A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                      R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
A;Accession: AB3334
                                                                                                                                                                                                                                                                        daunorubicin resistance transmembrane protein [imported] - Brucella melitensis (strain C;Species: Brucella melitensis (c;Date: 01-Feb-2002 #text_change 09-Jul-2004
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C;Superfamily: myb DNA-binding repeat homology
C;Keywords: transcription factor
[F:1-48/Domain: myb DNA-binding repeat homology (fragment) <MYB>
Score 38; DB 2; Length 146;
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                                                     0; Indels
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Pred. No. 59;
2; Mismatches
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Cross-references: EMBL:AF062882; PIDN:AAC83604.1
                            Pred. No. 2.3;
1; Mismatches
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  95.0%;
88.9%;
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ilarity 75.0%;
Conservative 2
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Best Local Similarity
6; Conserv?
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                 Best Local Similarity
Matches 8; Conserv
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A, Note: T13J8.220
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A,Gene: BMEI0656
  Query Match
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probable acyltransferase (AF232919) [imported] - Agrobacterium tumefaciens (strain C58, (C) Species: Agrobacterium tumefaciens (C) Species: Agrobacterium tumefaciens (C) Species: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 16-Aug-2004 (C) Accession: C94402 (A) Specience C94. (C) Allinger, M.; Miller, M.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A;Reference number: A97359; MUID:21608551; PMID:11743194
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C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 16-Aug-2004
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 16-Aug-2004
C;Accession: ACC220
C;Accession: ACCC
C;Acc
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A;Residues: 1-264 <KUR>
A;Cross-references: UNIPROT:08UIE2; GB:AE008688; PIDN:AAL41377.1; PID:g17738693; GSPDB:GR
A;Experimental source: strain C58 (Dupont)
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A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; MUID:21608550; PMID:11743193
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DB 2; Length 218;
54;
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A;Map position: circular chromosome
C;Superfamily: 1-acyl-sn-glycerol-3-phosphate acyltransferase
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C;Superfamily: 1-acyl-sn-glycerol-3-phosphate acyltransferase
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llarity 75.0%; Pred. No. 66;
Conservative 2; Mismatches
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C, Genetics:

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probable transport protein, similar to Wzx exoT [imported] - Sinorhizobium meliloti (stre C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: B95976
B;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernanc Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endos A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: B95976
A;Status: preliminary
A;Anclevile type: DMA
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A;Residues: 1-494 «KUR.
A;Cross-references: UNIPROT: P33699; GB: AL591985; PIDN: CAC49474.1; PID: g15140960; GSPDB:GR
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
B;Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
D; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C
A;Reference number: A96039; MUID: 21368234; PMID: 11474104
                             A;Cross-references: UNIPROT:Q9M0J5; GB:NC_001268; NID:g7269665; PIDN:CAB79613.1; GSPDB:GPC;Genetics:
A;Gene: A;Gene: A;Gene: A;Gene: A;Gene: A;Gene: A;Ap;S110: 4
C;Superfamily: barley myb-related protein 3; myb DNA-binding repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable succinoglycan transport protein ExoT - Rhizobium meliloti
C;Species: Rhizobium meliloti
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Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 0.
                                                                                                                                                                                                                                                                        80.0%; Score 32; DB 2;
100.0%; Pred. No. 70;
iive 0; Mismatches
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C;Superfamily: hypothetical protein b2046
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Best Local Similarity 100.
Matches 7; Conservative
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122 SLLIPLQL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 SLLLPLQ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SLLLPLQI 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SLLLPLQ 7
A;Residues: 1-282 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Contents: annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hepatocarcinogenesis-related transcription factor - rat
C;Species: Rattus norregicus (Norway rat)
C;Species: Rattus norregicus (Norway rat)
C;Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Jul-2004
C;Accession: JC4857
R;Kishimoto, T.; Kokura, K.; Kumagai, Y.; Makino, Y.; Tamura, T.
B;ochem. Biophys. Res. Commun. 224, 746-751, 1996
A;Title: HTP: A b-zip transcription factor that is closely related to the human XBP/TREE
A;Reference number: JC4857
                                                                                probable transcription factor MYB41 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85327
R;anonymous, The Buropean Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUD:20083488; PMID:10617198
A;Accession: B85327
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-267 <KIS>
A;Cross-references: UNIPROT:Q9R1S4
C;Comment: This is a basic-leucine zipper type transcription factor involved in hepatoce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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C;Superfamily: X box-binding protein 1; fos/jun DNA-binding domain homology
C;Keywords: leucine zipper; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: X box-binding protein 1; fos/jun DNA-binding domain homology C;Keywords: leucine zipper; transcription factor F;Se-98/Domain: fos/jun DNA-binding domain homology <FUD> F;Se-126/Region: leucine zipper motif
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A;Residues: 1-266 <MAS>
A;Cross-references: UNIPROT:Q9ESS3; DDBJ:AB036745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.0%; Score 32; DB 2
100.0%; Pred. No. 66;
tive 0; Mismatches
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Best Local Similarity 100...
7; Conservative
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Best Local Similarity 100.
L.c. 7; Conservative
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Search completed: July 13, 2005, 17:31:31
Job time : 14.5556 secs
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A;Map position: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable membrane protein YOR137c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein 03329; hypothetical protein YOR3329c
C;Species: Saccharomyces cerevisiae
C;Dactes: O9-Mar-1996 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: S61692; 867022
R;Benes, V.; Andrade, M.A.; Rechmann, S.; Teodoru, C.; Banrevi, A.; Sander, C.; Valencia Bubmitted to the EMBL Data Library, December 1995
A;Description: Nucleotide sequence and analysis of a 130 kb fragment of yeast chromosome A;Reference number: S61643
A;Accession: S61692
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A,Residues: 1-622 <BEN>
A,Cross-references: UNIPROT:Q12212; EMBL:X94335; NID:g1262139; PID:e217839; PID:g1164980
R,Vooss-references: UNIPROT:Q12212; EMBL:X94335; NID:g1262139; PID:e217839; PID:g1164980
R,Vooss-references: V.; Rechmann, S.; Teodoru, C.; Schwager, C.; Paces, V.; Ansorge, W. submitted to the Protein Sequence Database, July 1996
A,Reference number: S66965
                                                                                                                                                                                                                                                                             ExoT protein - Rhizobium meliloti
C;Species: Rhizobium maliloti
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 19-May-2000
C;Accession: $40176
R;Becker, A.; Kleickmann, A.; Kuester, H.; Keller, M.; Arnold, W.; Puehler, A.
submitted to the EMBL Data Library, April 1993
A;Description: Analysis of the Rhizobium meliloti genes exoU, exoW, exoW, and exoI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:Z75045; NID:g1420348; PID:e252028; PID:g1420349; MIPS:YOR137c
A;Experimental source: strain S288C
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Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 582;
80.0%; Score 32; DB 2; Length 494
75.0%; Pred. No. 1.2e+02;
ive 2; Mismatches 0; Indels
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C;Keywords: transmembrane protein
F;11-27/Domain: transmembrane #status predicted <TMM>
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75.0%; Pred. No. 1.5e+02;
iive 2; Mismatches 0;
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A,Residues: 1-582 <BEC>
A;Cross-references: EMBL:Z22646
C;Superfamily: hypothetical protein b2046
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Best Local Similarity 75.0
Matches 6; Conservative
                                                    6; Conservative
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141 SALIPLOVL 149
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||SLLIPLQL 129
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122 SLLIPLQL 129
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                                                                                                    1 SLLLPLQI 8
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                     Best Local Similarity
Matches 6; Conserv
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hes 6; Conserv
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A; Residues: 1-622 < VOS>
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A; Status: preliminary
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C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: G65039
A;Reference D.J.; Mau, B.; Shao, Y.
Silence 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MuID:97426617; PMID:9278503
A;Reference number: A64720; MuID:97426617; PMID:92367142; PIDN:AAC75661.1; PID:91788965; A;Residues: 1-196 <BLAT>
A;Residues: 1-196 <BLAT>
A;Cross-references: GB:AE000347; GB:U00096; NID:92367142; PIDN:AAC75661.1; PID:91788965; A;Experimental source: strain K-12, substrain MG1655
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-303 <5TO>
A,Residues: 1-303 <5TO>
A,Cross-references: UNIPROT:022910, GB:AE002093; NID:g2275214; PIDN:AAB63836.1; GSPDB:GNC
C;Genetics:
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77.5%; Score 31; DB 2; Length 196;
Best Local Similarity 87.5%; Pred: No. 77;
Matches 7; Conservative 0; Mismatches 1; Indels
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hypothetical protein b2612 - Escherichia coli (strain K-12)
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SEQUENCE FROM N.A
TISSUE=Brain;
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ID KLK7 HUMAN
AC P49862;
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Q6DTY1;
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                                                                                                                                          July 13, 2005, 16:15:23 ; Search time 62.2222 Seconds (without alignments) 74.069 Million cell updates/sec
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"Cloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase.";
J. Biol. Chem. 269:19420-19426(1994).
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01-OCT-1996 (Rel. 34, Last sequence update)
02-OCT-2004 (Rel. 45, Last annotation update)
Kallikrein 7 precursor (EC 3.4.21.-) (Stratum corneum chymotryptic enzyme) (hSCCE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AX(46152; AAT(66047.1; ''' SERIC392BCB22PDB CRC64;
SEQUENCE 66 AA; 7171 WW; 82EIC3922ECDB CRC64;
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                 0876R3
0922G5
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Name=KLK7; Synonyms=PRSS6, SCCE;
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Best Local Similarity 100.0%;
Matches 9; Conservative C
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Lucopean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Epidermal overexpression of stratum corneum chymotryptic enzyme in mice; a model for chronic ithchy dermatitis.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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Skytt A., Stroemqvist M., Egelrud T.;
"Primary substrate specificity of recombinant human stratum corneum
                                  Yousef G.M., Scorilas A., Diamandis E.P.;
Moblecular characterization, mapping and tissue expression of the
human stratum corneum chymotryptic enzyme gene.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                               PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6; Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J., Moss P., Paeper B., Wang K.; Squencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region."; Gene 257:119-130(2000).
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CHARACTERIZATION.
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SIGNAL 1
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THE REAL BRANKS AND BR
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Trausbesching,

W MEDLINE=2218825; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Klausner R.D., Celling F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Frange C.,

Brownstein M.J., Usdin T.B., ToSchiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McKennan K.J., Mallek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Halton B., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A shes S.J., Marra M.A.,

Young A.C., Shevching D.E., Schnerch A., Schein J.E.,

A shes S.J., Marra M.A.,

Young A.C., Shevching D.E., Schnerch A., Schein J.E.,

A shes S.J., Marra M.A.,

Young A.C., Shevching D.E., Schnerch A., Schein J.E.,

A shes S.J., Marra M.A.,

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                  (By similarity).
(By similarity).
(By similarity).
                                                                                                                                                                                                                  .) (Potential).
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                                                                                                                                                                                                                                                                                  Similarity 100.0%; Score 40; DB 1; Length 253; Similarity 100.0%; Pred. No. 6.4; 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. -- SIMILARITY: Belongs to peptidase family S1. EMBL; BC032005; AAH32005.1; -- HSSP; P00760; 1EZX.
                                                                                                                                                                                                                    -linked (GlcNAc. . .) (Pc
2D68B6B15A76A668 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:cpptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:trypsin activity; IEA.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Stratum corneum chymotryptic enzyme, preproprotein.
               Charge relay system (1)
Charge relay system (1)
Charge relay system (1)
By similarity.
N-linked (GlCNAC...)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 AA.
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01-OCT-2002 (TrEMBLrel. 22, Last seq
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                                                                                                                                                                                                                                           27525 MW;
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4 SLLLPLOIL 12
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253 AA;
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176
201
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Best Local S
Matches 9
CHAIN
ACT SITE
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"Generation and initial analysis of more than 15,000 full-length human
                                                MEDLINE-98152303; PubMed-9491603;
Engel S.R., Hogan K.M., Taylor J.F., Davis S.K.;
"Molecular systematics and paleobiogeography of the South American
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 AA; 23967 MW; 8AF1788697AED6A2 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
NON TER 208 208
SEQUENCE 208 AA; 23967 MW; 8AF1788697AED6A2
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STRAIN-FVB/N; TISSUE-Salivary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (TrEMBLrel. 20,
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les 8, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SLLLPLQIL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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MEDLINE=22511545; PubMed=12622808;

MEDLINE=22511545; PubMed=12622808;

A Cohen G.N., Barbe V., Plament D., Galperin M., Heilig R., Lecompte O.,

A Cohen G.N., Barbe V., Plament D., Galperin M., Heilig R., Lecompte O.,

A Cohen G.N., Weisenbach J., Ripp R., Thierry J.-C.,

An der Oost J., Weisenbach J., Zivanovic Y., Forterre P.;

An integrated analysis of the genome of the hyperthermophilic

T archaeon Pyrococcus abyssi.",

Mol. Microbiol. 47:1495-1512(2003).

EMBL; AJ248283; CAB49063.1; -.

REMBL; AJ248283; CAB49063.1; -.

REMBL; AJ248283; CAB49063.1; -.

REMBL; AJ248283; CAB49063.1; -.

REMBL; PFOSOR4; DUF819.

Refam; PFOSOR4; DUF819.

W Complete proteome: Hypothetical protein.

W Complete AA; 16092 MW; 7182941371258C1F CRC64;
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Arvicolinae;
Clethrionomys.
NCBI_TaxID=56223;
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                                                                                                                                                                                                                                                                    100.0%; Score 40; DB 2; Length 253; 100.0%; Pred. No. 6.4; ive 0; Mismatches 0; Indelg
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                   Pfam; PF00089; Trypsin; 1.

PRINTS, PR0072; CHYMOTRYPSIN.

SMART; SM00020; Tryp_SPc; 1.

PROSITE; PS02040; TRYPSIN DM; 1.

PROSITE; PS00134; TRYPSIN JH; UNKNOWN_1.

PROSITE; PS00135; TRYPSIN JES; UNKNOWN_1.

Hydrolase; Protease; Serine protease.

SEQUENCE 253 AA; 27608 MW; 2D68B6A41B22A668 CRC64;
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Last annotation update)
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01-JAN-1998 (TrEMBLrel, 05, Last sequ
01-OCT-2003 (TrEMBLrel, 25, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
InterPro; IPR009003; Pept_Ser_Cys
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                                                                                                                                                                                                                                                                                                                          9; Conservative
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nes 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   1 SULLPLOIL 9
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Matches 9; Conserv
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01-MAY-2000
01-MAY-2000
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021527;
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10 09V2D5

AC 099V2

DT 01-M

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Gaps

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2; Length 208; 0; Indels

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LLLPLOLL 13
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          2 LLLPLQIL
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                                                                                                                    Fkbp11 protein.
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                                                                        Q6PKE2
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Kakaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                      85.0%; Score 34; DB 2; Length 73; 87.5%; Pred. No. 32; 0; Indels ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-!-SIMILARITY: Belongs to the FKBP-type PPIase family.
EMBL; BC022900; AAH22900.1; -. HSSP; P18203; 1FKL.
Strausberg R.; Strausberg R.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. Submitted (JAN-2002) to the EMBL, BC021345; AAH21345.1; -- MGD; MGI:1913370; Fkbp11.. GO; 00:0005615; C:extracellular space; TAS. GO; 00:0016021; C:extracellular space; TAS. SEQUENCE 73 AA; 71819 MM; 93E8P53399BF3C11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prosite; Prosite; Prosite; 1.7
Prosite; Prosite; Prosite; 1.8
Sequence 104 AA; 11085 MW; 0534D57467566914 CRC64;
                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:913170; FKbp11.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
InterPro; IPR001179; FKBP_PPIase.
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STRAIN=CZECH II; TISSUE=Mammary tumor;
                                                                                                                                                                                          Created)
                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
                                                                              Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                     Mus musculus (Mouse).
                                                                                                                            6 LLLPLOLL 13
                                                                                                          2 LILIPLOIL 9
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                    Fkbp11 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
                                                                                                                                                                                                                            Name=Fkbp11;
                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                 Q8R5D6;
                                                                                                                                                                        Q8R5D6
                                                                                                                                                       RESULT 7
                                                                                                                                                               QBR5D6
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=FVBIN TISSUE=Mammary tumor;

MEDINE=2238257; PubMed=1247932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zebebrg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zebebrg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina R., Parmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., NcKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Ranking M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

RA Richards S., Grimwood J., Schnutz J., Myers R.M., Butterfield Y.S.,

RA Richards R.M., Touchman J.W., Green B.D., Dickson M.C.,

RA Richards R.M., Schalsku U., Smailus D.E., Schnerch A., Schein J.E.,

RA Richards M.I., Salsku U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PK11 MOUSE STANDARD; PRT; 201 AA.

Q9D1M7; Q9CRE4;
28-FEB-2003 (Rel. 41, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
05-UUL-2004 (Rel. 44, Last annotation update)
trans isomerase) (PPlase) (Rotamase) (19 kDa FK506-binding protein)
(FKBP-19).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRALM-FVB/N, TISSUE-Mammary tumor;
Stransberg R.
Stransberg (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50059; FKBP PPIASE; 1.
SEQUENCE 138 AA; 15105 MW; C138BBBOEFDDF59D CRC64;
                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
138 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, BC002311; AAH02311.1; -. GO.0005615; C.extracellular space; TAS. GO; GO.0016021; C.integral to membrane; TAS. InterPro; IPR001179; FKBP_PPIASE.
                                                                           Created)
   PRT;
                                                                           27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences."
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PRELIMINARY;
                                     Q6PKE2;
05-JUL-2004 (TrEMBLrel.
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STEALNESSTEERDLYO;

WEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

WEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

A Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Nikaido I., Osato N., Eatio R., Suzuki H., Yamanaka I., Kiyosawa H.,

A saidarellia R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Blake J.A., Bradt D., Matsuda H., Batalov S., Beisel K.W.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

A salla E., Dragani T.A., Fletcher C.F., Forrest A., Fuzers K.S.,

A casterland T.A., Gariboldi M., Gissi C., Godzik A., Gough J.,

Ramai A., Kawaji H., Kawasawa Y., Kedzierski R.M., Fuzers R.B.,

A konagaya A., Kurochkin I.V., Lew Y., Lenhard B., Lyons P.A.,

Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Rayashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pescle G.,

Retrovsky N., Pillai R., Pontius J.U., Oi D., Ramachandran S.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

Sandelin A., Schneider C., Semple C.A., Setcu M., Shimada K.,

Sandelin A., Schneider C., Semple C.A., Setcu M., Shimada K.,

A sultana R., Hashaw-Boris A., Yanaqisawa M., Yang I., Yang L.,

Nilming L.G., Wymshaw-Boris A., Yanaqisawa M., Yang I., Yang L.,

Nilming L.G., Wymshaw-Boris A., Yanaqisawa M., Yang I., Yang L.,

Nilming L.G., Wymshaw-Boris A., Yanaqisawa M., Yang I., Yang L.,

Nilming L.G., Wymshaw-Boris A., Yanaqisawa M., Yang I., Yang L.,

Nilming L.G., Wymshaw-Boris A., Yanaqisawa M., Yang I., Yang L.,

Nilming L.G., Wymshaw-Boris A., Yanaqisawa M., Yang I., Yang L.,

Nilming L.G., Wymshaw-Boris A., Yanaqisawa M., Yang I., Yang L.,

Nilming L.G., Wymshaw-Boris A., Yanaqisawa M., Yang I., Yang L.,

Nilming L.A., Sakai K., Sasaki J., Aizawa K., Arakawa T., Fukuda S.,

Nilming L.A., Sakai K., Sasaki J., Aizawa K., Shinaqawa R.,

Yasunsahi A., Yashirahi W., Materston R., Lander E.S., Rogers J.,

Natire A.D., Salayanizaki Y.;

Natire A.D., Salayanizaki Y.;

Natire A.D., Salayanizaki Y.;

Natire A.D., Salayanizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and a sits content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the FKBP-type PPIase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 420:563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein synthesis.
                  Mus musculus (Mouse)
                                                                           NCBI_TaxID=10090;
                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A.
MEDLINE=99027340; PubMed=9801457;
Vanmontfort D., Fidler A.E., Heath D.A., Lawrence S.B., Tisdall D.J.,
Vanmontfort D., McNatty K.;
"CDNA sequence analysis, gene expression and protein localisation of
the inhibin alpha subunit of Australian brushtail possum (Trichosurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: Dimeric, linked by one or more disulfide bonds. Inhibin is a dimer of alpha and beta-A. Inhibin B is a dimer of alpha and
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trichosurus vulpecula (Brush-tailed possum).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Metatheria, Diprotodontia, Phalangeridae, Trichosurus.
                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                            BAB31559).
                                                                                                                                                                                                                                                                                    85.0%; Score 34; DB 1; Length 201; larity 87.5%; Pred. No. 89; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                            PPIase, FKBP-type.
S -> F (in Ref. 1; BAB31559)
S -> R (in Ref. 1; BAB31559)
94D955C57264BD82 CRC64;
                                                                                                                                                                                             FK506 binding protein 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the TGF-beta family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Inhibin alpha chain precursor.
                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                Potential
                                        EMBL, AK00331; BAB22719.1; -.
EMBL, AK019132; BAB31559.1; -.
EMBL, BC037596; AA437596.1; -.
HSSP, P20071; ITCO.
MGD; MGI.1913370; FKbpl1.
INTERPRO; IPRO01179; FKBP_PFIASE.
Pfam, PF00254; FKBP_C; 1.
PROSITE; PS50059; FKBP_PPIASE; 1.
                                                                                                                                                                                             28 201 FK:
57 144 PP:
53 53 S S S
198 198 S C 201 AA; 22137 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF033340; AAC63945.1; -.
                                                                                                                                                             Isomerase, Rotamase, Signal 1 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                   2 LLLPLQIL 9
                                                                                                                                                                                                                                                                                                  Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9337;
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077755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=INHA;
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                                                                                                                                                                                                                                          CONFLICT
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                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                SIGNAL
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Matches
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Gaps

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Debagner From A. Truck BaA-98; PubMed=14704707; DOI=10.1038/nbt923; PubMed=14704707; DOI=10.1038/nbt923; PubMed=14704707; DOI=10.1038/nbt923; PubMed=14704707; DOI=10.1038/nbt923; PubMed=14704707; DOI=10.1038/nbt923; PubMer F.W., Chain P., Hauser L., Lang A.S., Tabita F.R., Gibson J.L., Hanson T.B., Bobst C., Torres y Torres J.L., Peres C., Harrison F.H., Gibson J., Harwood C.S.; Porces J.L., Peres C., Harrison F.H., Gibson J., Harwood C.S.; Porces J.L., Peres C., Harrison F.H., Gibson J., Harwood C.S.; PubMed C. Botterium Rhodopseudomonas palustris."; PubMed. Biotechnol. 22:55-61(2004).

EMBL, Biotechnol. 22:55-61(2004).

EMBL, BS70263; Interlevin J. UNKNOWN I.

Complete proteome; Hypothetical protein; Signal.
     Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A., Weidman J.F., Kahouri H.M., Feldblyum T.V., Utterback T.R., Van Aken S.E., Lovley D.R., Fraser C.M.; "Genome of Geobacter sulfurreducens: metal reduction in subsurface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                               Rhodopseudomonas palustris.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Rhodopseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.5%; Score 33; DB 2; Length 148; 77.8%; Pred. No. 1.1e+02; Live 1; Mismatches 1; Indels
                                                                                                                                                                          Score 34; DB 2; Length 373;
Pred. No. 1.6e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 148 AA; 16860 MW; 9501B7C6C2808F45 CRC64;
                                                                                                                                                   373 AA; 40412 MW; 94B9D6AFF570D4A2 CRC64;
                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein precursor.
OrderedLocusNames=RPA3183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                          InterProj IPR000412; ABC_2.
Pfam; PF01061; ABC2_membrane; 1.
Complete protecome.
SEQUENCE 373 AA; 40412 MW; 9.
                                            "Genome of Geobacter sulfurred
environments.";
Science 302:1967-1969(2003).
EMBL, AE017180; AAR36057.1; -.
TIGR; GSU2685; -.
                                                                                                                                                                            85.0%;
                                                                                                                                                                 Local Similarity 77.8
hes 7; Conservative
                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                             :|||||||
293 ILLPLOIL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||||||| :|
7 SLLLPLMLL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SLLLPLQIL 9
                                                                                                                                                                                                                              2 LLLPLOIL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGC80882 protein.
Name=MGC80882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                   Q6N500;
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                                                                                                                                                                                                                                                                                                                       Q6N500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
Q6GNT6
                                                                                                                                                                                                                                                                                               RESULT 12
Q6N500
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STRAIN=PGA / ATCC 51573;
PubMed=14671304; DOI=10.1126/science.1088727;
Methe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C., Heidelberg J.F., Wu D., Wu M., Ward N.L., Beanan M.J., Dodson R.J., Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Gwinn M.L., Kolonay J.F., Sullivan S.A., Haft D.H., Selengut J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Geobacter sulfurreducens.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales; Geobacteraceae; Geobacter.
NCBI_TaxID=35554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  By similarity.
By similarity.
By similarity.
Notation (By similarity).
Notation (Glow).
Notation (Glow).
Notation (Glow).
Notation (Glow).
Notation (Glow).
Notation (Glow).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85.0%; Score 34; DB 1; Length 361; 87.5%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -iinxed (Gichac. . .) (Pc
D661CDF93CDAA87D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                           By similarity.
Inhibin alpha chain.
                                                                                                                                                                                                                                                                                                                                                                                                   Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 373 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                             PRINTS, PROOGES, INTELNA.
Prodom; PD000357; TGFb; 1.
PRART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF BETA 1; 1.
Glycoprotein; Growth Factor; Horn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38945 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Membrane protein, putative. OrderedLocusNames=GSU2685,
                                                                                                                                                                                                                                                                                                                                     beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 87.5
es 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LLLPLQIL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 AA;
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DISULFID
DISULFID
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SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

STRAIN=306 / ATCC 13902 / XV 101;

MEDIINE=20202145; PubMed=12024217; DOI=10.1038/4174599;

A da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A da Silva A.C.R., Ferro J.A., Bertolini M.C., Camargo L.B.A.,

A laves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

A laves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

A laves L.M.C., Granavan F., Cardozo J., Chambergo F.C. Ciapina L.P.,

Cararelli R.M.S., Coulinion L.L., Cursino-Santos J.R., El-Dorry H.,

Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Pornighieri B.F., Franco M.C., Greggio C.C., Gruber A.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

Noratins B.C., Maddanis J.M., Madeira A.M.B.N., Martine Z-Rossi N.M.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

Stubal J.C., Kitajima J.P.,

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

Comparison of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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STRANN=16M / ATCC 23456 / Biotype 1;
MEDLINE=20020109; PubMed=11756688; DOI=10.1073/pnas.221575398;
MEDLINE=20020109; Rapatral V., Redkar R.J., Patra G., Mujer C., Los T., DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF_01206; -; 1.
InterPro; IPR000572; Oxidored_molyb.
InterPro; IPR006311; Tat.
Pfam; PF00174; Oxidored_molyb; 1.
TIGRFAMS; TIGR01409; TAT signal_seq; 1.
Complete proteome; Hypothetical_protein.
SEQUENCE 339 AA; 37901 MW; B926DFC9AA849438 CRC64;
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DAUNORUBICIN RESISTANCE TRANSMEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 417:459-463(2002).
-!- SIMILARITY: Belongs to the UPF0190 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               370 AA.
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                                       Kanthomonadaceae; Xanthomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 88. ک
است 8; Conservative
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                                                                               NCBI_TaxID=92829;
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MEDINES-2188257; PubMed=12477912; DOI=10.1073/pnas.242603899;
MALAUSER R.D., Colling F.S., Wargner L., Shenmen C.M., Schuler G.D.,
MALSCHOLS F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Maronstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
Man S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Menas S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
M. Halton D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
M., Miting M., Youchman J.W., Green E.D., Dickson M.C.,
M., Kaywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
M. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Mathain S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.; Poop 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Kenopodinae; Kenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.5%; Score 33; DB 2; Length 302;
87.5%; Pred. No. 2.1e+02;
tive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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GO, GO:0016431; F:oxidoreductase activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IRR002198; ADH short.
InterPro; IPR002347; Adh_short_C2.
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Hypothetical Up0190 protein XAC1647.
OrderedLocusNames-XAC1647;
Xanthomonas axonopodis (pv. citri).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dev. Dyn. 225:384-391(2002).
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PRINTS; PR00080; SDRFAMILY.
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Matches 7; Conservative
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                                                             NCBI_TaxID=8355;
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Q8PLY8;
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Selkov B., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N.C., Overbeek R.;
"The genome sequence of the facultative intracellular pathogen Brucella melitensis.";
Brucella melitensis.";
Brucella Acad. Sci. U.S.A. 99:443-448(2002).
EMBL; AR009507; AAL51837.1;
PIR, AB3334; AB1334.
Pfam; PF01061; ABCZ_membrane; 1.
Complete protecome.
SEQUENCE 370 AA; 40369 MW; 819AAD684305CB60 CRC64;
                                                                                                                                                                                                                                                             Query Match 82.5%; Score 33; DB 2; Length 370; Best Local Similarity 75.0%; Pred. No. 2.6e+02; Matches 6; Conservative 2; Mismatches 0; Indels
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Search completed: July 13, 2005, 17:29:25 Job time : 63.2222 secs

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7861, AP 22663, A 27921, A 6128, AP 10615, A 8947, AP 11785, A

6, Appli 10791, A

323, App 57, Appl 25215, A 9866, Ap 7, Appli 2, Appli 2, Appli 24, Appli

Perfect score:

Sequence:

Searched:

Database

OM protein

Run on:

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Sequence 36, Application US/09502600A
Patent No. 6294344
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer
FILE REPERENCE: D6223CIP-C
CURRENT FILING DATE: D6223CIP-C
CURRENT FILING DATE: 09/09/502,600A
PRIOR APPLICATION NUMBER: 09/09/502,600A
PRIOR APPLICATION NUMBER: 09/039,211
PRIOR FILING DATE: 03-14-1998
NUMBER OF EQ ID NOS: 136
SEQ ID NO 36
LENGTH: 9

MANDER PRIOR FILING DATE: D6200 DATE: D620
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Sequence 36, Application US/09918243

GENERAL INFORMATION:

APPLICANT: Cannon, Martin J.

APPLICANT: Cannon, Methods for the early diagnosis of ovarian cancer;

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

TITLE OF INVENTION NUMBER: US/09/918,243

CURRENT APPLICATION NUMBER: US/09/918,243

CURRENT PILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-07-31

NUMBER OF SEQ ID NOS: 136

LENGTH: 9
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                                          US-09-252-991A-22663

US-09-252-991A-22663

US-09-949-016-10618

US-09-949-016-10618

US-09-489-019A-8947

US-09-489-019A-11785

US-09-489-019A-10791

US-09-489-019A-10791

US-09-489-018-9866

US-09-248-76A-25215

US-09-248-76A-25215

US-09-248-76A-25215

US-09-9170-115-7

US-09-9170-115-7

US-08-9170-115-7

US-08-9170-115-7

US-08-9170-115-7

US-08-9170-115-7

US-08-9170-115-7

US-08-9170-115-7

US-08-9170-115-7

US-08-9170-115-7
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Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-502-600-36
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RESULT 2
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Sequence 3, Appl
Sequence 3, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 116, Appl
Sequence 116, Appl
Sequence 116, Appl
Sequence 116, Appl
Sequence 35, Appl
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Sequence 13, Appl
Sequence 10, Appl
Sequence 5049, Appl
Sequence 593, Appl
Sequence 58, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                     (without alignments)
34.552 Million cell updates/sec
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                                                                                                                                                               July 13, 2005, 16:58:04 ; Search time 19.4444 Seconds
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-20-018-2

US-09-90-016-7716

US-09-90-016-7716

US-09-918-24-33

US-09-918-24-33

US-09-918-24-35

US-09-918-24-36

US-09-918-24-36

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US-09-918-24-36

US-09-918-24-31

US-09-9177-24-33

US-09-9177-24-33

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US-09-9177-24-33

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US-09-9177-24-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                  - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                      US-09-905-083A-36
                                                                                                                                                                                                                                                                                                        1 SLLLPLQIL 9
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Match Length
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880.0
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Result

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UCMBER: US/09/154,344
16-SEP-1998
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 253 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 16-SEP-19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
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  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 SLLLPLOIL 12
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New York COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLONE: 532504
                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-824-874-3
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APPLICANT: Egelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Bnzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: New York
COUNTRY: U.S.A.
ZIP: 10036-2797
COMPUTER: U.S.A.
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM FC Compatible
COMPUTER: ISM FC Compatible
COMPUTER: ISM FC COMPATIBLE
OPERATING STERM: PAPELICATION DATA:
APPLICATION NUMBER: 14-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Stermer, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                Query Match 100.0%; Score 40; DB 4; Length 9; Best Local Similarity 100.0%; Pred. No. 4.1e+05; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                  ) NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 4-12 of the SCCE protein
US-09-918-243-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: White & Case, Patent Department STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 40; DB
Best Local Similarity 100.0%; Pred. No. 2.6
Matches 9; Conservative 0; Mismatches
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US-08-824-874-3
; Sequence 3, Application US/08824874
; Patent No. 5962300
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
; TITLE OF INVENTION:
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/08557146
; Patent No. 5834290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 253 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-557-146-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 SLLLPLQIL 12
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FEATURE:
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| Sequence 2, Application US/09154344
| Sequence 2, Application US/09154344
| Patent No. 5981266 |
| GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Egelrud, Torbjorn APPLICANT: Hansson, Lennart TITLE OF INVENTION: Enzyme (SCCE) NUMBER OF SEQUENCES: 17 |
| CORRESPONDENCE ADDRESS: ADDRESSEE:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: Filed Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto CITY: Palo Alto CONTY: USA COUNTY: USA ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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    100.0%; Score 40; DB 3; Length 253; 100.0%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSDG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
FILING DATE:
CLASSIFICATION:
APPLICATION:
APPLICATION:
APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION UNBER: 36,749
REFERRINGE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPAX: 415-845-416
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hillman, Jennifer L.
Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                          RESULT 7
US-09-210-084-3
Sequence 3, Application US/09210084
; Setent No. 6197511
; GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Freet,
; TITLE OF INVENTION:
NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
US-09-764-762-3
Sequence 3, Application US/09764762
Patent No. 6472195
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 253 amino acids amino acids
      Query Match
Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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LIBRARY: GenBank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: GenB
CLONE: 532504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94304
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APPLICANT: Dixon, Eric P.

APPLICANT: Johnstone, Edward M.

APPLICANT: Jittle, Sheila P.

TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND

TITLE OF INVENTION: RELATED NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 40; DB 2; Length 253; 100.0%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,188
                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIPICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEPHONE: (212) 819-8783
TELEPHONE: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                    1103326-181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-ARR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
RGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: 38,082
TELECOMMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION 117-277-1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Indiana
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STRET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08930188 Patent No. 6093397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                             : 253 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                           US-09-154-344-2
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APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
TELEFAX: 317-276-3861
                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 253 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 10v.
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: protein PCT-US96-04294-2
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GENERAL INFORMATION:
APPLICANT: Dixon, Bric P.
APPLICANT: Johnstone Edward M.
APPLICANT: Little, Shella P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND TITLE OF INVENTION: RELATED NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 253;
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                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPTUTER: IBM Compatible

COMPTUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASISEO for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/764,762

FILING DATE: 16-Jan-2001

CLASSIFICATION NUMBER: 09/210,084

FILING DATE: -UDKNOWN>

PRIOR APPLICATION NUMBER: 09/210,084

FILING DATE: -UDKNOWN>

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 96-0252 US

TELEPHONE: 415-85-0555

TELEPHONE: 415-845-4166

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARAC
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COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04294
FILING DATE:
                     ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 40; DB 4
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
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STRANDEDNESS: single
TOPOLOGY: linear
CORRESPONDENCE ADDRESS:
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PCT-US96-04294-2
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Sequence 7716, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
PAPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 7716
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Batent No. 629434

BATENT O' Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of FILE REFERENCE. D6223CIP-C
                                                         Gaps
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100.0%; Score 40; DB 5; Length 253; 100.0%; Pred. No. 2.6;
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                                                       0; Indels
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                                                       0; Mismatches
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CURRENT FILING DATE: 2000-02-11
CURRENT APPLICATION NUMBER: US/09/502,600A
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Gaps

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0; Indels

Length 812;

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Score 34; DB 4;
Pred. No. 1.3e+02;
1; Mismatches 0
               85.0%;
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Matches 7; Conservative
                                                        Conservative
Query Match
Best Local Similarity &
                                                                                                                            429 Lilipiqui 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAB FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PLING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12075
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APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Methods Cor the early diagnosis of ovarian cancer TILE REFERENCE: D6223CIP/C/D/CIP
FILE REFERENCE: D6223CIP/C/D/CIP
CURRENT APPLICATION NUMBER: US/09/918,243
CURRENT PILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-3
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 33
LENGTH: 9
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                                                                                                                                                                                                                   90.0%; Score 36; DB 3; Length 9; 100.0%; Pred. No. 4.1e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                             ; OTHER INFORMATION: Residues 5-13 of the SCCE protein US-09-502-600-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 5-13 of the SCCE protein
US-09-918-243-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 12075, Application US/09489039A; Patent No. 6610836
               09/039,211
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 33, Application US/09918243
Patent No. 6627403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Klebsiella pneumoniae
           PRIOR APPLICATION NUMBER: 09/0
PRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 33
LENGTH: 9
                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 8; Conservative
                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                               2 LLLPLQIL 9
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US-09-918-243-33
                                                                                                                                                                                                                       Query Match
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Sequence 16, Application US/09502600A

GENERAL INFORMATION:
APPLICAMT: O'ETINC Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer
FILLE REFERENCE: D6223CTP-C
CURRENT FILING DATE: 2000-00-11
CURRENT APPLICATION NUMBER: US/09/502,600A
PRIOR APPLICATION NUMBER: US/09/502,600A
PRIOR PILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 16
US-09-502-600-35

Sequence 35. Application US/09502600A

Patent No. 629434

GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION:
CURRENT PILING DATE:
CURRENT PILING DATE:
CURRENT APPLICATION NUMBER: US/09/502,600A

PRIOR APPLICATION NUMBER: US/09/502,600A

PRIOR PILING DATE:
CURRENT APPLICATION NUMBER: US/09/502,600A

PRIOR FILING DATE:
O3-14-1998

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 3-5

TENCH ID NO 3-5

TENCH ID NO 3-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Residues 6-14 of the SCCE protein US-09-502-600-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Residues 2-10 of the SCCE protein US-09-502-600-116
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100.0%; Score 40; DB 9; I
llarity 100.0%; Pred. No. 1.6e+06;
Conservative 0; Mismatches 0;
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9; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-918-243-36
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Best Local S
Matches 9
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Sequence 36, Appl
Sequence 92, Appl
Sequence 98, Appl
Sequence 3, Appli
Sequence 2, Appli
Sequence 48, Appli
Sequence 48, Appli
Sequence 90, Appli
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                                                                                                             July 13, 2005, 17:29:45; Search time 64.8889 Seconds . (without alignments) 53.584 Million cell updates/sec
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Sequence 36,
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(cgn2_6/ptodata1/pubpaa/USO7_PUBCOMB.ppp:
(cgn2_6/ptodata1/pubpaa/USO7_NEW_PUB.pep:*
(cgn2_6/ptodata1/pubpaa/USO6_NEW_PUB.pep:*
(cgn2_6/ptodata1/pubpaa/USO6_PUBCOMB.pep:*
(cgn2_6/ptodata1/pubpaa/USO7_NEW_PUB.pep:*
(cgn2_6/ptodata1/pubpaa/USO8_NEW_PUB.pep:*
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(cgn2_6/ptodata1/pubpaa/USO10_NEW_PUB.pep:*
(cgn2_6/ptodata1/pubpaa/USO0_NEW_PUB.pep:*
(cgn2_6/ptodata1/pubpaa/USO0_NEW_PUB.pep:*
(cgn2_6/ptodata1/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-905-083-36
US-10-372-521-36
US-10-31-075-36
US-10-262-511-96
US-10-262-511-96
US-09-764-762-3
US-09-764-762-3
US-10-071-214-2
US-10-71-214-2
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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Sequence 639, App
Sequence 95, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 31, Appl
Sequence 314, Appl
Sequence 10255, A
Sequence 10255, A
Sequence 104977,
Sequence 207950,
Sequence 265948,
Sequence 266948,
Sequence 266948,
Sequence 266948,
Sequence 266948,
Sequence 266948,
Sequence 116, Appl
Sequence 128, Appl
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APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
APPLICANT: Santin, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
FILE REFERENCE: D6223CIP/C/D/CIP
CURRENT APPLICATION NUMBER: US/09/918,243
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 36
     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CHAIN
OTHER INFORMATION: Residues 4-12 of the SCCE protein US-09-918-243-36
                                                                                                                  US-09-918-243-33

US-09-905-083-33

S US-010-831-035-083-33

S US-10-831-075-33

S US-10-424-593-10255

S US-10-424-599-207950

S US-10-424-599-207950

S US-10-424-599-207950

S US-10-424-599-207950

S US-10-424-599-205948

S US-10-424-599-205948

S US-10-424-599-205948

S US-10-424-599-205948

S US-10-424-599-205948

S US-10-425-115-264649

G US-10-918-243-35

US-09-918-243-35

US-09-918-243-31

US-09-91
US-10-295-027-498
US-10-173-999-48
US-10-408-765A-639
US-10-643-795A-95
US-10-948-518-95
US-10-344-394-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 36, Application US/09918243 Patent No. US20020142317A1
   TYPE: PRT
ORGANISM: Homo sapiens
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Gaps

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RESULT

Length 9; 0; Indels

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100.0%; Score 40; DB 16; 100.0%; Pred. No. 1.6e+06;
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               CURRENT APPLICATION NUMBER: US/10/831,075
CURRENT FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 10/372,521
PRIOR FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 140
SEQ ID NO 36
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
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PRIOR APPLICATION NUMBER: 60/326,483
PRIOR APPLICATION NUMBER: 60/33,815
PRIOR PILLING DATE: 2001-10-02
PRIOR PILLING DATE: 2002-04-19
PRIOR PILLING DATE: 2001-10-09
PRIOR PILLING DATE: 2001-10-09
PRIOR PILLING DATE: 2001-09
PRIOR PILLING DATE: 2002-05-17
PRIOR PELICATION NUMBER: 60/381,642
PRIOR PELICATION NUMBER: 60/326,029
PRIOR PILLING DATE: 2002-0-09
PRIOR PLILING DATE: 2002-10-09
PRIOR PLILING DATE: 2002-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 96, Application US/10262511
Publication No. US20040038223A1
GENERAL INFORMATION:
FILE REFERENCE: D6223CIP/C/D/CIP3
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Patturajan, Meera
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Shenoy, Suresh G.
Shimkets, Richard A.
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Miller, Charles E.
Rastelli, Luca
Stone, David J.
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Leach, Martin D.
Agee, Michele L.
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Edinger, Shlomit R.
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Malyankar, Uriel M.
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Anderson, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
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Catterton, Elina
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ort, Tatiana
                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SLLLPLQIL 9
                                                                                                                                                                                                                                                                                                                                                                                                               1 STITEPLOIL 9
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  Sequence 36, Application US/09905083
; Sequence 36, Application US/09905083
; Patent No. US20020146708A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: O'Arian Cancer
; FILE REFERENCE: D6223CIP/C/Div
; CURRENT APPLICATION NUMBER: US/09/905,083
; CURRENT FILING DATE: 2001-07-13
; PRIOR FILING DATE: 2001-07-13
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 36
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APPLICANT: Santin, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer
FILE REFERENCE: D6223CIP/CD/CDF2
CURRENT APPLICATION NUMBER: US/10/372,521
CURRENT FILING DATE: 2003-02-21
PRIOR PILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 136
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Publication No. US20040224891A1
GENERAL INFORMATION:
APPLICANT: O'Brien, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer.
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; OTHER INFORMATION: Residues 4-12 of the SCCE protein
US-10-372-521-36
                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CHAIN OTHER INFORMATION: Residues 4-12 of the SCCE protein
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100.0%; Pred. No. 1.6e+06;
ative 0; Mismatches 0;
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; Publication No. US20030223973A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
ses 9; Conservative
                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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US-09-905-083-36
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Matches
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Gaps
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TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
                                                                                                                                               ö
                                                                                                       Length 9;
                                                                                                                                               0; Indels
FEATURE:
NAME/KEY: CHAIN
OTHER INFORMATION: Residues 4-12 of the SCCE protein
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PRIOR APPLICATION NUMBER: 60/328,029
PRIOR FILING DATE: 2002-10-09
PRIOR PLING DATE: 2002-0-61
PRIOR PLING DATE: 2002-05-16
PRIOR PLING DATE: 2002-05-16
PRIOR FLING DATE: 2002-05-16
PRIOR PLING DATE: 2002-04-17
PRIOR PLING DATE: 2002-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 40; DB 15; Length 250; 100.0%; Pred. No. 26;
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APPLICANT: WHYTE, DAVID
APPLICANT: CARENEEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: SUDRESANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REPERENCE: 038602/1214
CURRENT FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 98
LENGTH: 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-888-615-98
; Sequence 98, Application US/0988615
; Patent No. US20020064856A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-92
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; ORGANISM: Homo sapiens
US-09-888-615-98
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US-09-764-762-3
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APPLICANT: Schenberg, Mark E.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Agee, Michele L.
APPLICANT: Bergh, Constance
ITILE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT PILING DATE: 2003-05-28
FRIOR PELING DATE: 2001-10-07
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR FILING DATE: 2001-10-07
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR FILING DATE: 2002-04-19
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                                  PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-09
PRIOR PLING DATE: 2002-04-17
PRIOR PLING DATE: 2002-04-19
PRIOR PLING DATE: 2002-04-19
PRIOR PILING DATE: 2002-04-19
PRIOR FILING DATE: 2001-10-05
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 439
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 96
LENGTH: 198
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PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR FILING DATE: 2002-05-17
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Publication No. US20040038223A1
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Spytek, Kimberly A.
Edinger, Shlomit R.
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Malyankar, Uriel M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zerhusen, Bryan D.
Anderson, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Charles E.
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Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
            FILING DATE: 2002-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Catterton, Elina
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Matches 9; Conservative
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ii, Li
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Miller, Char
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; ORGANISM: Homo sapiens
US-10-262-511-96
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APPLICANT: GRELRUD, Torbjorn
TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
TITLE REFERENCE: HANSON=3A
CURRENT APPLICATION NUMBER: US/10/071,214
CURRENT FILING DATE: 2002-02-11
PRIOR PAPLICATION NUMBER: US 60/267,422
PRIOR PAPLICATION NUMBER: US RA 2001 00218
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN Version 3.1
SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Deduced amino acid sequence from the C-terminal part of SCCE from OTHER INFORMATION: homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 14; Length 253;
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APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF OVARIAN CANCER
FILE REFERENCE: 210121.590
CURRENT APPLICATION NUMBER: US/10/264,283
CURRENT FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 111
SOFTWARE: OCTIXA INVENTION Disclosure Database
SEQ ID NO 90
LENGTH: 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                              Sequence 48, Application US/10071214
Publication No. US20030066099A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                        APPLICANT: HANSSON, Lennart
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Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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US-10-264-283-90
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US-10-295-027-498
                                                                                                                                                                      US-10-071-214-48
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APPLICANT: HANSSON, Lennart
APPLICANT: EGELRUD, Torbjorn
TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAWMALS AND THEIR USE AS MODELS OF HUMAN
TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAWMALS AND THEIR USE AS MODELS OF HUMAN
CURRENT APPLICATION NUMBER: US 60/267,422
PRIOR APPLICATION NUMBER: US 60/267,422
PRIOR APPLICATION NUMBER: DK 72 2001 00218
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                 COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SOFTWARE: FastSEQ for Windows Version 2.0
SOFTWARE: 16-Jan-2001
CLASSIFICATION NUMBER: US/09/764,762
FILING DATE: 16-Jan-2001
CLASSIFICATION NUMBER: 09/210,084
FILING DATE: cUhknown>
APPLICATION NUMBER: 09/210,084
FILING DATE: cUhknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
               ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 40; DB 9;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 0
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SEQUENCE DESCRIPTION: SEQ ID NO: 3:
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Publication No. US20030066099A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 253 amino acids
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                          ZIP: 94304
COMPUTER READABLE FORM:
CORRESPONDENCE ADDRESS:
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CORGANISM: Homo sapiens
US-10-071-214-2
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Best Local Similarity
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Sequence 95, Application US/10643795A Publication No. US20040241703A1 GENERAL INFORMATION:
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APPLICANT: GRETCHEN FRANTZ
APPLICANT: KENNETH J. HILLAN
APPLICANT: PAUL POLAKIS
APPLICANT: PAUL POLAKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VICTORIA SMITH
SUSAN D. SPENCER
THOMAS D. WU
ZEMIN ZHANG
                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 9; Conservative
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Best Local Similarity 100.
Matches 9; Conservative
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CRGANISM: Homo sapiens
US-10-408-765A-639
                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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US-10-408-765A-639
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                                                                                                                                                                   APPLICANT: Glynne, Richard.
APPLICANT: Glynne, Richard.
APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Mark, David H.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Methods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Screening for Modulators of Cancer CURRENT APPLICANTON NUMBER: US/10/295,027
CURRENT APPLICATION NUMBER: US 60/350,666
RIOR APPLICATION NUMBER: US 60/350,666
RIOR APPLICATION NUMBER: US 60/335,394
RIOR FILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-11-12
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-12
PRIOR PILING DATE: 2001-12-14
PRIOR PILING DATE: 2002-11-0
PRIOR PILING DATE: 2002-10-08
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-02-08
PRIOR PILING DATE: 2002-02-03
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Publication No. US20040005563A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mack, David H.
APPLICANT: Gash, Kurt C.
APPLICANT: Ess Biotechnology, Inc.
APPLICANT: Ess Biotechnology, Inc.
APPLICANT: Ess Biotechnology, Inc.
APPLICANT: Gos Biotechnology, Inc.
APPLICANT: Gos Biotechnology, Inc.
APPLICANT: Gos Biotechnology, Inc.
APPLICANT: Compositions
TITLE OF INVENTION: Cancer
FILE OF INVENTION: Cancer
FILE REFERENCE: 018501-002420US
CURRENT APPLICATION NUMBER: US/10/173,999
CURRENT FILING DATE: 2002-06-17
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PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US 60/315,287
PRIOR FILING DATE: 2001-08-27
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                                                        APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsh, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
Publication No. US20030232350A1
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Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapiens
US-10-295-027-498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 639, Application US/10408765A

Publication No. US20040101874A1

GENERAL INFORMATION:

APPLICANT: Pahy, Boin D.

APPLICANT: Gabon, Bradford W.

APPLICANT: Gibson, Bradford W.

APPLICANT: Glenn, Gary W.

APPLICANT: Glenn, Gary W.

APPLICANT: Glenn, Gary W.

APPLICANT: Glenn, Gary W.

TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REPERBENCE: 660088 465

CURRENT FILING DATE: 2003-04-04

NUMBER OF SEQ ID NOS: 3077

SEQ ID NO 639

LENGTH: 253
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PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 163
SOFTWARE: PALENT VET. 201
SEQ ID NO 48
LENGTH: 253
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100.0%; Score 40; DB 16; Length 253;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 9; Conservative 0; Mismatches 0; Indels 0
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FLILING DATE: 2002-08-19
; PRIOR FILING DATE: 2002-08-19
; PRIOR PILING DATE: 2002-09-21
; PRIOR APPLICATION NUMBER: US 60/413,192
; PRIOR PILING DATE: 2002-09-23
; PRIOR FILING DATE: 2002-09-15
; PRIOR FILING DATE: 2002-10-15
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/426,847
; PRIOR FILING DATE: 2003-11-15
; PRIOR APPLICATION NUMBER: US 60/484,959
; SEQ ID NO 95
; LENGTH: 253
; TYPE: PRT
; ORGANISM: HOMO Sapien
US-10-643-795A-95
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WO200159158-A1.
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Copyright (c) 1993 - 2005 Compugen Ltd.
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The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypain enzyme (SCCB). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is Human stratum corneum chymotrypsin enzyme peptide #50 (residues 207-215) Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia. Diagnosing cancer comprises detecting stratum corneum chymotrypsin 9 Length 4, N

us-09-905-083a-80.rag

(first entry)

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immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
                                                                                                                                                       numan; NOVX; antidiabetic; anorectic; antibacterial; virucide;
                                                                                                            Human NOV18d protein SEQ ID NO:98.
                                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-2002; 2002WO-US031373
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15-OCT-2001; 2
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                          ADA05738;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel method for vaccinating an individual against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating an individual with a SCCE peptide, which elicits an immune response in the individual. A peptide of the invention acts as a stratum corneum chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating an individual against SCCE, particularly an individual having, suspected or at risk of getting ovarian, lung, prostate, pancreatic or colon cancer. The oligonucleotide is useful for treating a neoplastic state in an individual, such as ovarian, breast, lung, colon, prostate, or peptides are also useful in the monitoring and development of immunotherapies for ovarian and other malignancies. The present sequence represents a peptide fragment of serine protease SCCE (stratum corneum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for vaccinating an individual against SCCE, and in monitoring and developing immunotherapies for ovarian and other malignancies.
                                                                                                                                                                                                                                                                                                                                                 Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:80.
                          Gaps
                            ö
                                                                                                                                                                                                                                                                                                                                                                                       serine protease; stratum corneum chymotrytic enzyme; SCCE;
immune response; ovarian cancer; lung cancer; prostate cancer;
pancreatic cancer; colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 50; DB 8; Length 9; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                          Indels
                          ö
  Pred. No. 1.8e+06; ; Mismatches 0;
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                                                                                                                                                                                                                   ADR68841 standard; peptide; 9 AA.
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100.08;
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                                                                                                                                                                                                                                                                                                       02-DEC-2004 (first entry)
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Best Local Similarity 100.
Matches 9; Conservative
                          9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O'brien IJ, Cannon MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYAR-) UNIV ARKANSAS
                                                                  σ
                                                                                           chymotrytic enzyme).
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                                                                  1 GPLVCRGTL
    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                             ADR68841;
                          Matches
                                                                                                                                                                    RESULT 2
ADR68841
ADR68841
ADR68841
ADR6
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ADDT 02-[
XXX
DT 02-[

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2001US - 0343629P 2001US - 0349575P 2001US - 0346357P 2002US - 0373260P 2002US - 0373815P

2002US-0374977P. 2002US-0381037P. 2002US-0381038P.

2002US-0373826P. 2002US-0373884P.

2002US-0381042P. 2002US-0381642P. 2002US-0383656P.

2002US-0383831P

20010S-0328056P-20010S-0328849P-20010S-0330414P-20010S-0330309P-20010S-0341058P-20010S-0341058P-20010S-0341058P-

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ng M, carretton B,
A, Shenoy SG;
Berghs C, Dipippo VA;
                                                                                                                                                                                                                                                                                                                                                                                                                        New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22
                                                                                                                                             Catterton E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes NOVX proteins, where X can be 1 to
                                                                                                    Malyankar UM;
                                                           Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, L. Patturajan M, Spytek KA, Edinger SR, Ellerman K, Ma Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Slyimkets RA, Rothenberg ME, Leach MD, Agee ML, Berg Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 171; 586pp; English.
(CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                WPI; 2003-381626/36.
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GPLVCRGTL GPLVCRGTL

ADA05738 standard; protein; 181 AA.

RESULT 3
ADA05738
ID ADA0

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comprising a polypeptide described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the above vector; (6) an antibody that immunospecifically comprising the above vector; (6) an antibody that immunospecifically comprising the above vector; (6) an antibody that immunospecifically comprising the above vector; (6) an enthods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or presisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide (12) a method of soreening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide. Novx (14) a method for producing the above polypeptide. Novx (14) a method for producing the above polypeptide or the nucleic and antilipaemic activities, and can be used in gene therapy. The amunomodulator, cyclostatic, noorcopic, neuroprotective, antiparkinsonian and antilipaemic activities, and can be used in gene therapy. The colympeptide is useful in manufacturing a medicament for treating a medicament and moderness and van be used to diagnose, treat or prevent metabolic activities, and can also be used as hybridisation associated with a human disease. The polypeptide or the nucleic acide sease or immune disorders such as allabetes or obesity, infections, canceri, immune disorders haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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100.0%; Pred. No. 1.7;
Ative 0; Mismatches 0; Indels
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05-OCT-2001; 2001US-0327449P.
09-OCT-2001; 2001US-0327917P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002; 2002US-00262511.
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Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 GPĽVČRĠŤĽ 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 181 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2004038223-A1.
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhueen BD, Anderson DW, Zhong M, Catterton B;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                             2002US-0373826P.
2002US-0373884P.
2002US-0374977P.
                                                                                                                                                               24-OCT-2001; 2001US-0339266P.
24-OCT-2001; 2001US-0343629P.
29-OCT-2001; 2001US-0349575P.
01-NOV-2001; 2001US-0346357P.
                                                                                                                                                                                                                                                                                            2002US-0373817P
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EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EISEN A.
GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZERHUSEN B D.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATTURAJAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MILLET I.
PEYMAN J A.
KEKUDA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZHONG M.
CATTERTON E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-213931/20.
N-PSDB; ADN62901.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MILLER C E.
RASTELLI L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMITHSON G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEACH M D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GORMAN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RASTELLI
                                                        12-OCT-2001; 2
15-OCT-2001; 2
17-OCT-2001; 2
18-OCT-2001; 2
22-OCT-2001; 2
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16-MAY-2002;
                                                                                                                                                                                                                                                                                                                19-APR-2002;
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(MILL/)
(PEYM/)
(XUJJ/)
(LILL/)
(GUOX/)
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(ZHON/)
(CATT/)
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(AGEE/)
(BERG/)
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(RAST/)
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(SHIM/)
(ROTH/)
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PARKER REPRESENTATION OF THE PROPERTIES OF THE PROPERTY OF THE
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The invention relates to isolated NOVX polypeptides and polynucleotides.

NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the abbrrant expression and activity of NOVX by supplementing the patient our polynucleotides may be used to treat disorders associated with decreased expression or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polynucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which pathents may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators anti-NOVX polypeptide antibodies, agonists and antagonists may also be used as anti-NOVX polypeptide antibodies, agonists and antagonists may also be used to modulate NOVX polypeptide expression and activity of NOVX polypeptides. The anti-NOVX polypeptide expression and activity of NOVX polypeptides and polynucleotide expression and activity of NOVX polypeptides and polynucleotide may be used in this way to prevent, diagnoses and treat: metabolic disorders, diabetes, obesity, infectious disorders, all also acceptable of the various dyslipidaemism, metabolic disorders, and antagonisms, and antipolic disorders, and antipolic d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
                                   Claim 1; SEQ ID NO 98; 395pp; English.
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Sequence 181 AA;

Gaps ; 0 100.0%; Score 50; DB 8; Length 181; 100.0%; Pred. No. 1.7; ative 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.00
Best Local Similarity

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ADA05736 standard; protein; 198 AA. ADA05736; ADA05736

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XX XX DE Hume

XX XX DE Hume

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06-NOV-2003 (first entry)

Human NOV18c protein SEQ ID NO:96.

immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alaheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia. human; NOVX; antidiabetic; anorectic; antibacterial; virucide;

Homo sapiens

WO2003029424-A2

10-APR-2003.

02-OCT-2002; 2002WO-US031373

02-OCT-2001; 2001US-0326483P. 05-OCT-2001; 2001US-0327435P. 05-OCT-2001; 2001US-032749P. 09-OCT-2001; 2001US-0328029P.

15-OCT-2001; 2001US-0329414P. 17-OCT-2001; 2001US-0330142P. 18-OCT-2001; 2001US-0341058P. 24-OCT-2001; 2001US-0341058P. 24-OCT-2001; 2001US-0343629P. 25-OCT-2001; 2001US-034957F. 01-NOV-2001; 2001US-0346357P. 17-APR-2002; 2002US-0373260P. 2002US-0373815P. 2002US-0373817P. 2002US-0373826P. 2002US-0373884P. 2002US-0374977P. 16-MAY-2002; 2002US-0381038P. 2002US-0381042P. 2002US-0381642P. 2002US-0383656P 2002US-0383831P 2002US-0391335P 2002US-00262511 22-APR-2002; 16-MAY-2002; 19-APR-2002; 28-MAY-2002; 19-APR-2002; 19-APR-2002; 19-APR-2002; 29-MAY-2002; 25-JUN-2002;

(CURA-) CURAGEN CORP.

01-OCT-2002;

Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM, Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Oif W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK; Kekuda R, Ju J, Li L, Guo X SR, Ellerman K, Malyankar UM; Peyman JA, Smithson G, Millet I,

WPI; 2003-381626/36. N-PSDB; ADA05735.

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New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or pharmacogenomics.

Claim 1; Page 170; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule described above; (3) an isolated nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the molecule described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a disease associated with altered levels of expression of the above colypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for use in treating an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of secreting a pathology associated with the polypeptide; (12) a method of cor preventing a pathology associated with the above polypeptide. NoVX sequences have antidiabetic, anorectic, antibacterial, virucide.

Cor preventing a pathology associated with the above polypeptide. NoVX sequences have antidiabetic, anorectic, antibacterial, virucide.

Cor preventing a pathology associated with the above polypeptide. NoVX sequences have antidiabetic, anorectic, antibacterial, virucide.

Cor preventing a pathology associated with the above polypeptide. NOVX sequences have antidiabetic, anorectic, antibacterial, virucide, and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a columnary has need to an ease and the polypeptide of the polype acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer,

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                                                                                                                                                                                                                          human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer, cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder;
       disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the present invention.
neurodegenerative disorders such as Alzheimer's disease or Parkinson's
                                                                                     Gaps
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                                                                                                                                                                                                                                                  haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
                                                                     100.0%; Score 50; DB 6; Length 198; 100.0%; Pred. No. 1.9; ive 0; Mismatches 0; Indels
                                                                                                                                                           ADN62900 standard; protein; 198 AA.
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2001US-0328029P.
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                                                            Query Match
Best Local Similarity 100...
Best and 9; Conservative
                                                                                                                                                                                            01-JUL-2004 (first entry)
                                                                                                                     152 GPLVCRGTL 160
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                                                                                                     1 GPLVCRGTL
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                                                                                                                                                                                                                                                           wasting disorder
                                                      Sequence 198 AA;
                                                                                                                                                                                                                                                                                         US2004038223-A1.
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22-OCT-2001;
24-OCT-2001;
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9-OCT-2001;
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                                                                                                                                                                                                           Human NOV18c
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The invention relates to isolated NOVX polypeptides and polynucleotides.

NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX by supplementing the patient our polynucleotides may be used to treat disorders associated with decreased expression or activity of NOVX by supplementing the patient our correctify mutations. Conversely, antisense NA molecules production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polypurcleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators anti-NOVX polypeptide sand antagonists and antigonists may also be used to modulate NOVX polymucleotide expression and activity of NOVX colappeptides. The anti-NOVX polypeptide expression and activity of NOVX colappeptides. The anti-NOVX polypeptide expression and activity of NOVX colappeptides and polymucleotide expression and activity of NOVX colappeptides and polymucleotide expression and activity of NOVX colappeptides and polymucleotide expression and activity of NOVX colappeptides and polymucleotides may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious disorders, and the various dyslipidaemias, metabolic chaematopoietic disorders, and the various dyslipidaemias, metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG, Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease
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                                                                                                                                                                                                                  SPYTEK K A.
EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
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RASTELLI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
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RIEGER D K.
SPADERNA S K.
ZYMAN J A.
KEKUDA R.
TU J.
                                                                                                                                                                                          PATTURAJAN M.
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ANDERSON D W.
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BERGHS C.
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(RIEG/)
(SPAD/)
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(ZERH/)
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(EISE/)
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Dipippo VA;

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Human NOV18g
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disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
                                                                                                                                                                                                                                     immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipemic; gene therapy; human disease;
metabolic disorder; diabetes; obesity; infection; cachaxia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
                                                                             Gaps
                                                                             .;
0
                                                                                                                                                                                                                             human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
                                                          100.0%; Score 50; DB 8; Length 198; 100.0%; Pred. No. 1.9;
                                                                            0; Indels
                                                                                                                                                                                                                                                                       immune disorder; haematopoietic disorder; dyslipidaemia
                                                                             Mismatches
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                                                                                                                                                         ADA05744 standard; protein; 224 AA.
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2001US - 0327917P
2001US - 0328049P
2001US - 0328056P
2001US - 0328056P
2001US - 03294149P
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2001US-0343629P.
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                                                                             9; Conservative
                                                                                                        1 GPLVCRGTL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP
                                                                    Local Similarity
                                          Sequence 198 AA;
                                                                                                                                                                                                                                                                                                         WO2003029424-A2
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12-067-2001;
11-067-2001;
18-067-2001;
22-067-2001;
24-067-2001;
24-067-2001;
29-067-2001;
29-067-2001;
29-067-2001;
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19-APR-2002;
19-APR-2002;
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16-MAY-2002;
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(e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVY protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (6) a cell comprising the nucleic acid molecule described above; (7) methods for determining the binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or a permotory of intentifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or a pathology associated with the polypeptide; (12) a method of carrivity of the polypeptide; (12) a method of carrivity of the polypeptide; (12) a method for modulating or preventing a pathology associated with the above polypeptide in a memmal; and (14) a method for producing the above polypeptide in a memmal; and (14) a method for producing the above polypeptide; NOVX immandal and (14) a method for producing the above polypeptide in a memmal; and contacterial, virucide,
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                                                                                                                                                                                    Dipippo VA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                Malyankar UM;
M, Catterton E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes NOVX proteins, where X can be 1 to 55
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UJ Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterto Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dil Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
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Best Local Similarity 100...
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                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ADA05743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pharmacogenomics
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Dipippo VA;

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The invention relates to isolated NOVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and activity of NOVX polypeptides and activity of NOVX polypeptides and conversely, antisense NA molecules expression or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX binding with the cells own genes and preventing their expression. NOVX binding with the cells own genes and preventing their expression. NOVX copymentered and quantitate the presence of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of significant of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX.

Copymeptides. The anti-NOVX polypeptide antibodies may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polymerial and polypeptides and polymerial and polypeptides and polymerial and polymerial and polypeptides and polymerial and polypeptides and polymerial and polymerial and polymerial and polymerial and disorders, immune disorders, disorders, disorders, and the various dyslipidaemias, metabolic disorders associated with obesity, the metabolic syndrome X and antibodies associated with obesity, the metabolic expenses an oresis.
                                                                                                                                                                                                                                                                                                                                     Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
                                                                                                                                 Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; TADG-15; cytostatic; vaccine; ovarian tumour; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 50; DB 8; Length 224; Best Local Similarity 100.0%; Pred. No. 2.1; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 104; 395pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB98502 standard; protein; 225 AA.
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                                   (EISE/) EISEN A.
(GANG/) GANGOLLI E A.
(RIEG/) RIEGER D K.
(SPAD/) SPADERNA S K.
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BERGHS C.
DIPIPPO V A.
                                                                                                                                                                                                                                                                           WPI; 2004-213931/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-2001
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BERG/)
                      DIPI/)
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                                                                                                                                                                                                                                                                                                                                                      2001US-0327917P.
2001US-0328029P.
2001US-0328044P.
2001US-0328056P.
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2001US-0330309P.
2001US-0341058P.
2001US-0339266P.
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2002US-0381037P.
2002US-0381038P.
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2001US-0329414P.
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2001US-0346357P.
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2001US-0327449P
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EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MILLER C E. RASTELLI L. STONE D J. SPENA C B A. SHENOY S G. SHIMKETS R A. ROTHENBERG M E. LEACH M D. AGEE M L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATTURAJAN M.
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PEYMAN J A.
KEKUDA R.
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                                                                                              wasting disorder.
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                                                                                                                                                                      US2004038223-A1
                                                                                                                                                                                                                                                                                                                                                                                                               09-OCT-2001;
12-OCT-2001;
15-OCT-2001;
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                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4-OCT-2001;
9-OCT-2001;
1-NOV-2001;
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(PEYM/)
(KEKU/)
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(GUOX/)
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(LEAC/)
(AGEE/)
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(EDIN/)
(ELLE/)
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(GORM/)
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(STON/)
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                                                                                                                                                                                              Novel extracellular serine protease, termed tumor antigen-derived gene 15 protein overexpressed in carcinomas and DNA encoding it, for diagnosis, treatment, prevention of cancer, particularly breast, ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obesity; infection; cachaxia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                numan; NOVX; antidiabetic; anorectic; antibacterial; virucide;
                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 50; DB 4; Length 225; ilarity 100.0%; Pred. No. 2.1; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune disorder; haematopoietic disorder; dyslipidaemia
 tumour antigen-derived gene 15; serine protease;
Stratum Corneum Chymotryptic Enzyme; SCCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human NOV18f protein SEQ ID NO:102.
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                                                                                          20-OCT-2000; 2000WO-US029095.
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                                                                                                                                                     O'brien TJ, Tanimoto H;
                                                                                                                                                                                                                                                                                                                                                                                                                                             179 GPLVCRGTL 187
                                                                                                                                   (UYAR-) UNIV ARKANSAS
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es 9; Conser
                                                                                                                                                                                                                                                                                                                                                              Sequence 225 AA;
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                                                  WO200129056-A1
                                                                                                                20-OCT-1999;
                                Homo sapiens
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PR 65-CCT-2001; 20018-03279179-
PR 90-CCT-20012 20018-03279179-
PR 90-CCT-20012 20018-03229029-
PR 90-CCT-20012 20018-0322040-
PR 90-CCT-20012 20018-0322040-
PR 90-CCT-20012 20018-0322040-
PR 90-CCT-20012 20018-0323040-
PR 90-CCT-20012 20018-0323040-
PR 90-CCT-20012 20018-0323260-
PR 90-CCT-20012 20028-0323319-
PR 90-CCT-20012 20028-033319-
PR 90-CCT-20012 20028-033319-
PR 90-CCT-20012 20028-0333103-
PR 90-CCT-20012 20028-033319-
PR 90-CCT-20012-0038-03319-
PR 90-CCT-20028-03319-
PR 90-CCT-20038-03319-
PR 90-CCT-20038-03319-
PR 90-CCT-20038
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                                                                                                                                                                                                                                                                      human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyplipidaemia; metabolic syndrome X;
associated with a human disease. The polypeptide or the nucleic
        acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslighdemias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
                                                                                                                        Gaps
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                                                                                                    100.0%; Score 50; DB 6; Length 247; 100.0%; Pred. No. 2.3; tive 0; Mismatches 0; Indels
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                                                                                                       100.0%;
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2001US-0328044P.
2001US-0328054P.
2001US-0328849P.
2001US-0328849P.
2001US-0330142P.
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2001US-0341058P.
2001US-0339266P.
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2001US-0346357P.
2002US-0373260P.
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2002US-0373817P.
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2002US-0383831P
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                                                                                                                                                                                                                                    01-JUL-2004 (first entry)
                                                                                                             Local Similarity 100.
                                                                                                                                                        193 GPĽVCRĠTĽ 201
                                                                                                                                       1 GPLVCRGTL 9
                                                                    present invention.
                                                                                                                                                                                                                                                                                                         wasting disorder.
                                                                                     Sequence 247 AA;
                                                                                                                                                                                                                                                                                                                                           US2004038223-A1.
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09-0CT-2001)
09-0CT-2001)
12-0CT-2001)
15-0CT-2001)
15-0CT-2001)
18-0CT-2001)
24-0CT-2001)
24-0CT-2001)
24-0CT-2001)
24-0CT-2001)
21-0CT-2001)
21-0CT-2001)
21-0CT-2001)
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19-APR-2002;
19-APR-2002;
19-APR-2002;
                                                                                                                                                                                                                                                       Human NOV18f.
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16-MAY-2002;
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                                                                                                     Query Match
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Matches
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25-JUN-2002; 2002US-0391335P.
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RIEGER D K.
SPADERNA S K.
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SHENOY S G.
SHIMKETS R A.
ROTHENBERG M E
                                                                                                                        MALYANKAR U M.
                                                                                                                                                   ZERHUSEN B D.
ANDERSON D W.
ZHONG M.
CATTERTON E.
                                                                                             SPYTEK K A.
EDINGER S R.
ELLERMAN K.
                                                                                    PATTURAJAN M.
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BERGHS C.
DIPIPPO V A.
                           MILLET 1.
PEYMAN J A.
KEKUDA R.
                                                                                                                                                                                                  MILLER C E.
RASTELLI L.
STONE D J.
                    SMITHSON G.
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                                                                                                                                            GORMAN L.
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                                                                          GUO X.
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                                                                                                     (EDIN/)
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton B; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA; Eisen A, Gangolli EA, Rieger DK, Spaderna SK;

WPI; 2004-213931/20. N-PSDB; ADN62905. Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease

Claim 1; SEQ ID NO 102; 395pp; English.

The invention relates to isolated NOVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX by supplementing the patient our polymentides may be used to treat disorders associated with decreased complements of the patient our controlled may be administered to down regulate expression of NOVX polypeptides by production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by colinding with the cells own genes and preventing their expression. NOVX polymucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators candiantage and antagonists of the expression and antagonists may also be used to modulate NOVX polypeptide expression and antagonists may also be used to modulate NOVX polypeptide expression and antagonists may also be used to modulate NOVX polypeptide expression and antagonists may also be used to modulate NOVX polypeptide antibodies, agonists and antagonists may also be cused to modulate NOVX polypeptide expression and antagonists may also be diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polymucleotides may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious

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  anorexía, cancer, cancer-associated cachexía, neurodegenerative
                          disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, haematopoietic disorders, and the various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obseity; infection; cachexia; cancer;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; NOVX; antidiabetic; anorectic; antibacterial; virucide;
                                                                                                                                                                                                                                                                                    8; Length 247;
                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                    100.0%; Score 50; DB 8 100.0%; Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                        Mismatches
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2001US-0328044P.
2001US-0328056P.
2001US-0328849P.
2001US-0329414P.
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2001US-0349575P.
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2001US-0339266P.
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2002US-0391335P.
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                                                                                                                                                                                                                                                                                                                                           9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 GPLVCRGTL 201
                                                                                                                                                                                                                                                                                                                                                                                             1 GPLVCRGTL 9
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                             Sequence 247 AA;
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18-0CT-2001;
24-0CT-2001;
24-0CT-2001;
29-0CT-2001;
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25-JUN-2002;
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19-APR-2002;
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16-MAY-2002;
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The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the mucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of secritity or of latency or predisposition to consprintly of the polypeptide described above; (13) methods of treating the activity or of latency or predisposition to consprending a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide. NoVX sequences have antidiabetic, anorectic, antibacterial, virucide, consprending a medicament for treating and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a colypeptide is and any present metable. The polypeptide is the polypeptide or produced and antilipaemic and any and or and any produced the polypeptide or produced and any produ
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                                                                                                                                                                                                                                                                                                                                                                                               obesity,
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                                                                                                                                                        Catterton E;
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                                                                                                                                                                                                                                                                                                                                                                 New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obecancer or dyslipidemia, and in chromosome mapping, tissue typing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cance
                                                                                                                                  Malyankar UM;
                                                                                                                                                                              Shenoy SG;
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                                                                                               Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li Patturajan M, Spytek KA, Edinger SR, Ellerman K, Mal Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Jiw, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Bergh Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 169-170; 586pp; English.
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01-OCT-2002; 2002US-00262511.
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                                                   (CURA-) CURAGEN CORP.
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The invention relates to isolated NOVX polypeptides and polymucleotides.

NOVX polypeptides and polymucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX by supplementing the patient our polymucleotides may be used to treat disorders associated with decreased expression or activity of NOVX by supplementing the patient our polymucleotides may be used to treat disorders associated with decreased complements of NOVX polypeptides by conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by conversely antisense may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of crestorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators the production of antibodies and in assays to identify modulators anti-NOVX polypeptides and antagonists and antagonists and antagonists of antibodies and in the expression and activity of NOVX. The anti-NOVX polypeptides may be used in this way to prevent, colypeptides and polymucleotide expression and activity of NOVX polypeptides may be used in this way to prevent, colypeptides and polymucleotides may be used in this way to prevent, colypeptides and polymucleotides may be used in this way to prevent, colypeptides and polymucleotides may be used in this way to prevent, colypeptides and polymucleotides may be used in this way to prevent, colypeptides and polymucleotides may be used in this way to prevent, colypeptides polypeptides. Parkinson's Disorder, immune disorders, alternating disorders, alternations dyslibutions dy
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Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Pott T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
                                                                                                                                                                                                                                                                                                                                                                                              Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 92; 395pp; English.
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    ROTHENBERG M E.
                                                                                                                 GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
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                                        AGEE M L.
BERGHS C.
DIPIPPO V A.
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N-PSDB; ADN62895.
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Matches
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                                                                           human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; morexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
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2001US-0327917P.
2001US-0328029P.
2001US-0328044P.
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2001US-0330142P.
2001US-0330309P.
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01-JUL-2004 (first entry)
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PENA C E A.
SHENOY S G.
SHIMKETS R A.
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EDINGER S R.
ELLERMAN K.
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ANDERSON D W.
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human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
Human NOV18b protein SEQ ID NO:94
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2001US-0328029P.
2001US-0328044P.
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17-OCT-2001;
18-OCT-2001;
22-OCT-2001;
24-OCT-2001;
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                                                                               Homo sapiens
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comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a disease associated with altered levels of expression of the above colypeptide or nucleic acid molecule in a first mammalian subject; (9) a complete of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for case in treating a pathology that is related to an aberrant expression or aberrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide in a corporate part of the activity of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide in a community of the polypeptide described above; (13) methods of treating or preventing a pathology associated with the above polypeptide or producing the above polypeptide or producing the above polypeptide or producing a medicament for treating a confidence associated with a human disease. The polypeptide or the nucleic caid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders und an also be used as hybridisation condisease in chromosome mapping, tissue typing, preventive medicine and probable, in chromosome mapping, tissue typing, preventive medicine and produced to mapping.
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Best Local Similarity
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Dipippo VA; New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK; Claim 1; Page 170; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell

09-0CT-2001; 2001US-0327917P. 09-0CT-2001; 2001US-0328029P. 09-0CT-2001; 2001US-0328044P. 12-0CT-2001; 2001US-0328056P. 15-0CT-2001; 2001US-0328049P. 02-0CT-2001; 2001US-0326483P. 05-0CT-2001; 2001US-0327435P. 05-0CT-2001; 2001US-0327449P.

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2001US-0343629P.
2001US-0349575P.
2001US-0346357P.
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2001US-0330142P
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SHENOY S G.
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ROTHENBERG M E
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BERGHS C.
DIPIPPO V A.
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PEYMAN J A.
KEKUDA R.
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Kekuda R, Ju J, Li L, Guo X;
RR, Ellerman K, Malyankar UM;
Berson DW, Zhong M, Catterton E;
Boly, Pena CEA, Shenoy SG;
MD, Agee ML, Berghs C, Dipippo VA;
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2004-213931/20. N-PSDB; ADN62897

Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease

Claim 1; SEQ ID NO 94; 395pp; English.

The invention relates to isolated NOVX polypeptides and polynucleotides. NOVX polypeptides and polynucleotides are used to prevent, diagnose or

activity of NOVX polypeptides. For example, NOVX polypeptides and polymucleotides may be used to treat disorders associated with decreased expression or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polymucleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX. The anti-NOVX polypeptide expression and activity of NOVX polypeptides and integers and antagonists may also be used as dispositic agents for detecting the presence of NOVX polypeptides and polymucleotides may be used as diagnoser and treat: metabolic disorders, diabetes, obesity, infectious ö rreat a medical condition in human related to the aberrant expression and disease, anorexia, cancer, cancer-associated cachexia, neurodegenerative disorders. Alzhabimer's Disease, Parkinson's Disorder, immune disorders, hamenatopoietic disorders, and the various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein. Gaps ö 100.0%; Score 50; DB 8; Length 252; 100.0%; Pred. No. 2.4; 0; Indels 0; Mismatches Ouery Match Best Local Similarity 100. 206 GPLVCRGTL 214 1 GPLVCRGTL 9 Sequence 252 AA; ઠ 셤

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A;Accession: Manazor. H2227, Marzor. M
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tissue kallikrein
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                                                                                                                                                                    July 13, 2005, 16:54:03; Search time 13.5556 Seconds (without alignments) 63.882 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283416 seqs, 96216763 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                 OM protein - protein search, using sw model
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A32297
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T35999
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Gapop 10.0 , Gapext 0.5
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S15395
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length: 2000000000
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Match Length
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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No.
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310	W W	74.	00	261 261	N N	A28062 A25606 ti	gamma-renin (EC 3. tissue kallikrein
32	37	74.0	0	261			
33	37	74.0	0	261		A29745 ti	
34	37	74.	٥.	261			tissue kallikrein
35	37	74.0	0	263			tissue kallikrein
36	37	74.0	0	264		S65663 gr	granzyme 3 (EC 3.4
37	37	74.0	0	599			riboflavin biosynt
38	36	72.	0	99			kallikrein - mouse
39	36	72.0	0	73	~		elastase (EC 3.4.2
40	36	72.0	0	149	-		tissue kallikrein
41	36	72.0	0	226	~	S69370 du	duodenase - bovine
42	36	72.0	0	229	-	TRDFS	trypsin (EC 3.4.21
43	36	72.0	0	231	-	TRPGTR	
44	36	72.0	0	231	~		(EC 3.4
45	36	72.0	. 0	236	-		44
						ALIGNMENTS	
RESILT 1							
serine proteinase SCCE precursor N, Alternate names: stratum corner	oteinas te name	3e SC	CE p: trati	recur!	3or rnet	serine proteinase SCCE precursor - human N/Alternate names: stratum corneum chymotryptic enzyme	
C;Species C;Date: 0	HOMO	8api 1995	ens #seq	(man) uence	re,	C;Species: Homo sapiens (man) C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004	nge 09-Jul-2004
C;Accession: A33966 R;Hansson, L.; Stro	L. S	3 roe	mavi	St. M.		Baeckman, A.; Wallbrandt, P.;	Carlstein, A.; Egelrud, T.
J. Biol.	Chem. 2	,69;	1942	0-1942	.92	J. Biol. Chem. 269, 19420-19426, 1994	
A; Title: (Cloning	3, ex	pres	sion,	and	A, Title: Cloning, expression, and characterization of stratum	n corneum chymotryptic enzyme
A; Reference number:	ice numb	Ser:	A539	68; M	ai.	A; Reference number: A53968; MUID:94308225; PMID:8034709	
A:Status: preliminary	prelim	ninar	>				
A; Molecule type: mRNA	e type:	mRN	٠ <u>۸</u>				
A; Residues: 1-253 <han></han>	8: 1-25	53 <h< td=""><td>AN></td><td></td><td></td><td></td><td></td></h<>	AN>				
A; Cross-references: UNIPROT: P49862;	eferenc	ea:	UNIP	ROT: P.	1986	62; GB:L33404; NID:g521214; F	GB:L33404; NID:g521214; PIDN:AAC37551.1; PID:g532504
	:8:	,	į.				
A;Gene: G	GDB: PRSS6; SCCE		3 C		,		
A;Cross-rererences: GDB:3///30	ererenc	7435	50B:	3///5	_		
C. Cuperfemily, tymein.	# 1 t	200	2	7	5	trumein homology	
F;30-245/Domain: trypsin homology <try></try>	Domain:	try		homod	60	V <try></try>	
Query Match	atch	· :	, .	100.08;	*0	e 50; DB 2; Length	253;
Best Local Similarity Matches 9; Conser	cal Sim	nilar Con	ity Berv	larity 100.0%; Conservative	*	; Pred. No. 0.092; 0; Mismatches 0; Indels	, 0, Gaps 0;
λ̈	1 GP	GPLVCRGTL		o			
q	207 GP	GPLVCRGTL		215			
RESULT 2							

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'PQAYHLHPSCTT',1-176 <RES>
A;Residues: 'PQAYHLHPSCTT',1-176 <RES>
A;Cross-references: GB:S7555; NID:g861469; PIDN:AAD14185.1; PID:g4261885
R;Christensson, A.; Lilja, H.

Bur. J Bloochen. 220, 45-55, 1994
A;Title: Complex formation between protein C inhibitor and prostate-specific antigen in N
A;Reference number: S41212; MUID:94164172; PMID:7509746
                                                                 A; Molecule type: protein
A; Residues: 25-261 <SC2>
R; Watt, K.W.K.; Lee, P.J.; M'Timkulu, T.; Chan, W.P.; Loor, R.
Proc. Natl. Acad. Sci. U.S.A. 83, 3166-3170, 1986
A; Title: Human prostate-specific antigen: structural and functional similarity with serir A; Reference number: A23937; MUID: 86205857; PMID: 2422647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Residues: 1-261 <MOR>
A,Cross-references: EMBL:U17040; NID:g595945; PIDN:AAA56764.1; PID:g595946
A;Cross-references: EMBL:U17040; NID:g595945; PIDN:AAA56764.1; PID:g595946
A;Cancer Res. 54, 6344-6347, 1994
A;Title: Molecular characterization of prostate-specific antigen messenger RNA expressed
A;Reference number: 152712; MUID:95079406; PMID:7527295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-261 <SCH>
A;Cross-references: UNIPROT:P20151; GB:M18157; NID:g186640; PIDN:AAA74454.1; PID:g386842
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                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 25-93,'T',95-164,'HL',166,'YDQM',169-174,'Q',176-261 <WAT>
R;Moreno, J.M.
submitted to the EMBL Data Library, November 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 25-30,'X',32-49 <CHR>
C;Comment: This enzyme preferentially cleaves after tyrosine residues.
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A,Reference number: A29586; MUID:88054467; PMID:2824146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A)Cross-references: GDB:119695; OMIM:176820
A;Map position: 19q13.3-19q13.3
A;Map position: 19q13.3-19q13.3
C;Superfamily: trypsin; trypsin; homology
C;Keywords: glycoprotein; hydrolase; prostate; serine prot
F;1-7/Domain: signal sequence #status predicted <SIG>F;18-24/Domain: propeptide #status predicted <SIG>F;25-24/Domain: trypsin homology <TRY>
F;25-253/Domain: trypsin homology <TRY>
F;55-253/Domain: trypsin homology <TRY>
F;55-253/Domain: trypsin homology <TRY>
F;55-253/Domain: trypsin homology <TRY>
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A; Reference number: S00232; MUID:88082806; PMID:3691515
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C;Species: Homo sapiens (man)
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989
C;Accession: A29586
R;Schedlich, L.J.; Bennetts, B.H.; Morris, B.J.
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A,Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Molecule type: protein
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                                           A; Accession: S00232
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                                                                                                                                                                                                R.Digby, M.; Zhang, X.Y.; Richards, R.I.
Nucleic Acids Res. 17, 2137, 1989
A;Title: Human prostate specific antigen (PSA) gene: structure and linkage to the kallik
A;Reference number: S03604; MUID:89183632; PMID:2467258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           foreserveferences: EMBL:X14810
Henttu, P.; Vihko, P.
Jochem. Biophys. Res. Commun. 160, 903-910, 1989
Jochem. Biophys. Res. Commun. 160, 903-910, 1989
Filtle: CDNA coding for the entire human prostate specific antigen shows high homologie; Reference number: A32546; MUID:89246551; PMID:2470373
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A;Title: Sequence of a cDNA clone encompassing the complete mature human prostate specif
A;Reference number: S02239; WUID:88289366; PMID:2456523
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A;Residues: 5-164, 'CTPGPDGAAGSPDAWV' <R14>
A;Cross-references: GB:M21897; NID:9189529; PIDN:AAA59997.1; PID:9189530
A;Note: the authors translated the codon GGC for residue 28 as Arg, TGG for residue 29
A;Note: the authors translated the codon GGC for matti, T.; Rickli, E.E.
Exchaller, J.; Akiyama, K.; Tsuda, R.; Hara, M.; Marti, T.; Rickli, E.E.
Eur. J. Biochem. 170, 111-120, 1987
A;Title: Isolation, characterization and amino-acid sequence of gamma-seminoprotein, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: mRNA
fResidues: 5-210, WNILITELIMPA', 223,'PMVLHGSLV',233,'WRGGV' <R13>
(Cross-references: GB:M21896; NID:9189525; PIDN:AAA59996.1; PID:9189526
(Note: the authors translated the codon GGC for residue 28 as Arg and TGG for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: GB-M21895; NID:g189523; PIDN:AAA59995.1; PID:g189524
Note: the authors translated the codon GGC for residue 28 as Arg and TGG for residue
Accession: A31567
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A'Residues: 5-261 <LU2>
R'Riegman, P.H.J.; Klaassen, P.; van der Korput, J.A.G.M.; Romijn, J.C.; Trapman,
Biochem. Biophys. Res. Commun. 155, 181-188, 1988
A'Title: Molecular cloning and characterization of novel prostate antigen cDNA's.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,Molecule type: mRNA
;Residues: 1-72,'T',74-85,'I',87-174,'P',176-183,'Q',185-259,'D',261 <HEN>
;Cross-references: GB:M26663
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A; Molecule type: DNA
A; Residues: 1-261 < KLL).
A; Cross-references: EMBL:X14810; NID:935732; PIDN:CAA32915.1; PID:9296671
A; Cross-references: EMBL:X14810; Schulz, P.; Arbusow, V.; Fittler, F.
R; Klobeck, H.G.; Combriato, G.; Schulz, P.; Arbusow, V.; Fittler, F.
A; Klobeck, H.G.; Sombriato, G.; Schulz, P.; Arbusow, V.; Fittler, F.
A; Title: Genomic sequence of human prostate specific antigen (PSA).
A; Reference number: 805467; MUID:89282407; PMID:2471958
                                                                                                                                                        ross-references: GB:M27274; NID:g190552; PIDN:AAA60192.1; PID:g190553
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A;Residues: 17-63, Tr',65-135, 'M',137-261 <SCH>
A;Cross-references: EMBL.X07730
R;Lundwall, A.; Lilja, H.
R;ESB Lett. 214, 317-322, 1987
A;Title: Molecular Choing of human prostate specific antigen CDNA.
A;Reference number: A26757, WUID:87190978; PMID:2436946
                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-261 < DIGS-
A; Residues: 1-261 < DIGS-
A; Cross-references: EMBL:X13940
R; Klobeck, H.G.; Combriato, G.; Schulz, P.; Arbusow, V.; Fittler,
Bubmitted to the EMBL Data Library, May 1989
A; Reference number: S05468
A; Accession: S05468
                                                                          A;Molecule type: DNA
A;Residues: 1-261 <LUN>
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Gaps

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A;Experimental source: pancreatic
R;Kato, H.; Nakanishi, E.; Enjyoji, K.; Hayashi, I.; Oh-Ishi, S.; Iwanaga, S.
J. Biochem. 102, 1389-1404, 1987
A;Title: Characterization of serine proteinases isolated from rat submaxillary gland: wit
A;Reference number: A41429; MUID:88198057; PMID:3482210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 115-265 <GER>
A;Residues: 115-265 <GER>
R;Inoue, H; Pukui, K; Miyake, Y.
R;Inoue, H; Pukui, S34-840, 1989
A; Biochem: 105, 834-840, 1989
A;Title: Identification and structure of the rat true tissue kallikrein gene expressed ir A;Reference number: JX0073; MUID:89327211; PMID:2753879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M23874; GB:J04701; GB:M23875; GB:M23876; NID:g205007; PIDN:AAA4144 C;Comment: The kallikreins liberate lysyl-bradykinin, a vasoactive decapptide, from kini C;Comment: The kallikreins assumes the uvo-chain form by cleavage between residues C;Comment: The protein presumably assumes the uvo-chain form by cleavage between residues C;Comment: Tissue kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to release l;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue kallikrein (EC 3.4.21.35) precursor - rat
NyAlternate names: glandular kallikrein; kininogenin; true tissue kallikrein
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A00944; A41429; A25137; JX0073; A23863; A33359
R;Swift, G.H.; Dagorn, J.C.; Ashley, P.L.; Cummings, S.W.; MacDonald, R.J.
Proc. Natl. Acad. Sci. U.S.A. 79, 7263-7267, 1982
A;Fitles: Rat pancreatic kallikrein mRNA: nucleotide sequence and amino acid sequence of A;Reference number: A00944; MUID:83117659; PMID:6961406
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A;Status: preliminary
A;Status: preliminary
A;Rolecule type: mRNA
A;Residues: 1-265 <ASHS
A;Cross-references: GB:M11563; NID:g205029; PIDN:AAA41464.1; PID:g205030
A;Experimental source: submaxillary gland
B;Wines, D.R.; Brady, J.M.; Pritchett, D.B.; Roberts, J.L.; MacDonald, R.J.
J. Biol. Chem. 264, 7653-7662, 1989
A;Title: Organization and expression of the rat kallikrein gene family.
A;Reference number: A33359; MUID:89214217; PMID:2708383
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F;18-28/Domain: activation peptide #status predicted <APT>
F;29-26/Product: tissue Kallikrain, pancreatic #status predicted <MPT>
F;29-25/Domain: trypsin homology <TRY>
F;35-177,54-70,156-23;188-202,213-238/Disulfide bonds: #status predicted
F;69,124,217/Active site: His, Asp, Ser #status predicted
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Cross-references: GB:D00448; NID:g220792; PIDN:BAA00346.1; PID:g220794
Experimental source: kidney
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Bochemistry 24, 4512-4520, 1985
A; Hitle: Kallikrein-related mRNAs of the rat submaxillary gland:
A; Reference number: A21863, MUID:86051477; PMID:2998455
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C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; pancreas; serine proteinase; zymogen
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A;Residues: 5-265 <WIN>
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A; Residues: 1-265 <SWI>
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A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: G7246
A;Accession: G7248
A;Accession: G7248
A;Accession: G7248
A;Amolecule type: DNA
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A;Experimental source: strain Kl
C;Genetics:
A;Gene: APE1675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable aminoglycoside acetyltransferase - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Objec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Accession: T35999 R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1999 A;Reference number: Z21574 A;Accession: T35999 A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: G72548
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C;Superfamily: Bscherichia coli aminoglycoside N3'-acetyltransferase
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A,Note: the authors translated the codon TAC for residue 43 as Trp
C,Genetics:
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                                                                                     Ajintrons: 16/1; 69/2; 165/1; 210/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
F;25-253/Domain: trypsin homology <TRY>
F;65,120,213/Active site: His, Asp, Ser #status predicted
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Pred. No. 6.5;
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88.9%;
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Best Local Similarity 77.0
77.0
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A; Regidues: 1-262 <SEE>
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Alternate names: glandular kallikrein

Cispecies: Mus musculus (house mouse)

Cispecies: Musculus (house kallikrein gene family suggests a role in specific processing A; Reference number: A00941; MUID:83219214; PMID:6602295
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A;Experimental source: Quakenbush inbred strain
A;Note: this sequence has been translated from two exons (11-147 and 522-674) located up:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: 149416
R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.
Ramm. Genome S, 349-355, 1994
A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A;Reference number: 148934; MUID:94319082; PMID:8043949
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C;Superfamily: trypsin; trypsin homology
N;Alternate names: gamma-seminoprotein; P-30 antigen; prostate-specific antigen; prostaté
                                                                                                                                                                                                                                                                                                                              A,Residues: 1261 <GAU>
A,Cross-references: UNIPROT:P33619; EMBL:X73560; NID:g311843; PIDN:CAA51957.1; PID:g31184
C,Comment: This enzyme preferentially cleaves after tyrosine residues.
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                                                         C,Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004 C;Accession: S35711; S34239  
R;Gauthier, B.R.; Chapdelaine, P.; Tremblay, R.R.; Dube, J.Y.
Biochim. Biophys. Acta 1174, 207-210, 1993
A;Title: Characterization of theus monkey prostate specific antigen cDNA. A;Reference number: S35711; MUID:93363642; PMID:7689340
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C;Species: Mus spretus (western wild mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolaes; prostate; serine proteinase
F;1-17.Domain: signal sequence #status predicted <SIG>
F;18-24/Domain: propeptide #status predicted <PRO>
F;25-261/Product: semenogelase #status predicted <MAT>
F;25-253/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 76.0%; Score 38; DB 1; Length 261; Local Similarity 77.8%; Pred. No. 15; 2; Indels nes 7; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 46
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Pred. No. 4.8;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                     C;Species: Macaca mulatta (rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.0%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 66.7
Matches 6; Conservative
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215 GPLVCDGVL 223
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A; Residues: 1-96 < MAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-46 < RES>
                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: I49416
                                                                                                                                                                                                                                                                 A;Accession: S35711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                complement factor D (EC 3.4.21.46) precursor [validated] - human (fragment)
N,Alternate names: adipsin; C3 convertase activator
C,Species: Homo abajens (man)
C,Species: Homo abajens (man)
C,Species: Homo apajens (man)
C,Species: 28-Aug-1985 #sequence revision 31-Dec-1992 #text_change 09-Jul-2004
C,Accession: A40197; A00936; A60571; S66645
C,Accession: A40197; A00936; A60571; S66645
D, Biol. Chem. 267, 9210-9213, 1992
A;Fitle: Human adipsin is identical to complement factor D and is expressed at high leve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein

A; Molecule type: protein

A; Molecule type: Journal (185-235),

A; Molecula for the previously published sequence of Reid et A; Molec: a few residues were assigned from the previously published sequence of Reid et B; Miyata, T.; Oda, O.; Inagi, R.; Sugiyama, S.; Miyama, A.; Maeda, K.; Nakashima, I.; Ya Mahl. Immunol. 27, 637-644, 1990

A; Title: Molecular and functional identification and purification of complement component A; Reference number: A60571; MUID: 90370044; PMID: 2395435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 19-20,'XX',23-27,'XX',30-31,'XX',34,'X',36-40 <MIY>
K;Balke, N.; Holtkamp, U.; Hoerl, W.H.; Tschesche, H.
FEBS Lett. 371, 300-302, 1995
A;Title: Inhibition of degranulation of human polymorphonuclear leukocytes by complement A;Reference number: S66645; MUID:96013156; PMID:7556615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Status: preliminary
MyNolecula type: protein
A.Racidues: 19-44, 'C',46-48 <BAL>
C.Comment: Factor D cleaves factor B when the latter is complexed with factor C3b, activ
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C;Superfamily: trypsin; trypsin; homology
C;Keywords: complement alternate pathway; hydrolase; plasma; serine proteinase
F;118/Domain: signal sequence #status predicted <SIG>
F;19-246/Product: complement factor_D (fragment) #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Amino acid sequence of human D of the alternative complement pathway.
A;Reference number: A00936; MUID:85000441; PMID:6383466
                                                                                                     Gaps
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F;44-60,141-207,172-188,197-222/Disulfide bonds: #status predicted
F;59,105,201/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 246;
                                 Length 265;
                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Molecule type: mRNA;
;Residues: 1-246 <WHI>
;Cross-references: UNIPROT:P00746; GB:M84526
;Niemann, M.A.; Bhown, A.S.; Bennett, J.C.; Volanakis, J.E.
iochemistry 23, 2482-2486, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gemenogelase (EC 3.4.21.77) precursor - rhesus macaque
                              Score 39; DB 1;
Pred. No. 10;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.0%; Score 38; DB 77.8%; Pred. No. 14; rative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: GDB:132645; OMIM:134350
                              78.0%;
66.7%;
                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                            219 GPLICNGVL 227
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                                                                                                                                                                  1 GPLVCRGTL 9
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Best Local Similarity
Local 7; Conserve
Query Match
Best Local Similarity
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tissue kallikrein (BC 3.4.21.35) 3 - rat (fragment)

tissue kallikrein (BC 3.4.21.35) 3 - rat (fragment)

Cibgecies: Rattus norvegicus (Norway rat)

Cibate: 22-Nov-1989 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

CiAccession: B32340

Rishai, S.Y.; Woodbay-Willer, C.; Chao, J.; Chao, L.

Biochemistry 28, 5334-5343, 1989

A;Title: Characterization of genes encoding rat tonin and a kallikrein-like serine protes

A;Reference number: A32340; MUID:89375248; PMID:2550051

A;Residues: Draiminary

A;Rolecule type: DNA

A;Residues: 1-188 < SHA>

A;Residues: 1-188 < SHA>

A;Cross-references: UNIPROT:P15950; GB:M26534; NID:g206773; PIDN:AAA42080.1; PID:g206774;

C;Superfamily: trypsin; 
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tissue kallikrein (EC 3.4.21.35), prostatic - guinea pig
N.Alternate names: glandular kallikrein
C.Species: Cavia porcellus (guinea pig)
C.Species: Cavia porcellus (guinea pig)
C.Spate: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 09-Jul-2004
C.Accession: A27207
R.Punubar, J.C.; Bradshaw, R.A.
Blochemistry 26, 3471-3479, 1987
A.Title: Amino acid sequence of guinea pig prostate kallikrein.
A.Reference number: A27207; MUID:88000549; PMID:3307909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Dactes 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 19-May-2000
C;Accession: S45356
R;Dihanich, M.; Spiess, M.
Biochim. Babophs. Acta 1219, 225-228, 1994
A;Title: A novel serine proteinase-like sequence from human brain.
A;Reference number: S45356; MUID:94289486; PMID:8018728
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A;Cross-references: EMBL:X75363; NID:g407137; PIDN:CAA53145.1; PID:g940540
A;Experimental source: Alzheimer's disease patient brain cortex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;1-180/Domain: trypsin homology (fragment) <TRY>
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Pred. No. 20;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74.0%; Score 37; DB 66.7%; Pred. No. 17; cive 1; Mismatches
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C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74.0%;
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Best Local Similarity 77.8
Matches 7; Conservative
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                  110 GPLICDGVL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 GPLICDGVL 150
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Matches 6; Conserv
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A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue kallikrein-related proteinase (EC 3.4.21.-) klo - rat (fragments)
Cispecies: Rattus norvegicus (Norway rat)
Cispecies: Rattus norvegicus (Norway rat)
Cibate: 18-Feb-1994 #sequence_revision 19-Jul-1996.#text_change 17-Oct-1997
CiAccession: 515395; 815448
R;Gutman, N.; Elmoujahed, A.; Brillard, M.; Monegier du Sorbier, B.; Gauthier, F.
R;Gutman, N.; Elmoujahed, A.; Brillard, M.; Monegier du Sorbier, B.; Gauthier, F.
A;Title: Microheterogeneity of rat submaxillary gland kallikrein klo, a member of the ka
A;Reference number: 515395; MUID:91224135; PMID:2026164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fill(4/Domain: trypsin homology (fragments) <TRY> Fill(4/Domain: trypsin homology (fragments) <TRY> Fill(3/Product: tissue kallikrein-related protein k10 light chain (fragment) #status exp F;24-51/Product: tissue kallikrein-related protein k10 heavy chain (fragment) #status exp F;52-104/Product: tissue kallikrein-related protein k10 heavy chain (fragment) #status exp F;52-104/Product: tissue kallikrein-related protein k10 heavy chain (fragment)
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C,Superfamily: trypsin, trypsin homology
C,Keywords: hydrolase; serine proteinase
C;Comment: Glandular kallikreins cleave Met-Lys and Arg-Ser bonds in kininogen to releas
C;Genetics:
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NyAlternate names: glandular kallikrein; kininogenin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Unl-1987 #sequence_revision 22-Jul-1987 #text_change 09-Jul-2004
C;Accession: B23863
R;Ashley, P.L.; MacDonald, R.J.
Biochemistry 24, 4512-4520, 1985
A;Title: Kallikrein-related mRNAs of the rat submaxillary gland: nucleotide sequences A;Reference number: A23863; MUID:86051477; PMID:2998455
                                                                                                                                                A;Introns: 45/3
C;Superfamily: trypsin; trypsin homology
C;Keywords: glycoprotein; hydrolase; saliva; serine proteinase; submandibular gland
F;1-88/Domain: trypsin homology (fragment) <TRY>
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A;Experimental source: submaxillary gland
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase
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Best Local Similarity 66.77,
6, Conservative
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Best Local Similarity 66.7
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A; Residues: 1-156 <ASH>
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A; Molecule type: protein
A; Residues: 1-23 < DUN>
A; Residues: 1-23 < DUN>
A; Cross-references: UNIPROT: P12323
A; Note: 50-Trp was also found
C; Superfamily: trypsin; trypsin homology
C; Keywords: hydrolase; serine proteinase
C; Keywords: hydrolase; serine proteinase
F; 1-231/Domain: trypsin homology < TRY>
F; 1-231/Domain: trypsin homology < TRY>
F; 1-231/Active site: His, Asp, Ser #status predicted
Query Match
Query Match
Hest Local Similarity 66.7%; Score 37; DB 2; Length 239;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Search completed: July 13, 2005, 17:31:31 Job time : 13.5556 secs

1 GPLVCRGTL 9 |||:|| | 193 GPLICDGVL 201

상 음 anopheles g anopheles g anopheles g homo sapien

drosophila

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 26, Last annotation update)
Kallikrein 7 short variant protein.
Homo sapiens (Human).
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(Rel. 45, Last annotation update)
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KLK7 HUMAN
ID KLK7, HUMAN
AC P49862;
DT 01-0CT-1996
DT 25-0CT-2004
  Q8NFV7;
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O63zf4 rattus norv
O9ukg9 homo sapien
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                                                                                                              (without alignments)
74.069 Million cell updates/sec
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              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Q9XSN6
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Q8QG86
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NRPN RAT
Q71QH9
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KLK7 HUMAN
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KLK9 HUMAN
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Q63Z11
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Listing first 45 summaries
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Q8NCW4
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Genew; HGNC:6368; KLK7.

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Skin;
MEDLINE=94308225; PubMed=8034709;
Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chymotryptic enzyme.",
Biochem. Biophys. Res. Commun. 211:586-589(1995).
-!- FUNCTION: May catalyze the degradation of intercellular cohesive
structures in the cornified layer of the skin in the continuous
shedding of cells from the skin surface. Specific for amino acid
residues with aromatic side chains in the PI position. SCGE
cleaves insulin B Chain is at the PI position. SCGE
cleaves insulin B Chain is in the PI position. SCGE
activation of precursors to inflammatory cytokines.
-!- TISSUE SPECIFICITY: Abundantly expressed in the skin and is
expressed by keratinocytes in the epidermis. Very low levels are
also seen in the brain and kidney.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hansson L., Backman A., Ny A., Edlund M., Edholm E., Tornell J., Wallbrandt P., Egelrud T.;
"Epidermal overexpression of stratum corneum chymotryptic enzyme in mice; a model for chronic ithchy dermatitis.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95314630; PubMed=7794273;
Skytt A., Stroemqvist M., Egelrud T.;
"Primary substrate specificity of recombinant human stratum corneum
Kallikrein 7 precursor (EC 3.4.21.-) (Stratum corneum chymotryptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yousef G.M., Scorilas A., Diamandis E.P.; Molecular characterization, mapping and tissue expression of the human stratum corneum chymotryptic enzyme gene."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                               rouno apptens (naman).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moss P., Paeper B., Wang K.; "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase.", J. Biol. Chem. 269:19420-19426 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig
Moss P., Paeper B., Wang K.;
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 23-53
                                                                                  Name=KLK7; Synonyms=PRSS6, SCCE;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF166330; AAD49718.1; -.
EMBL; AF243527; AAG33360.1; -.
EMBL; AF332583; AAK69624.1; -.
PIR; A53968; A53968.
HSSP; P00760; 1ECX.
MEROPS; S01.300; -.
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                                       (hSCCE)
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bahat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergene E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Multing M., Madan A., Young A.C., Shevcheko Y., Boutfard G.G.,
Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                          InterPro; IPR009003; Pept, Ser Cys.
InterPro; IPR009003; Pept, Ser Cys.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR001214; Peptidase_S1.
InterPro; IPR001214; Peptidase_S1.
PROMP: PR00089; Trypsin; 1.
PROMP: PR00172; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS001134; TRYPSIN_HIS; 1.
PROSITE; PS001134; TRYPSIN_HIS; 1.
Direct protein sequencing; Glycoprotein; Hydrolase; Serine protease; Signal; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                 (By similarity) (By similarity) (By similarity)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 50; DB 1; Length 253; illarity 100.0%; Pred. No. 0.24; Conservative 0; Mismatches 0: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2D68B6B15A76A668 CRC64;
                                          GO; GO:0008236; F:serine-type peptidase activity; TAS. GO; GO:0008544; P:epidermal differentiation; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 26, Last annotation update)
Stratum corneum chymotryptic enzyme, preproprotein.
                                                                                                                                                                                                                                                                                              Charge relay system (Charge relay system (Charge relay system (Charge relay system (By similarity.
By similarity.
By similarity.
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Kallikrein 7.
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              H-InvDB; HIX0015373; -.
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253
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Best Local Similarity
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176
201
246
253 AA;
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                             MIM; 604438; -.
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KLK9_HUMAN
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Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=15203212; DOI=10.1016/j.ygeno.2004.01.009; Olsson A.Y., Lilja H., Lundwall A.; Taxon-specific evolution of glandular kallikrein genes and identification of a progenitor of prostate-specific antigen."; Genomics 84:147-156(2004).

-- MISCELLAMBEUUS: The sequence shown here is derived from an EMBL/GenBank/DDBJ third party annotation (TPA) entry.
                                                                                                                                                                         100.0%; Score 50; DB 2; Length 253; 100.0%; Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.0%; Score 47; DB 2; Length 258; 88.9%; Pred. No. 0.91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PERMIT PP00089, TYTYDEN; 1.

PRINTS, PR00722; CHYMORRYPSIN.

PROSTIE, PS00400; TYTYD SPC; 1.

PROSITE, PS00400; TRYPSIN DM; 1.

PROSITE; PS00134; TRYPSIN LIS; UNKNOWN 1.

PROSITE; PS00135; TRYPSIN LIS; 1.

Hydrolase; Protesse; Serine protesse.

SEQUENCE 253 AA; 27608 MW; 2D68B6A41B22A668 CRC64;
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5933AE83F6BE4461 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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21 258 g
258 AA; 28581 MW;
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                                                   and mouse cDNA sequences.
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les 9; Conser
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                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
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SIGNAL
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1||||:||| 206 GPLVCKGTL 214

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1 GPLVCRGTL 9

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PubMed=15057824; DOI=10.1038/nature02399;

PubMed=15057824; DOI=10.1038/nature02399;

A Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,

A Lamerdin J.B., Hellsten U., Goodstein D., Courone O., Tran-Gyamfi M.,

A Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,

A Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,

A Cleland C.A., Copeland A., Dain E., Denal P., Denys M., Detter J.C.,

RA Cleland C.A., Copeland A., Dain E., Denal P., Denys M., Detter J.C.,

RA Escobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M.,

A Bordia T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,

RA Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,

RA Kobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,

Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,

RA Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,

RA Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,

RA Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,

RA Plazak T., Solovyev V., Thayer N., Trice H., Tsai M., Ustassewska A.,

RA Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,

RA Rubin E.M., Lucas S.M.;

Nature 4281529-352 (2004)

RA Rubin E.M., Stokhsar D.S., Myers R.M.,

RA Rubin E.M., Lucas S.M.;

Nature 4281529-352 (2004)
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 MEDLINE=20247258; PubMed=10783266; DOI=10.1006/geno.2000.6159;
Yousef G.M., Diamandis E.P.;
"The expanded human kallikrein gene family: locus characterization and molecular cloning of a new member, KLK-L3.";
Genomics 65:184-194(2000).
 16-001-2001 (Rel. 40, Created)
116-001-2001 (Rel. 40, Last sequence update)
25-001-2004 (Rel. 45, Last annotation update)
Kallikrein 9 precursor (EC 3.4.21.-) (Kallikrein-like protein 3) (KLK-
 ature 428:529-535(2004).
!- SUBCELLULAR LOCATION: Secreted (Probable).
!- TISSUE SPECIFICITY: Skin, thymus, trachea, cerebellum and spinal
 SEQUENCE FROM N.A.
MEDLINE=20118156; PubMed=10652563;
Yousef G.M., Luo L.-Y., Diamandis B.P.;
"Identification of novel human kallikrein-like genes on chromosome
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
Moss P., Paeper B., Wang K.;
 "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region."; Gene 257:119-130(2000).
 -!- SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
 Anticancer Res. 19:2843-2852(1999)
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 19q13.3-q13.4.";
 subfamily.
KLK9 HUMAN
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"Functional annotation of a full-length mouse cDNA collection.";
 Query Match
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Matches
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 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
clone:1200016C12 product:similar to KALLIKREIN 9 (EC 3.4.21.-)
(KALLIKREIN-LIKE PROTEIN 3) (KLK- L3).
 STRAIN=C57BL/6J; TISSUE=Lung;
STRAIN=C57BL/6J; TISSUE=Lung;
MEDINE=99579253; VubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
 Gaps
 Potential.
Kallikrein 9.
Charge relay system (By similarity).
Charge relay system (By similarity).
Charge relay system (By similarity).
By similarity.
N-linked (GlCNAC. . .) (Potential).
N-linked (GlCNAC. . .) (Potential).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
 similarity).
similarity).
similarity).
 ;
0
 MIM, 605504;

R GO; GO:0005576; C:extracellular; NAS.
R GO; GO:0006508; P:serine-type endopeptidase activity; NAS.
R GO; GO:0006508; P:proceolysis and peptidolysis; NAS.
R GO; GO:0006508; P:proceolysis and peptidolysis; NAS.
R InterPro; IPR001254; Peptidase_S1.
R InterPro; IPR001254; Peptidase_S1A.
R PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SM0020; Trypsin; 1.
R PROSITE; PS50240; TRYPSIN DOM; 1.
R PROSITE; PS00134; TRYPSIN DM; 1.
R PROSITE; PS00134; TRYPSIN HIS; 1.
R PROSITE; PS00135; TRYPSIN Est; 1.
R PROSITE; PS00135; TRYPSIN Est
 90.0%; Score 45; DB 1; Length 250; 88.9%; Pred. No. 2.1; ive 0; Mismatches 1; Indels
 SEQUENCE FROM N.A.
STRAIN-CSTBL/6J; TISSUE=Lung;
MEDLINE-21085660; PLOMBEd=11217851; DOI=10.1038/35055500;
RIKEN FANTOM COMSORTIUM;
 N-linked (GlcNAc. .) (Po
F2785245B063E98B CRC64;
 251 AA
 01-JUN-2001 (TrEMBLrel. 17, Created)
 EMBL, AF135026; AAD26427.2; --
EMBL, AF243527; AAG33362.1; --
EMBL, AC011473; AAG23255.1; --
HSSP; P00746; 1FDP.
MEROPS; S01.307; --
Genew; HGNC:6370; KLK9.
MIM; 605504; --
 27512 MW;
 Conservative
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 206 GPLVCNGTL 214
 1 GPLVCRGTL 9
 211 2
250 AA;
 Mus musculus (Mouse)
 Local Similarity
es 8; Conser
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63
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204
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1136
1143
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ACT_SITE
ACT_SITE
DISULFID
 DISULFID
 CARBOHYD
 Query Match
 DISULFID
 DISULFID
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 CARBOHYD
 09DBQ8
 CHAIN
 Matches
 RESULT 6
유
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SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUB=Lung;
Arakawa T., Azawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayateu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kosukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Kawai J., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito R., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagawi M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
- SIMILARITY: Balongs to peptidase family Sl.

HSSP, P00746; IFDP.
 The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; Manlysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
 STRAIN=C57BL/6J; TISSUB=Lung; MEDILINB=20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDILINB=20499374; PubMed=11042159; DOI=10.101/gr.145100; Carrinci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Nokazaki Y., Pubbraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
 STRAIN=C57BL/6J; TISSUE-Lung;
STRAIN=C57BL/6J; TISSUE-Lung;
STRAIN=C57BL/6J; TISSUE-Lung;
STRAIN=C90313; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Nokazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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GG; GG:0005515; C:extracellular space; TAS.
InterPro; IPR001354; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR00933; Peptidase_S1A.
 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Lung;
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Nature 409:685-690(2001)
 206 GPLVCEGTL 214
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 SEQUENCE FROM N.A.
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Name=KLK14; Synonyms=KLKL6;
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 SEQUENCE FROM N.A.
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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.R., Bahat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcarane P.H.,
A Richards S., Worley K.C., Hale S., Garcarane R.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
 ö
 Gaps
 Hypothetical protein.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Kallikrein 14 precursor (EC 3.4.21.-) (Kallikrein-like protein 6)
 "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 ö
 88.0%; Score 44; DB 2; Length 210; 88.9%; Pred. No. 2.8;
 1; Indels
 Klein S., Gerhard D.S.;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC082936; AAH82936.1; -.
Hypothetical protein.
SEQUENCE 210 AA; 22897 WW; 7543224C2227DA35 CRC64;
 Last sequence update)
Last annotation update)
 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 PubMed=12477932; DOI=10.1073/pnas.242603899;
 251 AA
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 Created)
 (TrEMBLrel. 28, (TrEMBLrel. 28, I
 Dev. Dyn. 225:384-391 (2002).
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 8; Conservative
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25-OCT-2004
 25-OCT-2004
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 KLKE HUMAN
ID KLKE HUMAN
AC Q9P0G3;
 initiative.
 Query Match
 063ZI1;
 063211
 Matches
 RESULT 8
 844488
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Districts (Numban).

Shieryces Rectared (Nordits) Cranists vertebrats; Biteleostomis, Memmaliar Entheria; Primates; Catarrinis; Hostinidae, Homo.

Memmaliar Entheria; Primates; Catarrinis; Hostinidae, Homo.

Memmaliar Entheria; Primates; Catarrinis; Hostinidae, Homo.

Memmaliar Entheria; Primates; Catarrinis; Hostinidae, Homo.

Mischart (M.) Diamandia E.P.;

M. Yousef G.M., Diamandia E.P.;

M. Shahited (GNT):1993) to the BEBI/Centank (DDBJ databases.

M. Shahited (GNT):1993) to the BEBI/Centank (DDBJ databases.

M. Hospier J.D., Buil LT. Rea F.K.; Harvey T.J.; Myster S.A.; Myster S.A.; Harvey T.J.; Myster S.A.; Harvey T.J.; Myster S.A.; Myster S.A.; Harvey T.J.; Myster S.A.; Myster S.A
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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STRAIN-CS7BL/6J; TISSUE=Tongue;
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 88.98;
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nes 8; Conserv
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Name=2310015108Rik;
 1 GPLVCRGTL
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 NCBI_TaxID=10090;
 Query Match
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 090078
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 Straubberg R.L., Feingold E.A., Grouse L.H., Darge JG.,

Straubberg R.L., Feingold E.A., Grouse L.H., Darge JG.,

Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheez T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S.W., Wizey D.M., Sodersen R.J., Lu X., Ginbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nillalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Ritting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schnutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

and mouse cDNA sequences.";
 ö
 Gaps
 Charge relay system (By similarity).
Charge relay system (By similarity).
Charge relay system (By similarity).
By similarity.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 MIM, 606135; -

R GO, 6000576; C:extracellular; NAS.

R GO; GO:0006508; P:proteolysis and peptidolysis; NAS.

R GO; GO:0006508; P:proteolysis and peptidolysis; NAS.

R InterPro; IPR001254; Peptidase_S1.

R InterPro; IPR001254; Peptidase_S1.

R InterPro; IPR001254; Peptidase_S1.

R PRIME; PR00139; Trypsin; 1.

R PRNSTT; SR00020; Tryp SPC; 1.

R PROSITE; PS00134; TRYPSIN_DOM; 1.

R PROSITE; PS00135; TRYPSIN_SER; 1.
 Activation peptide (Potential).
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 Last sequence update)
Last annotation update)
 88.0%; Score 44; DB 1; 88.9%; Pred. No. 3.3;
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 (TrEMBLrel. 28, C
(TrEMBLrel. 28, I
(TrEMBLrel. 28, I
 8; Conservative
 PRELIMINARY;
Genew; HGNC:6362; KLK14.
 67
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204
164
68
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 25-OCT-2004
 25-OCT-2004
 25-OCT-2004
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 SEQUENCE
 DISULFID
 PROPEP
 Q6B089
 Matches
 RESULT 9
06808
06808
07 06800
07 25-06
07 25-06
08 Name
08 Nam
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the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(002).
 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
05-JUD-2004 (TrEMBLrel. 27, Last annotation update)
Mus musculus adult male tongue cDNA, RIKEN full-length enriched
library, clone:2310081E03 product:protease, serine, 20, full insert
sequence (Mus muscullus adult male tongue cDNA, RIKEN full-length
enriched library, clone:310021N04 product:protease, serine, 20, full
insert sequence) (Fragment).
 SEQUENCE FROM N.A.
STRAIN=CS7BL/60; ILSSUE=Tongue;
MEDLINE=99279213; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
 Gaps
 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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 Score 44; DB 2; Length 251;
Pred. No. 3.3;
 GO: GO: 0004295; F: chymotrypsin activity; IEA.
GO: GO: 0004295; F: chymotrypsin activity; IEA.
GO: GO: 0004295; F: chymotrypsin activity; IEA.
GO: GO: 0004295; F: chymotrypsin activity; IEA.
InterPro; IPR001294; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR009003; Pept_Ser_Gys.
FEan; PF00089; Trypsin; 1.
PFNITS; PR00172; CHYMOTRYPSIN.
SMART; SM00120; Tryp_SPO; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
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STRAIN=C57BL/6J; TISSUB=Tongue;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 databases
TISSUE=Lung;
Director MGC Project;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ .
-! SINLARITY Belongs to peptidase family S1 EMBL; BC074905; AAH74905.1; -.
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Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
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A rakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Imocani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A Saaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
A Sano H., Sasaki D., Shibata K., Shibata Y., Shihaqawa A., Shiraki T.,
Sogabe Y., Suzuki H., Yamamura T., Yamunishi R., Yoshida K., Yoshida K., Sobino M.,
Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

R EMBL; AKO19451: BAB26297.1; -.
 SEQUENCE FROM N.A.

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Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Adachi J., Aizawa K., Akahira S., Pukuda S., Fukunishi Y., Furuno M.,
A Arakawa T., Bono H., Carninoi P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,
A Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
A Sano H., Sasaki D., Shibata K., Shibata Y., Shinaki T.,
A Fojima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
A Muramatsu M., Hayashizaki Y.,
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
 MEDLINE=20499374; PubMed=11042i59; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
 STRAIN=CSTBL/6J; TISSUE=Tongue;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
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Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watshiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RIKIS integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
 Length 87;
 87 AA; 9549 MW; B988D0CD62926EAA CRC64;
 Score 41; DB 2;
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GO; GO:0005615; C:extracellular space; TAS.
 Hydrolase, Protease, Serine protease.
 InterPro; IPR001254; Peptidase SI.
InterPro; IPR009003; Pept_Ser_Cys.
 PEAM; PF00089; Trypsin; 1. PMRRT; SM00020; Tryp SPC; 1. PROSITE; PS0240; TRYPSIN DOM; 1. PROSITE; PS00135; TRYPSIN_SER; 1.
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77.8%;
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 HSSP; P00760; 1EZX
 MEROPS; S01.257; -
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Riausberg R.L., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Ruhing M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Raheslesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmuz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 'Generation and initial analysis of more than 15,000 full-length human
 Gaps
 TISSUE=Embryo;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
 Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 ö
 82.0%; Score 41; DB 2; Length 163; 77.8%; Pred. No. 8.1;
 Indels
 (SEP-2004) to the EMBL/GenBank/DDBJ databases
 Hydrolase; Protease; Serine protease.
SEQUENCE 163 AA; 17881 MW; DC90CAEAA755BAFB CRC64;
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 Last sequence update)
Last annotation update)
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 Created)
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InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR009003; Pept_Ser_Cys.
Pfam: PP00089; Trynsin; 1.
 PERM; PF00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
BMART; SM00200; Tryp SP07; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00135; TRYPSIN DSH; 1.
 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
 (TrEMBLrel. 28,
 Dev. Dyn. 225:384-391(2002)
 Best Local Similarity 77.8 Matches 7; Conservative
 cDNA sequences.
PRELIMINARY;
 Klein S., Gerhard D.S.;
Submitted (SEP-2004) to
 Jones S.J., Marra M.A.
 Xenopodinae; Xenopus
 SEQUENCE FROM N.A.
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Name=MGC97901;
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 and mouse
 SEQUENCE
 Query Match
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Gaps

ö

1; Indels

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PubMed=15203212; DOI=10.1016/j.ygeno.2004.01.009;
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22 2
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01-MAY-2000
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 090YN3
 CHAIN
 RESULT 14
 090YN3
SORETTE
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 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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 Mitsui S., Okui A., Kominami K., Uemura H., Yamagushi N.; "cDNA cloning and tissue-specific splicing variants of mouse hippostasin/TLSP (PRSS20).";
 Length 249;
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 25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Last annotation update)
 82.0%; Score 41; DB 2; 77.8%; Pred. No. 12; ive 1; Mismatches
 250 AA
 249 AA
 Biochim. Biophys. Acta 1494:206-210(2000).
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 Best Local Similarity
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01-MAY-2000
 118
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 Matches
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STRAIN=C57BL/6J; TISSUE=Tongue;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I all Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
 01-MAY-2000 (TrEMBLrel: 13, Last sequence update)
25-OCT-2004 (TrEMBLrel: 28, Last annotation update)
4 ippostatin profester trype (Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310015108 product:protease, serine, 20, full insert sequence) (Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310040F07 product:protease, serine, 20, full insert sequence).
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STRAIN=C57BL/6J; TISSUE=Tongue;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
 TISSUE=Prostate;
MEDLINE=20525460; PubMed=11072088; DOI=10.1016/S0167-4781(00)00206-2;
 Gaps
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
Olsson A.Y., Lilja H., Lundwall A.;
"Taxon-specific evolution of glandular kallikrein genes and identification of a progenitor of prostate-specific antigen.";
Genomics 84:147-156 (2004).
-!- MISCELLANEOUS: The sequence shown here is derived from an EMBL/Genbank/DDBJ third party annotation (TPA) entry.
 ö
 Mitsui S., Okui A., Kominami K., Uemura H., Yamagushi N.; "CDNA cloning and tissue-specific splicing variants of mouse hippostasin/TLSP (PRSS20).";
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Mochizuki S., Hiratsu K., Suwa M., Ishii T., Sugino F., Yamada K.,
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The large linear plasmid pSLA2-L of Streptomyces rochei has an
unusually condensed gene organization for secondary metabolism.";
Mol. Microbiol. 48:1501-1510(2003).
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
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Hypothei.al protein.
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 Plasmid pSLA2-L.
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Adachi J., Aizawa K., Akhimura T., Arai A., Aono H.,

Adachi J., Aizawa K., Akhalira S., Akhimura T., Arai A., Aono H.,

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A Arakawa T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

Okazaki Y., Okido T., Owa C., Saito R., Sakai C., Sakai K.,

Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

Muramatsu M., Hayashizaki Y.;

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

- Shwilarny: Bablongs to peptidase family Sl.

EMBL; AK009360; BAB26241.2; -.

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Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Togawa Y., Izawa M., Ohara E., Watshikai M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,

RIKEN integrated sequence analysis (RISA) system 384-format

sequencing pipeline with 384 multicapillary sequencer.";
 STRAIN=C57BL/6J; TISSUB=Tongue;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazadi Y., Muramatsu M., Hayashizaki Y.;
Konno H., Okazadi Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
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Nature 420:563-573(2002).
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Suwa M., Sugino H., Sasaoka A., Mori E., Fujii S., Shinkawa H.,
Nimi O., Kinashi H.;
Nimi O., Kinashi H.;
Identification of two polyketide synthase gene clusters on the linear plasmid pSLA2-L in Streptomyces rochei.";
Gene 246:123-131(2000).
STRAIN=7434AN4;
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Hiratsu K., Mochizuki S., Kinashi H.;
Hiratsu K., Mochizuki S., Kinashi H.;
"Cloning and analysis of the replication origin and the telomeres of the large linear plasmid pSLA2-L in Streptomyces rochei.";
Mol. Gen. Genet. 263:1015-1021(2000).
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 MEDLINE=99053144; PubMed=9836424; Kinashi H., Shinkawa H.; Kinashi H., Fujii S., Hatani A., Kurokawa T., Shinkawa H.; Pujais S., Hatani A., Kurokawa T., Shinkawa H.; Pupayaisal mapping of the linear plasmid pSLA2-L and localization of the eryAl and acti homologs."; Biosci. Biotechnol. Biochem. 62:1892-1897(1998). BMSGIL, AB08824; BACK55881.; Phypothetical protein; Plasmid. SEQUENCE 612 AA; 66525 MW; 9BF0EIEEBD3110FC CRC64;
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US-09-654-600A-4
US-08-557-146-2
US-08-154-344-2
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US-08-130-188-2
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 US-08-944-483-33
US-08-557-146-12
US-09-027-337-4
 US-08-096-946-10
US-08-096-946-11
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 Title:
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 GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of FILE REFERENCE: D6223CIP-C CURRENT FILING DATE: 2000-02-11
CURRENT APPLICATION NUMBER: US/09/502,600A
PRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 80
LENGTH: 9
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US-08-767-820A-16

US-08-622-046B-1

US-08-622-046B-7

US-08-622-046B-7

US-08-944-483-37

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US-09-100-264-12

US-09-103-339-2

US-08-843-076D-1

US-08-843-076D-1

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US-08-843-076D-1

US-08-843-076D-1
 PCT-US94-07329-10
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US-09-502-600-80
; Sequence 80, Application US/09502600A
; Patent No. 6294344
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GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tollocto, Hirotosh,
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
TITLE OF INVENTION: Breast and Ovarian Carcinomas
TITLE OF INVENTION: Breast and Ovarian Carcinomas
CURRENT FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 13
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OTHER INFORMATION: Serine protease catalytic domain of Scce homologous to
 Gaps
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Matches 9; Conservative 0; Mismatches 0; Indels
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COUNTRY: U.S.A.
ZIP: 10036-2787
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COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PATEMIT Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: 424
ATTORNEY/ABENT INFORMATION:
NAME: Greener piakraid
 US-08-557-146-12

Sequence 12, Application US/08557146

Fatent No. 5834290

GENERAL INFORMATION:

APPLICANT: Egelrud, Torbjorn

APPLICANT: Hansson, Lennart

TITLE OF INVENTION: Recombinant Stratum Corneum

TITLE OF INVENTION: Brzyme (SCCE)

CORRESSONDENCE ADDRESS:

ADDRESSEE: White & Case, Patent Department
 NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 819-8783
TELEPAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
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 Sequence 4, Application US/09027337B Patent No. 5972616
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 STRANDEDNESS: single
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 CITY: New York
STATE: New York
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ORGANISM: Unknown
 US-08-557-146-12
 RESULT 5
US-09-027-337-4
 SEQ ID NO 4
LENGTH: 225
 STREET:
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 APPLICANT: COHEN, MAURICE
APPLICANT: COLPITS, TRACEY L.
APPLICANT: COLPITS, TRACEY L.
APPLICANT: PRIBOMAN, PAULA N.
APPLICANT: RASS, MICHAEL R.
APPLICANT: STEWARD N.
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; OTHER INFORMATION: Residues 207-215 of the SCCE protein
US-09-918-243-80
 SOFTWARE: PSESED for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/944,483 FILLING DATE:
 6183.US.01
 SEE: Abbott Laboratories
: 100 Abbott Park Road
Abbott Park
 Sequence 33, Application US/08944483
Patent No. 6232456
GENERAL INFORMATION:
 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BECAET, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183
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TELECHONE: 847/938-1629
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 ADDRESSEE:
 US-08-944-483-33
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 COUNTRY:
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Sequence 4, Application US/09654600A

Fatent No. 6649741

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

APPLICANT: Tanimoto, Hirotoshi

TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease

TITLE OF INVENTION: Overexpressed in Carcinomas

TITLE OF INVENTION: Overexpressed in Carcinomas

FILE REFERENCE: D606417/D

CURRENT APPLICATION NUMBER: US/09/654,600A

CURRENT APPLICATION NUMBER: 09/421,213

09/027,337

PRIOR FILING DATE: 1999-10-20
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CURRENT FILING DATE: 2000-08-23
PRIOR PILING DATE: 1999-10-20
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PRIOR FILING DATE: 1999-10-20
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 APPLICANT: Egelrud, Torbjorn APPLICANT: Hansson, Lennart
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 US-08-557-146-2
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 Gaps
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 GENERAL INFORMATION:
APPLICANT: Bgelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Brzyme (SCCE)
NUMBER OF SEQUENCES: 17
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Matches 9; Conservative 0; Mismatches
 ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
; OTHER INFORMATION: similar domain in TADG-15 US-09-027-337-4
 ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REPERENCE/DOCKET NUMBER: 1103326-181
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FILING DATE: 14-DEC-1995
CLASSIFICATION:
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 12, Application US/09154344
Patent No. 5981256
 Sequence 4, Application US/09644600; Patent No. 6451500; GENERAL INFORMATION: APPLICANT: O'Brien, Timothy J.
 STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 MOLECULE TYPE: polypeptide
 single
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 TYPE: amino acids
 linear
 STRANDEDNESS:
 TOPOLOGY:
 US-09-154-344-12
 US-09-154-344-12
 US-09-644-600-4
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 Sequence 2, Application US/09154344
Parent No. 5981256
GENERAL INFORMATION:
APPLICANT: BEALTH, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Brzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
 100.0%; Score 50; DB 2; Length 253; illarity 100.0%; Pred. No. 0.22; Conservative 0; Mismatches 0; Indels
 100.0%; Score 50; DB 2; Length 253; 100.0%; Pred. No. 0.22;
 STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2797
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING STEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
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FILING DATE: 16-SEP-1998
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/154,344
FILING DATE: 16-SEP-1998
GLASSIFICATION:
TO CLASSIFICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
GLASSIFICATION:
 0; Indels
 0; Mismatches
 NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REPERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
 INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 253 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear INMEDIATE SOURCE:
 TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
 ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 100.
Matches 9; Conservative
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 Query Match
Best Local Similarity
 LIBRARY: GenBank
CLONE: 532504
 New York
 TOPOLOGY:
 US-08-824-874-3
 US-09-154-344-2
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 Gaps
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 100.0%; Score 50; DB 2; Length 253; 100.0%; Pred. No. 0.22;
 COUNTRY: U.S.A.

ZIP: 10036-2787

COMPUTER READABLE FORM:
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SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
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FILING DATE: 14-DEC-1995
CLASSIPICATION: 424
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEN for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
CLASSIFICATION: 514
PRIOR APPLICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ADDRESSEE: White & Case, Patent Department
 US-08-824-874-3

Sequence 3, Application US/08824874

Sequence 3, Application US/08824874

Fatent No. 5962300

APPLICANT: Hillman, Jennifer L.

APPLICANT: Hallman, Jennifer L.

TITLE OF INVENTION: NOVEL KALLIKREIN

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE Incyte Pharmaccuticals, Inc.

STREET: 3174 Porter Drive
 0; Mismatches
 ATTORNEY AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION UNBER: 33,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEPHONE: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
 NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERNCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION:
TELEPHONE: 415-855-0555
 1155 Avenue of the America
 TYPE: amino acida
TOPOLOGY: 11-
 FILING DATE: ATTORNEY/AGENT INFORMATION:
 Conservative
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 MOLECULE TYPE: protein
 207 ĠPĽVĊŘĠŤĽ 215
 1 GPLVCRGTL 9
 New York
: U.S.A.
 Query Match
Best Local Similarity
Matches 9; Conserv
 New York
 USA
 COUNTRY: US
 94304
 US-08-557-146-2
 STATE:
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,762
FILLING DATE: 16-Jan-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter prive
 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
CLASSIFICATION:
 ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERRACE DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION:
TELEPHONE: 415-685-0555
 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy,
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
 APPLICANT: Hillman, Jennifer L.
Lal, Preeti
TILLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
 APPLICATION NUMBER: 09/210,084
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
 Sequence 3, Application US/09764762; Patent No. 6472195; GENERAL INFORMATION:
 TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
 COMPUTER READABLE FORM:
 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
 CITY: Palo Alto
 STRANDEDNESS: single
TOPOLOGY: linear
COMPUTER READABLE FORM
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 GenBank
 STATE: CA
 IMMEDIATE SOURCE:
 ; LIBRARY: GenB;
; CLONE: 532504
US-09-210-084-3
 US-09-764-762-3
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 Sequence 2, Application US/08930188

Patent No. 6093397

GENERAL INFORMATION:
APPLICANT: Dixon, Eric P.
APPLICANT: Johnstone, Edward M.
APPLICANT: Little, Sheila P.
TITLE OF INVENTION: AMYLOID PRECURSOR PROTEIN PROTEASE AND TITLE OF INVENTION: RELATED NUCLEIC ACIDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Eli Lilly and Company
STREET: Lilly Company
CITY: Indianapolis
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 Query Match 100.0%; Score 50; DB 3; Length 253; Best Local Similarity 100.0%; Pred. No. 0.22; Matches 9; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/930,188
 ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto CITY: Palo Alto COUNTRY: USA COUNTRY: USA ZIP: 94304
 Sequence 3, Application US/09210084
; Patent No. 6197511
; GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-ARR-1995
ATTORNEY/AGENT INFORMATION:
 United States of America
 NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFRENCE/DOCKET NUMBER: X923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
TELEPAX: 317-276-3861
 TELEFAX: 317-276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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 single
 , MOLECULE TYPE: protein US-08-930-188-2
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 TOPOLOGY: linear
 STATE: Indiana
COUNTRY: Unite
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 US-09-210-084-3
 JS-08-930-188-2
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207 GPLVCRGTL 215

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; Sequence 2, Application PC/TUS9604294
; GENERAL INFORMATION:
; APPLICANT: Dixon, Eric P.
; APPLICANT: Johnstone, Edward M.
; APPLICANT: Little, Sheila P.
; TITLE OF INVENTION: RELATED NUCLEIC ACIDS
; VUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
; TIT: Indiana
; STATE: Indiana
; COUNTRY: United States of America
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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APPLICATION NUMBER: PCT/US96/04294
 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APP-1995
ATTORNEY, AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-277-1090
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TELEPHONE: ALTO-276-3861
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LENGTH: 253 amino acide
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 LIBRARY: GenBank
CLONE: 532504
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SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
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STRANDEDNESS: single
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IMMEDIATE SOURCE:
 TYPE: amino acid
STRANDEDNESS: single
 MOLECULE TYPE: protein
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207 GPLVCRGTL 215
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US-09-918-243-80
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 US-09-905-083A-80
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| Description                      | Sequence 80, Appl | Sequence 80, Appl | Sequence 80, Appl | Sequence 80, Appl | Sequence 98, Appl | Sequence 96, Appl | Sequence 33, Appl | Sequence 104, App | Sequence 4, Appli | Sequence 102, App | Sequence 92, Appl |
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| 19   | 20 | 100.0 | 253 | 15 | US-10-173-999-48     | 48, A             |
| 20   | 20 | 100.0 | 253 | 16 | US-10-408-765A-639   | 639,              |
| 21   | 20 | 100.0 | 253 | 16 | US-10-643-795A-95    | 95, A             |
| 22   | 20 | 100.0 | 253 | 17 | US-10-948-518-95     | 95,               |
| 23   | 20 | 100.0 | 253 | 17 | US-10-868-490A-1     | Ļ,                |
| 24   | 20 | 100.0 | 257 | 15 | US-10-344-394-38     | 38,               |
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| 29   | 45 | 90.0  | 250 | 15 | US-10-055-569A-69    | 69,               |
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| 34   | 44 | 88.0  | 251 | 15 | US-10-344-394-27     | 27,               |
| 35   | 44 | 88.0  | 267 | 17 | US-10-480-988-20     |                   |
| 36   | 42 | 84.0  | 8   | 15 | US-10-424-599-210636 |                   |
| 37   | 41 | 82.0  | 23  | 14 | US-10-071-214-6      | Sequence 6, Appli |
| . 38 | 41 | 82.0  | 80  | 16 |                      |                   |
| 39   | 41 | 82.0  | 249 | 15 | US-10-055-569A-68    | Sequence 68, Appl |
| 40   | 41 | 82.0  | 276 | 15 | US-10-055-569A-67    | 67,               |
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| 45   | 40 | 80.0  | 237 | 10 | US-09-860-739-1      | 'n                |

## ALIGNMENTS

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 APPLICANT: O'Brien, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer; FILE REPERENCE: D6223CIP/C/D/CIP
CURRENT APPLICATION NUMBER: US/09/918,243
FRIOR PRILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 80
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 Length 9;
 100.0%; Score 50; DB 9; Length 9; larity 100.0%; Pred. No. 1.6e+06; Conservative 0; Mismatches 0; Indels
 FEATURE:
NAMB/KEY: CHAIN
OTHER INFORMATION: Residues 207-215 of the SCCE protein US-09-918-243-80
Sequence 80, Application US/09918243; Patent No. US20020142317A1; GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2004-04-23
PRIOR PILING DATE: 2003-02-21
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CORGANISM: Homo sapiens
 PRIOR APPLICATION NUMBER: 60/373,815
PRIOR PELING DATE: 2002-04-19
PRIOR PELING DATE: 2001-10-09
PRIOR PAPLICATION NUMBER: 60/327,917
PRIOR APPLICATION NUMBER: 60/381,642
PRIOR PILING DATE: 2002-05-17
PRIOR PELING DATE: 2002-05-09
PRIOR PILING DATE: 2002-09
PRIOR PLING DATE: 2002-10-09
 Sequence 98, Application US/10262511
Publication No. US20040038223A1
GENERAL INFORMATION:
APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Fekuda, Ramesh
 Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
 Miller, Charles E. Rastelli, Luca Stone, David J. Pena, Carol E. A. Shenoy, Suresh G. Shinkets, Richard A. Rothenberg, Mark E. Leach, Martin D. Agee, Michele L.
 FILE REFERENCE: D6223CIP/C/D/CIP3
 Malyankar, Uriel M.
 Zerhusen, Bryan D.
Anderson, David W.
 Zhong, Mei
Catterton, Elina
 Ellerman, Karen
 Best Local Similarity 100.
Matches 9; Conservative
 Ort, Tatiana
Gorman, Linda
 Ju, Jingfang
Li, Li
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NAME/KEY: CHAIN
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 APPLICANT
 APPLICANT
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 Sequence 80, Application US/09905083

Patent No. US20020146708A1

GENERAL INFORMATION:

APPLICANT: O'BIEN, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of

TITLE OF INVENTION: Covarian Cancer

FILE REPERBNCE: D5223CIP/C/Div

CURRENT APPLICATION NUMBER: US/09/905,083

CURRENT FILING DATE: 2001-07-13

PRIOR PILING DATE: 2000-02-11

SEQ ID NO 80

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 APPLICANT: Cannon, Martin J.
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APPLICANT: Santin, Alessandro.
TITLE CARLON: Alessandro.
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer FILE REFERENCE: D6223CIP/C/D/CIP2
CURRENT APPLICATION NUMBER: US,10/372,521
CURRENT FILING DATE: 2003-02-21
PRIOR FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 136
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Publication No. US20040224891A1
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
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0
 ö
 100.0%; Score 50; DB 15; Length 9; 100.0%; Pred. No. 1.6e+06; Ltive 0; Mismatches 0; Indels
 100.0%; Score 50; DB 9; Length 9; 100.0%; Pred. No. 1.6e+06;
 0; Indels
 FEATURE:
NAME/KEY: CHAIN
OTHER INFORMATION: Residues 207-215 of the SCCE protein US-09-905-083-8
 ; NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 207-215 of the SCCE protein
US-10-372-521-80
 0; Mismatches
 ; Sequence 80, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION:
 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
 9; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
 ORGANISM: Homo sapiens
 1 GPLVCRGTL 9
 1 GPLVCRGTL 9
 1 GPLVCRGTL 9
 1 GPLVCRGTL 9
 Query Match
Best Local Similarity
Matches 9; Conserv
 RESULT 3
US-10-372-521-80
 US-10-831-075-80
US-09-905-083-80
 TYPE: PRT
 FEATURE:
 ò
 ð
```

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Gaps
 APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPREBLICA: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/326,483
 ö
 Length 9;
 Indels
; OTHER INFORMATION: Residues 207-215 of the SCCE protein US-10-831-075-80
 100.0%; Score 50; DB 16; 100.0%; Pred. No. 1.6e+06;
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PRIOR APPLICATION DATA:
 Conservative
 152 ĠPĽVĊŘĠŤĽ 160
 STATE: IL
COUNTRY: USA
 TYPE: PRT
ORGANISM: Homo sapiens
 Query Match
Best Local Similarity
Matches 9; Conserv
 1 GPLVCRGTL
 US-10-262-511-96
 RESULT 7
 ö
 APPLICANT: Shinket, Richard A.
APPLICANT: Shinket, Richard A.
APPLICANT: Rothenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Leach, Michele L.
APPLICANT: Berghs, Constance
ITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERENCE: 21402-462.
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT PILING DATE: 2003-62.8
PRIOR PILING DATE: 2001-10-02
PRIOR PPLICATION NUMBER: 60/326,483
PRIOR PILING DATE: 2002-04-19
PRIOR PLING DATE: 2002-04-19
PRIOR PLING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR PLING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR PILING DATE: 2002-04-17
PRIOR PILING DATE: 2002-04-17
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-10-05
PRIOR FILING DATE: 2001-10-05
SOFTWARE: CuraSequist version 0.1
SEQ ID NO 98
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 100.0%; Score 50; DB 15; Length 181; 100.0%; Pred. No. 0.97;
 0; Indels
 0; Mismatches
 US-10-262-511-96
; Sequence 96, Application US/10262511
; Publication No. US20040038223A1
 Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
Malyankar, Uriel M.
 APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
 Zerhusen, Bryan D.
Anderson, David W.
 Ji, Weizhen
Miller, Charles E.
 Rastelli, Iuca
Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
 Zhong, Mei
Catterton, Elina
 Best Local Similarity 100.
Matches 9; Conservative
 Gorman, Linda
 Ort, Tatiana
 133 GPLVCRGTL 141
 TYPE: PRT
ORGANISM: Homo sapiens
 1 GPLVCRGTL 9
 US-10-262-511-98
 Query Match
 APPLICANT:
APPLICANT:
APPLICANT:
 ઠે
 셤
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```
GRANADOS, EDWARD N.
KLASS, MICHAEL R.
RUSSELL, JOHN C.
STEWARLT, KENT D.
STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERING PROTEASE REAGENTS
OF THE PROSTATE
 ö
PRIOR FILING DATE: 2002-10-09

PRIOR PELING DATE: 2002-05-16

PRIOR FILING DATE: 2002-05-16

PRIOR PELING DATE: 2002-05-16

PRIOR PELING DATE: 2002-05-16

PRIOR FILING DATE: 2001-05

PRIOR PILING DATE: 2001-0-17

PRIOR PILING DATE: 2002-04-17

PRIOR PILING DATE: 2002-04-17

PRIOR PILING DATE: 2002-04-17

PRIOR PILING DATE: 2002-04-17

PRIOR PILING DATE: 2002-04-19

PRIOR PILING DATE: 2001-0-05

PRIOR PILING DATE: 2001-0-05

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 439

SOFTWARE: CuraSeqList version 0.1

SEQ ID NO 96

TYPE: nnm
 Gape
 ..
0
 100.0%; Score 50; DB 15; Length 198; 100.0%; Pred. No. 1.1;
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 COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
COMPUTER: TOOR
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/789,210
FILING DATE: 20-Feb-2001
CLASSIFICATION: <UNKNOWN>
 APPLICATION NUMBER: 08/944,483
APPLING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
NAME: BECKET, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
 Mismatches
 NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
 RESULT ;

18-09-789-210-33

1 Sequence 33, Application US/09789210

1 Publication No. US20040241646A1

2 GENERAL INFORMATION:

APPLICANT: COHEN, MAURICE

COLPITTS, TRACEY L.

FRIEDMAN, PAULA N.
 STREET: 100 Abbott Park Road CITY: Abbott Park
```

```
Ju, Jingfang
Li, Li
Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
 APPLICANT: Smithson, Glennda
APPLICANT: Milet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: U, Jingfang
APPLICANT: Li, Li,
APPLICANT: Guo, Xiaojia (Sash
 Best Local Similarity 100.
Matches 9; Conservative
 FEATURE:
COTHER INFORMATION: SCCE
US-10-600-187-4
 179 GPLVCRGTL 187
 193 GPLVCRGTL 201
 TYPE: PRT
ORGANISM: Homo sapiens
 1 GPLVCRGTL 9
 1 GPLVCRGTL 9
 US-10-262-511-104
 US-10-262-511-102
 US-10-600-187-4
 APPLICANT:
APPLICANT:
 Query Match
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 Gaps
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 Query Match 100.0%; Score 50; DB 11; Length 224; Best Local Similarity 100.0%; Pred. No. 1.2; Matches 9; Conservative 0; Mismatches 0; Indels
 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: None
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-789-210-33
 ; Sequence 104, Application US/10262511
; Publication No. US20040038223A1
; GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
 Guo, Xiaojia (Sasha)
Patturajan, Meera
 Malyankar, Uriel M.
Ort, Tatiana
Gorman, Linda
 Spytek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
 Ji, Weizhen
Miller, Charles E.
Rastelli, Luca
Stone, David J.
 Zerhusen, Bryan D.
Anderson, David W.
 Shimkets, Richard
 Pena, Carol E. A.
Shenoy, Suresh G.
 APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
 Zhong, Mei
Catterton, Elina
TELEX: <Unknown>
 Ju, Jingfang
Li, Li
 178 GPLVCRGTL 186
 1 GPLVCRGTL 9
 US-10-262-511-104
 APPLICANT:
APPLICANT:
APPLICANT:
 APPLICANT:
 APPLICANT:
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PRIOR FILING DATE: 2002-04-13

PRESURE OF CARRAVISH: Reme sapisms

US-10-50-137-140

PRESURE OF CARRAVISH: Reme sapisms

OF I GOLINGARI 100.04; SCORE 60; DB 15; Length 224;

PRESURE OF CARRAVISH: Reme sapisms

OF I GOLINGARI 100.04; PRIOR DATE: 2003-04-10-10

PRESURE OF CARRAVISH: Reme sapisms

OF I GOLINGARI 100.04; PRIOR DATE: 2003-04-10-10

PRESURE OF CARRAVISH: REME CARRAVISH: REME PRIOR PRI
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```
APPLICANT: Ages, MICHELE D.
APPLICANT: AGES, MICHERE D.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPREBRENCE: 21402-462C
CURRENT APPLICATION NUMBER: 60/326,483
FRIOR APPLICATION NUMBER: 60/326,483
FRIOR APPLICATION NUMBER: 60/326,483
FRIOR APPLICATION NUMBER: 60/326,483
FRIOR APPLICATION NUMBER: 60/327,917
FRIOR APPLICATION NUMBER: 60/327,917
FRIOR APPLICATION NUMBER: 60/327,917
FRIOR APPLICATION NUMBER: 60/327,917
FRIOR FILING DATE: 2002-06-17
FRIOR FILING DATE: 2002-06-17
FRIOR FILING DATE: 2002-06-16
FRIOR FILING DATE: 2001-10-05
FRIOR
 100.0%; Score 50; DB 15; Length 250; 100.0%; Pred. No. 1.3;
 Mismatches
 ö
 Shimkets, Richard A. Rothenberg, Mark E. Leach, Martin D. Agee, Michele L.
Guo, Xiaojia (Sasha)
 Zerhusen, Bryan D.
Anderson, David W.
Zhong, Mei
Catterton, Elina
 Malyankar, Uriel M.
Ort, Tatiana
Gorman, Linda
 Ji, Weizhen
Miller, Charles E.
Rastelli, Luca
Stone, David J.
 Pena, Carol E. A.
Shenoy, Suresh G.
 3llerman, Karen
 Conservative
 204 GPLVCRGTL 212
 ; ORGANISM: Homo sapiens
US-10-262-511-92
 1 GPLVCRGTL 9
 Query Match
Best Local Similarity
Matches 9; Conserv
 US-10-262-511-94
 RESULT 12
 ö
 APPLICANT: Berghs, Constance
APPLICANT: Berghs, Constance
TITLE OF INVERTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
FURNER PELICATION NUMBER: 60/326,483
PRIOR APPLICATION NUMBER: 60/326,483
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR PILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR PLILNG DATE: 2002-05-17
PRIOR PLILNG DATE: 2002-05-17
PRIOR PLILNG DATE: 2002-05-17
PRIOR PLILNG DATE: 2002-10-09
PRIOR PLILNG DATE: 2002-10-09
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR PLILNG DATE: 2002-10-09
PRIOR PPLICATION NUMBER: 60/339,056
PRIOR PLILNG DATE: 2002-05-16
PRIOR PLILNG DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/333,260
PRIOR PLILNG DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR PLILNG DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,436
PRIOR PLILNG DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/327,435
PRIOR PLILNG DATE: 2002-04-17
PRIOR PLING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/327,435
PRIOR PLILNG DATE: 2002-04-17
PRIOR PLING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/327,435
 Gaps
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 100.0%; Score 50; DB 15; Length 247; 100.0%; Pred. No. 1.3; tive 0; Mismatches 0; Indels
 Sequence 92, Application US/10262511; Publication No. US20040038223A1; GENERAL INPORMATION: APPLICANT: Smithson, Glenda; APPLICANT: Millet, Isabelle; APPLICANT: Peyman, John A.; APPLICANT: General APPLICANT: Ju, Jingfang; APPLICANT: Ju, Jingfang; APPLICANT: Li, Li
Edinger, Shlomit R.
 Malyankar, Uriel M
Ort, Tatiana
 Rastelli, Luca
Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
 Rothenberg, Mark E
Leach, Martin D.
Agee, Michele L.
 Zerhusen, Bryan D.
Anderson, David W.
 Ji, Weizhen
Miller, Charles E.
 Shimkets, Richard
 Catterton, Elina
 Query Match . 100.
Best Local Similarity 100.
Matches 9; Conservative
 Sorman, Linda
 193 GPLVCRGTL 201
 TYPE: PRT
GRGANISM: Homo sapiens
US-10-262-511-102
 Shong, Mei
 US-10-262-511-92
 SEQ ID NO 102
LENGTH: 247
 셤
```

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ö
Gaps
;;
Indels
 Sequence 94, Application US/10262511; Publication No. US20040038223A1; GENERAL INFORMATION:
 APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
```

```
ö
 100.0%; Score 50; DB 9; Length 253; 100.0%; Pred. No. 1.3;
 0; Indels
 COMPUTER: FAILO ALLOS

STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compactible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/764,762
FILING DATE: 16-Jan-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 09/210,084
FILING DATE: «UNKnown»
ATTORNEY/AGENT INFORMATION:
NAME: BILLION:
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
 Sequence 3, Application US/09764762; Sequence 3, Application US/09764762; Patent No. US20020068341A1
GENERAL INFORMATION:
HILLMAN, Jennifer L.
Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: 5
STREET: 3174 Porter Drive
APPLICANT: PLOWMAN, GREGORY
APPLICANT: WHYTE, DAVID
APPLICANT: CRAENEELS, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
TILE COF INVENTION: NOVEL PROTEASES
FILE REPERBNCE: 038602/1214
CURRENT FILING DATE: 2001-06-26
CURRENT FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTHARE: PatentIn Ver: 2.1
SEQ ID NO 98
LENGTH: 253
 0; Mismatches
 TELECOMMUNICATION INFORMATION
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
 LENGTH: 253 amino acids
 Query Match
Best Local Similarity 100...
Pest Local 9; Conservative
 207 GPLVCRGTL 215
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-98
 IMMEDIATE SOURCE:
 1 GPLVCRGTL 9
 RESULT 14
US-09-764-762-3
 임
 ઠે
 ö
 APPLICANT: Stankers, Algorian A.
APPLICANT: Rechenberg, Mark E.
APPLICANT: Leach, Martin D.
APPLICANT: Age, Michele L.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: 06/326,483
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR PILING DATE: 2002-05-16
PRIOR PILING DATE: 2002-05-16
PRIOR PELING DATE: 2002-05-16
PRIOR PELING DATE: 2002-05-16
PRIOR PELING DATE: 2002-05-16
PRIOR PELING DATE: 2002-04-19
PRIOR PELING DATE: 2002-04-17
PRIOR PELING DATE: 2001-10-05
PRIOR PERIOR PELING DATE: 2001-10-05
PRIOR PELING
 Gaps
 ö
 Query Match
100.0%; Score 50; DB 15; Length 252;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels C
 ; Sequence 98, Application US/09888615; Patent No. US20020064856A1; GENERAL INFORMATION:
 Rastelli, Luca
Stone, David J.
Pena, Carol E. A.
Shenoy, Suresh G.
Shimkets, Richard A.
 Guo, Xiaojia (Sasha)
 Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
 Malyankar, Uriel M.
Ort, Tatiana
 Zerhusen, Bryan D.
Anderson, David W.
 Charles E
 Zhong, Mei
Catterton, Elina
 Ellerman, Karen
 Kekuda, Ramesh
 Gorman, Linda
 Ju, Jingfang
Li, Li
 Ji, Weizhen
Miller, Char
 206 GPLVCRGTL 214
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-94
 1 GPLVCRGTL 9
 RESULT 13
US-09-888-615-98
 APPLICANT:
APPLICANT:
APPLICANT:
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
 APPLICANT
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Gaps

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RESULT 15

US-10-071-214-2

i Sequence 2, Application US/10071214

i Publication No. US20030066099A1

i GENERAL INFORMATION:

APPLICANT: HANSSON, Lemart

APPLICANT: HANSSON, Lemart

ITTLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN

TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN

TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN

TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN

TITLE OF INVENTION UNMBER: US 60/267,422

PRIOR FILING DATE: 2001-02-09

RRIOR PRIOR DATE: 2001-02-09

NUMBER OF SEQ ID NOS: 50

SEQ TAMARE: PATENTIN VERSION 3.1

SEQ ID NO 2

LENGTH: 253

LENGTH: 253
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 Gaps
 0; Gaps
 ö
 Query Match 100.0%; Score 50; DB 14; Length 253; Best Local Similarity 100.0%; Pred. No. 1.3; Matches 9; Conservative 0; Mismatches 0; Indels (
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; SEQUENCE DESCRIPTION: SEQ ID NO: 3: US-09-764-762-3
 207 GPLVCRGTL 215
 TYPE: PRT;
CRGANISM: Homo sapiens
US-10-071-214-2
 1 GPLVCRGTL 9
 1 GPLVCRGTL 9
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Search completed: July 13, 2005, 18:23:41 Job time : 65.8889 secs

207 GPLVCRGTL 215

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AAE10657 AAE02609 ABB78618

440

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100.0%; Score 41;
475
475
475
85.4
85.4
85.4
 35
35
 Query Match
 26
27
28
 Human NOV
Human str
Human sCC
Human SCC
Amino aci
Protein d
Protein d
Human str
 Cancer/an
Human tum
Antipsori
Human ova
Human HSC
 Novel hum
Human NOV
 Ovarian c
Human hea
 Aae08291 Human str
Adr68847 Human str
 Human ser
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 July 13, 2005, 16:12:23; Search time 76.6667 Seconds (without alignments) 45.402 Million cell updates/sec
 Description
 Adr68847 Abg23378 Abg23378 Adr62900 Adr62900 Adr62900 Adr86290 Abb84421 Abb84421 Abb84421 Abb84421 Abr58471 Abr58471 Abr58471 Adr6883 Adr6983 Adr6983 Adr6982 Adr2880 Adr2880 Adr2886 Adr68877 Adr69820 Adr2886 Adr68877 Adr688977 Adr68877 Adr6887 Adr6887 Adr68877 Adr
 2105692
 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 2105692 seqs, 386760381 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 ADR68847
ABG23378
ADR62900
ADR62900
AAR6788
AAW62313
ABB8440
ABB84406
ABB84406
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Gapop 10.0 , Gapext 0.5
 geneseqp2002s:*
geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*
 US-09-905-083A-86
 seq length: 0
seq length: 200000000
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 1 MARSLLLPL 9
 Length
 Query
Match
 Scoring table:
 Title:
Perfect score:
 Score
 Minimum DB &
Maximum DB &
 Sequence:
 Searched:
 Database
 Run on:
 Result
 Š.
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| AMENGES AND STATES AND | A 6 ;                              | 01-NOV-2001 (first entry)  Human stratum corneum chymotrypsin enzyme peptide #56 (residues 1-9).  Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia. | 1.<br>2001WO-US003977.                                                   | 2000US-00502600.<br>ARKANSAS.<br>676/56. | cancer comprises detecting stratum corneum chymotrypsin<br>Page 114; 127pp; English. | The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide |                |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------|------------------------------------------|--------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------|
| 220<br>333<br>331<br>331<br>331<br>331<br>331<br>331<br>33                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | .08291 standard;                   | 01-NOV-2001 (first entry)  Human stratum corneum chymotrypsin  Stratum corneum chymotrypsin enzyme  cancer; ovarian; breast; lung; colc  antisense therapy; malignant hyper                                                                                                           | Homo saptens.<br>WO200159158-A1.<br>16-AUG-2001.<br>07-FEB-2001; 2001WO- | 4                                        | osing<br>e.<br>125;                                                                  | The invention relates to diagnosing screening for stratum corneum chymoconsidered to be an integral part of the diagnosis of cancer. The method carcinoma and malignant hyperplasia to treat a cancer selected from ovan and other cancers in which SCCE is human SCCE peptide                                                                                                                                                                                                                                                                  | sequence 9 AA; |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | RESULT 1 AAE08291 ID AAE XX AC AAE | **************************************                                                                                                                                                                                                                                                | P X B X B X S                                                            | <b>X # X # X #</b> X # X #               | XX E E X X S                                                                         | ¥88888888888                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | <u>ر</u><br>م  |

Length 9;

DB 4;

a

Matches

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RESULT 2 ADR68847

us-09-905-083a-86.rag

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCN) primeras, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cerivity of (II) as useful in gene therapy techniques to restore normal ectivity of (II) are to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in issue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from MIPO at (ftp. wipo.int/pub/published_pct_sequences)
 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
 4; Length 136;
 0; Indels
 100.0%; Score 41; DB 4 ilarity 100.0%; Pred. No. 1.9; Conservative 0; Mismatches
 claim 20; SEQ ID NO 53737; 103pp; English.
 Novel human diagnostic protein #23369.
 ADA05736 standard; protein; 198 AA.
 31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
 30-MAR-2001; 2001WO-US008631.
 Tang YT;
 (first entry)
 7 MARSLLLPL 15
 δ
 Drmanac RT, Liu C,
 WPI; 2001-639362/73
 Query Match
Best Local Similarity
 1 MARSLLLPL
 (HYSE-) HYSEQ INC
 N-PSDB; AAS87565.
 Sequence 136 AA;
 WO200175067-A2.
 biodiversity.
 18-FEB-2002
 ٠
;
 11-OCT-2001.
 ABG23378;
 ADA05736;
 Matches
 RESULT 4
 ADA05736
ID ADA
XX
AC ADA
 유
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 The invention relates to a novel method for vaccinating an individual against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating an individual with a SCCE peptide, which elicits an immune response in the individual. A peptide of the invention acts as a stratum corneum chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating an individual against SCCE, particularly an individual having, suspected or at risk of getting ovarian, lung, prostate, pancreatic or colon cancer. The oligonucleotide is useful for treating a neoplastic state in an individual, such as ovarian, breast, lung, colon, prostate, or peptides are also useful in the monitoring and development of immunotherapies for ovarian and other malignancies. The present sequence represents a peptide fragment of serine protease SCCE (stratum corneum
 Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for vaccinating an individual against SCCE, and in monitoring and developing immunotherapies for ovarian and other malignancies.
 Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:86.
 Gaps
 Gaps
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0
 serine protease; stratum corneum chymotrytic enzyme; SCCE; immune response; ovarian cancer; lung cancer; prostate cancer; pancreatic cancer; colon cancer.
 100.0%; Score 41; DB 8; Length 9; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
 Indels
 ..
0
 Pred. No. 1.8e+06;
 Mismatches
 Claim 5; SEQ ID NO 86; 117pp; English
 ABG23378 standard; protein; 136 AA.
 Santin A;
100.0%; FIE
 ADR68847 standard; peptide; 9 AA.
 20-FEB-2004; 2004WO-US005134.
 21-FEB-2003; 2003US-00372521
 02-DEC-2004 (first entry)
 9; Conservative
 Conservative
 O'brien TJ, Cannon MJ,
 (UYAR-) UNIV ARKANSAS
 0
 1 MARSLLLPL 9
 |||||||||
1 MARSLLLPL 9
 σ
 chymotrytic enzyme).
 WPI; 2004-653294/63.
 1 MARSLLLPL
 Query Match
Best Local Similarity
Matches 9; Conserv
 MARSLLLPL
 Best Local Similarity
 WO2004075723-A2
 Sequence 9 AA;
 Homo sapiens.
 10-SEP-2004.
 ADR68847;
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Gaps

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RESULT 3 ABG23378 ID ABG2

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The present invention describes NOVX proteins, where X can be 1 to 55 (e.g. NOV1). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more
 Claim 1; Page 170; 586pp; English
 06-NOV-2003 (first entry)
 Smithson G, Millet I, Pe
Patturajan M, Spytek KA,
Ort T, Gorman L, Zerhuse
 (CURA-) CURAGEN CORP.
 WPI; 2003-381626/36.
N-PSDB; ADA05735.
 pharmacogenomics
 WO2003029424-A2.
 18-OCT-2001;
22-OCT-2001;
24-OCT-2001;
24-OCT-2001;
29-OCT-2001;
 09-0CT-2001;
12-0CT-2001;
-15-0CT-2001;
17-0CT-2001;
 19-APR-2002;
19-APR-2002;
19-APR-2002;
 01-OCT-2002;
 Homo sapiens
 02-OCT-2001;
 -NOV-2001;
 19-APR-2002;
 22-APR-2002;
 16-MAY-2002;
 16-MAY-2002;
 16-MAY-2002;
 10-APR-2003
 17-APR-2002
 17-MAY-2002
 29-MAY-2002
 28-MAY-2002
 25-JUN-2002
 09-OCT-2001
 Eisen AJ,
 Ji W, Mi
Shimkets
 09-OCT-
 09-OCT-
 05-0CT
 05-OCT-
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containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or berrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to a pathology associated with the polypeptide; (12) a method for modulating or preventing a pathology associated with the above polypeptide in a mammal; and (14) a method for producing the above polypeptide in a mammal; and (14) a method for producing the above polypeptide in a mammal; and (14) a method for producing the above polypeptide in a mammal; and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a considered with a polypeptide or the nucleic and antilipaemic activities and can be used in gene therapy.
 human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
 probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
 acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various
 dyslipidaemias. The nucleic acids can also be used as hybridisation
 100.0%; Score 41; DB 6
100.0%; Pred. No. 2.9;
tive 0; Mismatches
 ADN62900 standard; protein; 198 AA
 01-OCT-2002; 2002US-00262511
 (first entry)
 Conservative
 1 MARSLLLPL 9
 1 MARSLLLPL 9
 Local Similarity
nes 9; Conserv
 wasting disorder.
 Sequence 198 AA;
 JS2004038223-A1
 Human NOV18c.
 Homo sapiens.
 01-JUL-2004
 26-FEB-2004.
 ADN62900;
 Query Match
 Matches
 RESULT 5
 ADN62900
 g
 ઠે
 New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
 Dipippo VA;
 Peyman JA, Kekuda R, Ju J, Li L, Guo X;
A, Edinger SR, Ellerman K, Malyankar UM;
usen BD, Anderson DW, Zhong M, Catterton E;
elli L, Stone DJ, Pena CEA, Shenoy SG;
 human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; disetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
 Berghs C,
 ajon v. Zernusen BD, Anderson DW, Zhong Miller CE, Rastelli L, Stone DJ, Pena CEA, its RA, Rothenberg ME, Leach MD, Agee ML, Bt AJ, Gangolli EA, Rieger DK, Spaderna SK;
 Human NOV18c protein SEQ ID NO:96
 2001US - 0327449P
2001US - 0327917P
2001US - 0328049P
2001US - 0328056P
2001US - 032849P
2001US - 0329414P
2001US - 0330414P
2001US - 033099P
 2001US-0326483P.
2001US-0327435P.
 2001US-0341058P.
2001US-0339266P.
 2002US-0373815P.
2002US-0373817P.
2002US-0373826P.
 2002US-0373884P.
 2002US-0381042P.
 2002US-0381642P.
2002US-0383656P.
 2001US-0343629P
 2001US-0349575P
 2001US-0346357P.
2002US-0373260P.
 2002US-0374977P
 2002US-0381037P
 02-OCT-2002; 2002WO-US031373
 2002US-0381038P
 2002US-0383831P
 2002US-00262511
 2002US-0391335P
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Gaps

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2001US-0326483P. 2001US-0327435P. 2001US-0327449P. 2001US-0327917P. 2001US-0328029P.

05-OCT-2001; 09-OCT-2001; 09-OCT-2001; 09-OCT-2001;

02-OCT-2001; 05-OCT-2001;

6; Length 198; 0; Indels

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AAR6788
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 셤
 Dipippo VA;
 Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 2001US-0349575P.
2001US-0346357P.
2002US-0373260P.
2002US-0373815P.
 2002US-0381037P.
2002US-0381038P.
2002US-0381042P.
2002US-0381642P.
2002US-0383656P.
 2001US-0339266P
 2002US-0373817P.
 2002US-0374977P.
 2001US-0330309P
 2001US-0343629P
 25-JUN-2002; 2002US-0391335P
 PATTURAJAN M.
SPYTEK K A.
EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
 STONE D J.
PENA C B A.
SHENOY S G.
SHIMKETS R A.
ROTHENBERG M B.
LEACH M D.
AGER M L.
BERGHS C.
DIPIPPO V A.
 GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
 ZERHUSEN B D.
ANDERSON D W.
 SMITHSON G.
MILLET I.
PEYMAN J A.
KEKUDA R.
 CATTERTON E.
 2004-213931/20.
 MILLER C E.
RASTELLI L.
 GORMAN L.
 EISEN A.
 ZHONG M.
 GUO X.
 18-OCT-2001;
22-OCT-2001;
24-OCT-2001;
24-OCT-2001;
 01-NOV-2001;
 29-OCT-2001;
 19-APR-2002;
 16-MAY-2002;
16-MAY-2002;
 7-MAY-2002;
 39-MAY-2002;
 19-APR-2002;
 22-APR-2002;
 17-APR-2002;
 19-APR-2002;
 (EISE/)
(GANG/)
(RIEG/)
(SPAD/)
 (LEAC/)
(AGEE/)
 (PATT/)
 ELLE/)
 (MILL/)
(RAST/)
(STON/)
 (SHIM/)
 (ZERH/)
(ANDE/)
 (MILL/
 GORM/
 ZHON/
 JIWM/
 GUOX/
 EDIN/
 PENA/
 SHEN/
 (BERG/
 (KEKU/
 (ORTT/
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Claim 1; SEQ ID NO 96; 395pp; English

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The INVENTION FLATEURS TO ISOLATED AND EXPENSION AS A PROPERTY OF STATE AND EXPENSION AND ADDITION ADDITION AND ADDITION L ADDITION
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The invention relates to isolated NOVX polypeptides and polynucleotides.
 Nucleotide sequences encoding stratum corneum chymotryptic enzyme - and
 Gaps
 Stratum corneum chymotryptic enzyme; skin disorder; acne; psoriasis; callosities; keratosis pilaris; ichthyoses; eczema.
 ö
 duman stratum corneum chymotrophic recombinant enzyme (SCCE).
 100.0%; Score 41; DB 8; Length 198; 100.0%; Pred. No. 2.9; o; Mismatches 0; Indels
 AAR67888 standard; protein; 253 AA.
 94WO-IB000166.
 93DK-00000725
 Query Match
Best Local Similarity luv...
Best Local Similarity
 (first entry)
 Egelrud T, Hansson L;
 (revised)
 WPI; 1995-052088/07.
N-PSDB; AAQ81203.
 (SYMB-) SYMBICOM AB.
 1 MARSLLLPL
 1 MARSLLLPL
 Sequence 198 AA;
 20-JUN-1994;
 18-JUN-1993;
 Homo sapiens
 WO9500651-A1
 09-AUG-1995
 25-MAR-2003
 05-JAN-1995.
 AAR67888;
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Pred. No.

100.08;

S

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Human amyloid precursor protein protease (AAW05383) is involved in the processing or clearance of amyloid precursor protein to form beta-amyloid peptide. Its amino acid sequence was deduced from a cDNA clone (AAT39783) obtd. from a human lung library. Recombinant protease can be produced in transformed or transfected prokaryotic (partic. B. coli) or eukaryotic and testing of cpds. useful for develop products for the design and testing of cpds. useful for treating or preventing conditions associated with beta-amyloid peptide, esp. Alzheimer's disease
related vectors, transformed cells and polypeptides, useful for treating skin disorders, e.g. acne or psoriasis, and for identification of specific inhibitors.
 The enzyme encoded by this sequence is used in pharmaceutical, cosmetic and skin care products, especially to treat and prevent acne, xeroderma, or other hyperkeratotic conditions (e.g. callosities or keratosis pilaris), ichthyoses, psoriasis, etc. It is produced recombinantly following mammal, insect, plant, or microorganism transformation with plasmid p5507. (Updated on 25-MAR-2003 to correct PN
 New isolated human amyloid precursor protein protease - used to develop
 . for the treatment or diagnosis of associated conditions, esp.
 Amyloid precursor protein protease; Alzheimer's disease; diagnosis;
 100.0%; Score 41; DB 2; Length 253; 100.0%; Pred. No. 3.8; tive 0; Mismatches 0; Indels
 Human amyloid precursor protein protease.
 Little SP
 Disclosure; Page 97; 137pp; English
 AAW05383 standard; protein; 253 AA.
 Claim 1; Page 44-45; 55pp; English.
 96WO-US004294
 95US-00416257
 31-DEC-1996 (first entry)
 Local Similarity 100.
 Dixon EP, Johnstone EM,
 (ELIL) LILLY & CO ELI
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 prods. for the treat
Alzheimer's disease.
 WPI; 1996-464694/46.
 MARSLLLPL
 MARSLLLPL
 N-PSDB; AAT39783
 Sequence 253 AA;
 02-APR-1996;
 04-APR-1995;
 Homo sapiens
 WO9631122-A1
 -
 AAW05383;
 Query Match
 therapy
 field.)
 datches
 RESULT 7
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100.0%; Score 41; DB 2; Length 253;

Sequence 253 AA;

Query Match

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Gaps

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This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of anucleotide sequence coording for a stratum corneum chymotryptic enzyme (SCCE) or its variant, coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant, corneum chymotryptic enzymention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or testing of a composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or composition effective for the prevention or treatment of an compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of an abnormal or unwanted phenotype, and for screening or identifying a compound or composition effective for the prevention or treatment of puritus, acopic dermatitis, eczema, acne and inherited skin diseases consisting of epidermal hyperkratosis. The mammal of the invention said of potential compounds and compositions for relieve of various skin diseases a model for the human statum corneum chymotryptic enzyme, SCCE cramsgenic mammals described in the invention
 ö
 Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.
 SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protease; ktin cancer; hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermatitis; eczema; acne; itch; KLK7; enzyme.
 Gaps
 ö
 Indels
 ö
 Human SCCE protein N-terminal fragment SEQ ID 48.
 Mismatches
 ABB84421 standard; peptide; 253 AA.
 Example 6; Page 37; 74pp; English.
 ö
 08-FEB-2002; 2002WO-IB001300.
 09-FEB-2001; 2001CA-02332655.
 (first entry)
 Conservative
 Egelrud T, Hansson L;
 1 MARSLLLPL 9
 WPI; 2002-643380/69
Best Local Similarity
Matches 9; Conserv
 1 MARSLLLPL
 (EGEL/) EGELRUD T. (HANS/) HANSSON L.
 Sequence 253 AA;
 WO200262135-A2
 Homo sapiens
 08-NOV-2002
 15-AUG-2002.
 ABB84421;
 RESULT 8
 ABB8442
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transgenic mammals described in the invention

Sequence 253 AA;

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This invention describes a novel non-human transgenic mammal or mammalian embryo having integrated within its genome, a heterologous nucleotide sequence comprising at least a significant part of a nucleotide sequence coding for a bratum corneum chymotryptic enzyme (SCCE) or its variant, operably linked to a promoter that drives expression of heterologous scce or its variant in skin. The product of the invention is useful as a model for the study of disease with the aim of improving treatment, to relieve or ameliorate a pathogenic condition, for development or testing of a cosmetic or a pharmaceutical formulation, and for the development of a disgnostic method. It can also be used as a model for a skin disease or skin cancer. The invention is also useful for screening or identifying a compound or composition effective for the prevention or treatment of an compound or composition effective for the prevention or treatment of compound or composition effective for the prevention or treatment of inflammatory skin diseases selected from diseases consisting of epidermal hyperkeratosis, eczema, acno and inherited skin diseases with epidermal hyperkeratosis. The mammal of the invention is also useful as a model for further studies of itch mechanisms and the testing of where itch is a component. This sequence represents the human stratum corneum chymotryptic enzyme, SCCE which is a serine protease synonymous corneum kallikrein 7 (KLK7) and is used in the development of the
 ö
 Transgenic mammal or its embryo useful as model for human disease, has heterologous nucleotide sequence coding for stratum corneum chymotryptic enzyme operably linked to promoter that drives its expression in skin.
 SCCE; human; stratum corneum chymotryptic enzyme; kallikrein 7; serine protease; krangganic mammal; skin; skin disease; skin cancer; hyperkertatosis; acanthosis; epidermal inflammation; dermal inflammation; pruritus; atopic dermaltitis; eczema; acne; itch; KLK7; enzyme.
 Gaps
 ö
100.0%; Score 41; DB 5; Length 253; 100.0%; Pred. No. 3.8;
 0; Indels
 0; Mismatches
 Claim 10; Page 58-59; 74pp; English.
 ABB84406 standard; protein; 253 AA.
 08-FEB-2002; 2002WO-IB001300.
 09-FEB-2001; 2001CA-02332655.
09-FEB-2001; 2001DK-00000218.
 08-NOV-2002 (first entry)
Query Match
Best Local Similarity 100.
Matches 9; Conservative
 Egelrud T, Hansson L;
 σ
 WPI; 2002-643380/69.
N-PSDB; ABQ76226.
 Human SCCE protein.
 1 MARSLLLPL
 1 MARSLLLPL
 (EGEL/) EGELRUD T.
(HANS/) HANSSON L.
 WO200262135-A2
 Homo sapiens
 15-AUG-2002.
 ABB84406;
 RESULT 9
ABB84406
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The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. restenosis and coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obssity), inflammatory disorders (e.g. restenosis and remarties and psoriasis), central or peripheral nervous system the seases, migraines, pain, sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypotension, hypotension, psychotic disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's disease) and dyskinesias The nucleic acids and polypeptides are also useful for treating viral infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. virus (HIV), and mon-viral infections such as ocular disease (e.g.
 ö
 Human; protease; cancer; immune-related disorder; cardiovascular disease; neuronal-associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain; mood disorder; hypertension; psychotic disorder; neurological disorder; disorder; viral infection; human immunodeficiency virus; HIV; non-viral infection; ocular disease; cytostatic; enzyme.
 Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
 Gaps
 ö
 Sudarsanam S, Manning G, Caenepeel S;
 5; Length 253;
 0; Indels
 Amino acid sequence of novel human protease #39.
 100.0%; Score 41; DB 5
100.0%; Pred. No. 3.8;
 0; Mismatches
 AAU82740 standard; protein; 253 AA
 human proteases of the invention
 Claim 6; Fig 2N; 313pp; English.
 26-JUN-2001; 2001WO-US020171.
 26-JUN-2000; 2000US-0214047P.
Query Match
Best Local Similarity luv.v.
9; Conservative
 (first entry)
 Plowman G, Whyte D,
 σ
 σ
 WPI; 2002-139913/18.
 1 MARSLLLPL
 1 MARSLLLPL
 (SUGE-) SUGEN INC
 N-PSDB; ABK31782
 Sequence 253 AA;
 WO200200860-A2.
 Charydczak G;
 Homo sapiens.
 23-APR-2002
 03-JAN-2002.
 disorders.
 AAU82740
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The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises to prostate cancer. (I) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves contermining the expression levels in a sample comprising prostate cancer. Preferably, the expression levels of at least 10 genes are determined. (I) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells, which involves contexting a polypeptide differentially-regulated in prostate cancer cells with a test agent under conditions effective for the test agent to modulate a biological activity of the polypeptide, and eternining whether the test agent modulaces the biological activity. (I) is useful as molecular markers, as afture targets, and for detecting, determining predisposition to diseases and conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer conditions especially relating to prostate cancer. (I) and its expression conditions especially relating to prostate earcer. (I) and its expression conditions especially relating to prostate earce. (I) and its expression conditions especially relating to present earce. (I) and its safety etc. (I) is useful for assessing cancer eg., to determine the type of cancer. The polypeptide encoded by (I) can be used as target for therapy or drug
 Novel genes which are differentially regulated in prostate cancer, usef for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.
 Gaps
 Prostate cancer; gene expression; differential regulation;
molecular marker; drug target; cancer detection; cancer diagnosis;
cancer staging; cancer grading; cancer assessing; cancer monitoring.
 ..
 100.0%; Score 41; DB 5; Length 253; 100.0%; Pred. No. 3.8; ive 0; Mismatches 0; Indels
 Protein differentially regulated in prostate cancer #43.
 Claim 1; Page 293-294; 416pp; English.
 ABU07440 standard; protein; 253 AA.
 (ORIG-) ORIGENE TECHNOLOGIES INC.
 08-APR-2002; 2002WO-US010824.
 06-APR-2001; 2001US-0281731P.
 28-JAN-2003 (first entry)
Query Match
Best Local Similarity 100.
Matches 9; Conservative
 6
 2003-058520/05
 1 MARSLLLPL
 MARSLLLPL
 N-PSDB; ABX10343
 WO200281638-A2
 Jay G;
 Homo sapiens
 17-OCT-2002.
 ABU07440;
 Sun Z,
 RESULT 11
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 The invention describes genes (I) which are differentially regulated in prostate cancer. (I) Is useful for diagnosing a prostate cancer in a sample comprising prostate tissue, which involves determining the number of target genes which are differentially-regulated in the sample, where the number is indicative of the probability that the sample comprises prostate cancer. (I) Is useful for assessing a therapeutic or preventive intervention in a subject having a prostate cancer, which involves determining the expression levels in a sample comprising prostate tissue of target genes which are differentially-regulated in prostate cancer. Preferably, the expression levels of at least 10 genes are determined. (I) is also useful for identifying agents that modulate a biological activity of a polypeptide differentially-regulated in prostate cancer cells, which involves contexting a polypeptide differentially-regulated in prostate cancer cells with a test agent under conditions effective for
 Novel genes which are differentially regulated in prostate cancer, useful for diagnosing prostate cancer in prostate tissue sample and assessing therapeutic or preventive intervention in prostate cancer patients.
discovery. (I) can also be used for expressing the polypeptide and thus for searching specific binding partners of the polypeptide. (I) is useful in therapeutic applications to tract prostate cancer. The identification of specific genes, and groups of genes, expressed in pathways physiologically relevant to prostate cancer permits the definition of functional and disease pathways and the delineation of targets in these pathways which are useful in diagnostic, therapeutic, and clinical applications. This is the amino acid sequence of a protein diferentially
 Gaps
 Prostate cancer; gene expression; differential regulation;
molecular marker; drug target; cancer detection; cancer diagnosis;
cancer staging; cancer grading; cancer assessing; cancer monitoring.
 ö
 100.0%; Score 41; DB 6; Length 253; 100.0%; Pred. No. 3.8;
 Indels
 Protein differentially regulated in prostate cancer #74.
 .
0
 0; Mismatches
 ABU07471 standard; protein; 253 AA.
 Claim 1; Page 351; 416pp; English.
 (ORIG-) ORIGENE TECHNOLOGIES INC.
 08-APR-2002; 2002WO-US010824.
 06-APR-2001; 2001US-0281731P.
 regulated in prostate cancer
 (first entry)
 Conservative
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 WPI; 2003-058520/05.
 1 MARSLLLPL
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 Local Similarity
 N-PSDB, ABX10375
 Sequence 253 AA;
 WO200281638-A2.
 Jay G;
 Homo sapiens.
 28-JAN-2003
 17-OCT-2002.
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 ABU07471;
 Query Match
 Sun Z,
 Best Loc
Matches
 RESULT 12
 ABU07471
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Gaps

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0; Indels

Mismatches

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Conservative σ Q

1 MARSLLLPL

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1 MARSLLLPL

Query Match Best Local Similarity

Sequence 253 AA;

9

100.0%; Score 41; DB 6 100.0%; Pred. No. 3.8;

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the test agent to modulate a biological activity of the polypeptide, and determining whether the test agent modulates the biological activity. (I) is useful as molecular markers, as drug targets, and for detecting, diagnosing, staging, grading, assessing, monitoring, prognosticating, preventing or treating, determining predisposition to diseases and conditions especially relating to prostate cancer. (I) and its expression products are used in the diagnostic test to assay for presence of cancer. (I) is useful for assessing cancer e.g., to determine the type of cancer, its stage of development, the nature of genetic defect, etc. The polypeptide encoded by (I) can be used as target for therapy or drug discovery. (I) can also be used for expressing the polypeptide and thus cor specific genes, and groups of genes, expressed in pathways as specific genes, and groups of genes, expressed in pathways of functional and disease pathways and the delineation of targets in these pathways which are useful in diagnostic, therapeutic, and clinical applications. This is the amino acid sequence of a protein differentially
 New polynucleotide and polypeptide useful for diagnosing and/or treating cancer, particularly ovarian cancer, and as a vaccine.
 Human stratum corneum chymotryptic enzyme - ovarian cancer clone 01676P.
 Gaps
 Human; cytostatic; gene therapy; vaccine; cancer; ovarian cancer
 ;
0
 100.0%; Score 41; DB 6; Length 253; 100.0%; Pred. No. 3.8;
 0; Indels
 Mismatches
 ABR58471 standard; protein; 253 AA.
 ;
0
 02-OCT-2002; 2002WO-US031467.
 02-OCT-2001; 2001US-0327135P.
30-MAY-2002; 2002US-0384531P.
 regulated in prostate cancer
 07-JUL-2003 (first entry)
 9; Conservative
 Mannion J;
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 (CORI-) CORIXA CORP
 WPI; 2003-372001/35
 |||||||||
1 MARSLLLPL
 1 MARSLLLPL
 Local Similarity
 Sequence 253 AA;
 WO2003029468-A1.
 Homo sapiens.
 10-APR-2003
 Algate PA,
 ABR58471;
 Query Match
 Matches
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 The invention relates to a method of detecting an ovarian cancerassociated transcript in a cell from a patient, by contacting a biological sample from the patient with a polymucleotide that selectively hybridizes to a sequence at least 80% identical to any of one of 80 mucleic acid sequences given in the specification. The method is useful in diagnosing ovarian cancer and in identifying and using agents and/or targets that inhibit ovarian cancer. The nucleic acid melecule, polypoptide and the antibody may also be used in detecting ovarian cancers, monitoring and early detection of relapse following treatment, monitoring response to therapy, selecting patients for post-operative chemotherapy or radiation therapy, in selecting mode of therapy, determining tumour prognosis, early detection of pre-cancerous lesions, and as vaccines. This sequence corresponds to one of the proteins used
 Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
 Gaps
 cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis; post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection.
 ..
0
 100.0%; Score 41; DB 7; Length 253; llarity 100.0%; Pred. No. 3.8; Conservative 0; Mismatches 0; Indels
 detection method of the invention.
 Ovarian cancer-associated protein #24
 Claim 13; Page 291; 332pp; English.
 ADB80484 standard; protein; 253 AA
 (EOSB-) EOS BIOTECHNOLOGY INC
 18-JUN-2001; 2001US-0299234P.
27-AUG-2001; 2001US-0315287P.
05-SEP-2001; 2001US-0310544P.
13-NOV-2001; 2001US-0350666P.
 18-JUN-2002; 2002WO-US019297.
 12-APR-2002; 2002US-0372246P.
 WPI; 2003-167431/16.
 Best Local Similarity
Matches 9; Conserv
 Mack DH, Gish KC;
 N-PSDB; ADB80483
 Sequence 253 AA;
 WO2002102235-A2
 Homo sapiens.
 04-DEC-2003
 27-DEC-2002.
 ADB80484;
 Query Match
ADB80484
```

polynucleotides of the invention have cytostatic activity, and may have a use in gene therapy, and in a vaccine. The composition and methods are useful in diagnosing and/or treating cancer, particularly ovarian cancer. The composition may also be as a vaccine to prevent cancer. The present sequence is used in the exemplification of the invention

The invention relates to a novel isolated polynucleotide. The

Claim 2; Page 157-158; 169pp; English.

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This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRP) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic.
 Leber's hereditary optic neuropathy; LHON; mitochondrial encephalopathy lactic acidosis and stroke; MELAS; myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer; neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic; osteopathic; ophthalmological; cytostatic.
 Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating with the disease.
 Human heat mitochondrial protein as a therapeutic target SeqID639.
 anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart
 Glenn GM;
 mitochondrial; human; screening assay; diabetes mellitus;
 Gibson BW, Taylor SW,
 Claim 1; SEQ ID NO 639; 180pp; English.
 mitochondrial protein of the invention
 osteoarthritis;
 ADJ68833 standard; protein; 253 AA.
 Fahy ED, Zhang B,
 12-APR-2002; 2002US-0372843P.
17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
 04-APR-2003; 2003WO-US010870.
 06-MAY-2004 (first entry)
 (MITO-) MITOKOR.
(BUCK-) BUCK INST AGE RES.
 Huntington's disease;
 σ
 WPI; 2003-845369/78.
 |||||||||
1 MARSLLLPL
MARSLLLPL
 Sequence 253 AA;
 WO2003087768-A2.
 Homo sapiens.
 Ghosh SS, F
Warnock DE;
 23-OCT-2003
 ADJ68833;
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Search completed: July 13, 2005, 17:19:56 Job time : 77.6667 secs
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Gaps

; 0

100.0%; Score 41; DB 7; Length 253; 100.0%; Pred. No. 3.8; tive 0; Mismatches 0; Indels

Query Match
Best Local Similarity 100.
Matches 9; Conservative

1 MARSLLLPL

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

OM protein - protein search, using sw model

July 13, 2005, 16:54:03 ; Search time 13.5556 Seconds Run on:

(without alignments) 63.882 Million cell updates/sec

US-09-905-083A-86

1 MARSLLLPL 9

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query March Length DB Result

| Description  | serine proteinase | suppressor protein | conserved hypothet | hypothetical prote | matrix metalloprot | matrix metalloprot | hypothetical prote |        | hypothetical prote | conserved membrane | ionotropic glutama | probable ligand-ga | hypothetical prote | sodium channel alp | -      | ۳.     | cell division inhi | hypothetical prote | NADH2 dehydrogenas | probable transamin | probable transamin | PTS system, n-acet | m      | inulinase (EC 3.2. | cytolysin B transp | Ħ      | polyk  | corazonin precurso | hypothetical prote |
|--------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------|--------|--------------------|--------------------|
| ID           | A53968            | A46394             | B87343             | E96550             | 148673             | 184471             | B97856             | C82169 | A83060             | B87102             | T51136             | F84732             | T38055             | 148107 .           | S28698 | AB0627 | B29016             | B86450             | T11364             | C71917             | H64597             | A83734             | JC6197 | S31330             | T43109             | B25019 | T17464 | JC2384             | T17834             |
| E C          | ~                 | ~                  | ~                  | ~                  | 7                  | ~                  | ~                  | ~      | 7                  | 7                  | ~                  | ~                  | 7                  | 0                  | 7      | 7      | 7                  | ~                  | ~                  | ~                  | ~                  | ~                  | 7      | ٦                  | N                  | ~      | 7      | ~                  | 7                  |
| Match Length | 253               | 461                | 397                | 571                | 582                | 582                | 81                 | 126    | 432                | 909                | 921                | 923                | 1628               | 138                | 147    | 169    | 169                | 294                | 346                | 375                | 375                | 452                | 491    | 556                | 708                | 2005   | 5069   | 72                 | 74                 |
| Match        | 100.0             | 82.9               |                    | 80.5               | 80.5               | 80.5               | 78.0               | 78.0   | 78.0               | 78.0               | 78.0               | 78.0               | 78.0               | 75.6               | 75.6   | 75.6   | 75.6               |                    |                    |                    |                    |                    |        |                    |                    | 75.6   |        | 73.2               |                    |
| Score        | 41                | 34                 | 33                 | 33                 | 33                 | 33                 | 32                 | 32     | 32                 | 32                 | 32                 | 32                 | 32                 | 31                 | 31     | 31     | 31                 | 31                 | 31                 | 31                 | 31                 | 31                 | 31     | 31                 | 31                 | 31     | 31     | 30                 | 30                 |
| So           | -                 | ~                  | ო                  | 4                  | S                  | 9                  | 7                  | ۵      | σ                  | 10                 | 11                 | 12                 |                    | 14                 | 15     | 16     | 17                 | 18                 | 19                 | 20                 | 21                 | 22                 | 23     | 24                 | 52                 | 56     | 27     | 28                 | 29                 |

| histone-like DNA-b | DRE/CRT-binding pr | transcription fact | hypothetical prote | hypothetical prote | transcription acti | transcription acti | probable transcrip | probable transcrip | probable transcrip | protein ZC155.4 (i | hypothetical prote | hypothetical prote | conserved hypothet | hypothetical prote | transmembrane glyc |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| S43476             | JE0297             | T51830             | D82132             | T17832             | D85294             | T05799             | S47741             | B86025             | A91179             | A88452             | T25122             | A97482             | AI2699             | G87494             | A48931             |
| 7                  | ~                  | ~                  | 7                  | ~                  | ~                  | 7                  | 7                  | ~                  | ~                  | 7                  | ~                  | ~                  | 7                  | 7                  | ~                  |
| 170                | 216                | 216                | 222                | 299                | 314                | 314                | 323                | 323                | 323                | 325                | 325                | 325                | 325                | 331                | 354                |
| 73.2               | 73.2               | 73.2               | 73.2               | 73.2               | 73.2               | 73.2               | 73.2               | 73.2               | 73.2               | 73.2               | 73.2               | 73.2               | 73.2               | 73.2               | 73.2               |
| 30                 | 30                 | 30                 | 30                 | 30                 | 30                 | 30                 | 30                 | 30                 | 30                 | 30                 | 30                 | 30                 | 30                 | 30                 | 30                 |
| 30                 | 31                 | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

Serine proteinase SCCE precursor - human
N;Alternate names: stratum corneum chymotryptic enzyme
C;Species: Homo sapiens (man)
C;Accesion: A53968
R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T.
J. Biol. (Chem. 269, 19420-19426, 1994
A;Title: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme
A;Reference number: A53968, MuID:94308225; PMID:8034709
A;Accession: A5396
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-253 <HAN>
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A;Residues: 1-253 <HAN>
A;Cross-references: UNIPROT:P49862; GB:L33404; NID:9521214; PIDN:AAC37551.1; PID:9532504
A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A

A;Map position: 7q35-7q35 C;Superfamily: trypsin; trypsin homology F;30-245/Domain: trypsin homology <TRY>

Gaps ö 100.0%; Score 41; DB 2; Length 253; 100.0%; Pred. No. 0.34; tive 0; Mismatches 0; Indels Best Local Similarity 100. Matches 9; Conservative Query Match

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mutation, is essential for transla

Anglessor protein SSL1 - yeast (Saccharomyces cerevisiae)
NyAlternate names: protein L1531; protein YLR005w
C,Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 18-May-1994 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004
C;Accession: A46394; S64827
R;Yoon, H.; Miller, S.F.; Pabich, E.K.; Donahue, T.F.
Genes Dev. 6, 2463-2477, 1992
A;Title: SSL1, a suppressor of a HIS4 5'-UTR stem-loop mutation, is essential for A;Reference number: A46394; MUID:94040711; PMID:1340463
A;Reference number: A46394
A;References: UNIPROT:Q04673; GB:Z17385; NID:g2695; PID:g2696
B;Vandenbol, M.; Portetelle, D.; Hilger, F.
Submitted to the Protein Sequence Database, May 1996
A;Reference number: S64742
A;Accession: S64827

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Gaps

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C;Accession: I48673
R;Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, P. Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
A;Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cel A;Reference number: I38046; MUID:95224014; PMID:7708715
 A,Cross-references: EMBL:X83536; NID:g804999; PIDN:CAA58520.1; PID:g805000
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F;24-97/Domain: activation peptide #status predicted <PRO>F;24-97/Domain: matrix metalloproteinase homology <MMP>
 F.313-508/Domain: hemopexin repeat homology <PXNS'
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F.339,243,249/Binding site: zinc, catalytic (His) (active) #status predicted
F;240/Active site: Glu #status predicted
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 C;Species: Rattus norvegicus (Norway rat)
C;Abate: 0.2-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 184471; 161946
R;Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset, P. Proc. Natl. Acad. SGi. U.S.A. 92, 2730-2734, 1995
A;Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cel A;Reference number: 138046; MUID:95224014; PMID:7708715
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 C,Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Jun-1999
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 matrix metalloproteinase (EC 3.4.24.-) membrane type precursor - rat
N;Alternate names: membrane-type metalloproteinase
 Length 582;
 1; Indels
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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87.5%; Pred. No. 43;
iive 1; Mismatches
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Pred. No.
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77.0
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 332 MLRSLLVPL 340
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8 SRSLLLPL 15
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A; Gene: F11M15.13
 A; Map position: 1
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 C, Genetics:
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Matches
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 RESULT 6
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 Conserved hypothetical protein CC0757 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: B87343
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Haidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
J, J; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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S.Superfamily: NMA polymerase II transcription initiation/nucleotide excision repair fac
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.; Li, J., Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
 A;Cross-references: UNIPROT:Q9SYC9; GB:AE005173; NID:g4836937; PIDN:AAD30639.1; GSPDB:GN
C;Genetics:
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 Length 397
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Pred. No. 29;
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77.8%;
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 Conservative
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 216 MARGLLLPV 224
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Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-571 <STO>
 A; Residues: 1-461 <VAN>
 A; Accession: E96550
 C; Genetics:
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Cispecies: Mycobacterium leprae Cispecies: Mycobacterium reprae Cispecies: Mycobacterium leprae Cispecies: Mycobacterium leprae Cispecies: Mycobacterium leprae Cispecies: Mycobacterium leprae Cispecies: No. 20-Apr-2001 #sequence_revision 20-Apr-2001 #sequence_revision 20-Apr-2001 #sequence_revision 20-Apr-2001 #sequence_revision No.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, ean, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq. A;Reference number: A66909; MulD:21128732; PMID:11234002
A;Reference number: A66909; MulD:21128732; PMID:11234002
 A;Cross-references: UNIPROT:09HVB1; GB:AE004882; GB:AE004091; NID:g9950939; PIDN:AAG08071
A;Experimental source: strain PAO1
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoç
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83060
 A,Cross-references: UNIPROT:Q9Z513; GB:AL450380; NID:g13093364; PIDN:CAC30495.1; GSPDB:GR
 Cispecies: Pseudomonas aeruginosa
Cibate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
CiAccession: A83060
Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, i. Lory, S.; Olson, M.V.
 ionotropic glutamate receptor glr5 [imported] - Arabidopsis thaliana ("Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 09-Jul-2004
C; Accession: T51136
R; Davenport, R.J.; Kiegle, E.A.; Tester, M.
Bubmitted to the EMBL Data Library, December 1999
A; Description: GLR5, an ionotropic glutamate receptor ortholog from Arabidopsis.
 hypothetical protein PA4684 [imported] - Pseudomonas aeruginosa (strain PAO1)
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 A;Gene: ML1544
C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1782
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 conserved membrane protein ML1544 [imported] - Mycobacterium leprae
 Score 32; DB 2; Length 506;
Pred. No. 62;
1; Mismatches 1; Indels
 Length 432
 Indels
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 DB 2;
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 0; Mismatches
 78.0%;
77.8%;
 Query Match
Best Local Similarity 87.5
 Query Match
Best Local Similarity 77.8
Lagrand 7, Conservative
 223 MNRSVLLPL 231
 245 ARBLLLPL 252
 σ
 2 ARSLLLPL 9
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 A;Status: preliminary
A;Molecule type: DNA
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 A;Status: preliminary A;Molecule type: DNA
 A;Gene: PA4684
 C, Genetics
 C, Genetics
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 C;Accession: B97856
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rc Science 29; 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
 C;Accession: C82169
K;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. J. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
 A;Cross-references: UNIPROT:Q92G73; GB:AE006914; PIDN:AAL03788.1; PID:g15620385; GSPDB:C
C;Genetics:
 A;Cross-references: UNIPROT:Q9KRE6; GB:AE004247; GB:AE003852; NID:g9656204; PIDN:AAF9484
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
 F;313-508/Domain: hemopexin repeat homology <PXN>
F;93,239,243,249/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F;239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted
F;240/Active site: Glu #status predicted
 DNA-binding protein inhibitor Id-2-related protein VC1696 [imported] - Vibrio cholerae C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #text_change 09-Jul-2004
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 hypothetical protein RC1250 [imported] - Rickettsia conorii (strain Malish 7)
 C.Species: Rickettsia conorii
C.Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
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 Length 126;
 Length 582;
 Score 32; DB 2; Length 81;
Pred. No. 9.4;
2; Mismatches 0; Indels
 1; Indels
 0; Indels
;61-284/Domain: matrix metalloproteinase homology <MMP>
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Conservative 2
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43 ARSLLIPI 50
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 A; Status: preliminary A; Molecule type: DNA
 A; Map position: 1
 A; Gene: RC1250
 A; Gene: VC1696
 Query Match
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Cispecies: Agrobacterium tumefaciens plasmid pTil5955
Cispecies: Agrobacterium tumefaciens
Cispecies: Safe98
Ribarker, R.F.; Idler, K.B.; Thompson, D.V.; Kemp, J.D.
Plann Mol. Biol. 2, 335-350, 1983
A;Title: Nucleotide sequence of the T-DNA region from the Agrobacterium tumefaciens octor
 A;Status: translation not shown
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-147 <BAR>
A;Cross-references: UNIPROT:Q44395; EMBL:X00493; NID:g39062; PIDN:CAA25178.1; PID:g39078
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 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-138 cRES>
A;Cross-references: UNIPROT:Q60463; GB:M87540; NJD:g191067; PIDN:AAA36978.1; PID:g191068
C;Genetics:
 C;Accession: 148107

R;Lalik, P.H; Krafte, D.S.; Ciccarelli, R.B.

R;Lalik, P.H; Krafte, D.S.; Ciccarelli, R.B.

R;Lalik, P.H; Krafte, D.S.; Ciccarelli, R.B.

R;Lelis, C, Boysiol. 264, 803-809, 1993

A;Title: Characterization of endogenous Sodium channel gene expressed in chinese hamster A;Reference number: 148107

A;Reference number: 148107
 sodium channel alpha subunit - long-tailed hamster (fragment)
C,Species: Cricetulus longicaudatus (long-tailed hamster)
C,Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 75.6%; Score 31; DB 2; Length 138; 75.0%; Pred. No. 27;
Pred. No. 2e+02;
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3
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 2; Mismatches
 Search completed: July 13, 2005, 17:31:32
Job time : 14.5556 secs
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C;Keywords: duplication
 75.6%;
87.5%;
 Best Local Similarity 100.
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Best Local Similarity 87.5
Matches 7; Conservative
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583 RSLLLPL 589
 1 MARSLLLP 8
 3 RSLLLPL 9
 1 MARSVLVP
 1 MARYLLLP
 1 MARSLLLP
 A;Genome: plasmid
 Query Match
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 A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q09779; EMBL:Z69239; PIDN:CAA93223.1; GSPDB:GN00066; SPDB:SE
R;Lye, G.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
A;Lye, G.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
A;Molecule to the EMBL Data Library, October 1995
A;Accession: T38177
 A;Status: preliminary
A;Molecule type: DNA
A;Resdues: 1-923 <STO>
A;Cross-references: UNIPROT:Q9SDQ4; GB:AE002093; NID:g3831456; PIDN:AAC69938.1; GSPDB:GN
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A;Cross-references: EMBL:Z54285; NID:g1008429; PIDN:CAA91079.2; GSPDB:GN00066; SPDB:SPAC
C;Genetics:
 probable ligand-gated ion channel subunit [imported] - Arabidopsis thaliana (Gispecies: Arabidopsis thaliana (mouse-ear cress) (Cispecies: Arabidopsis thaliana (mouse-ear cress) (Cispecies: 02-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 09-Jul-2004 (Ciscossion: F84732 (Ciscossion: Fa4732 (Ciscossion: Fa4732 (Ciscossion: Fa4732 (Ciscossion: Fa4732 (Ciscossion: Fa4732 (Ciscossion: Ciscossion: A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
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 hypochetical protein SPAC22F3.14c - fission yeast (Schizosaccharomyces pombe) C; Species: Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe C; Date: 20-Apr-2000 #sequence revision 20-Apr-2000 #text_change 09-Jul-2004 C; Accession: 718055; T38177; $52429 R; Lyo, G.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, February 1995
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 A;Residues: 1-921 <DAV>
A;Cross-references: UNIPROT:Q9SDQ4; EMBL:AF210701; PIDN:AAF21042.1
A;Experimental source: cultivar Columbis
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 Length 921;
 Length 923;
 1; Indels
 Score 32; DB 2; L
Pred. No. 1.1e+02;
1; Mismatches 1;
 Score 32; DB 2; I
Pred. No. 1.1e+02;
1; Mismatches 1;
 78.0%; Score 32;
 78.0%;
77.8%;
 78.0%;
77.8%;
 Query Match
Best Local Similarity 77.0
77. Conservative
 Query Match 78.0
Best Local Similarity 77.8
Matches 7; Conservative
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707 MARSRLVPL 715
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705 MARSRLVPL 713
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 1 MARSLLLPL 9
 1 MARSLLLPL 9
 A; Molecule type: mRNA
 A; Accession: T38055
 A;Gene: SPAC1D4.14
A;Map position: 1L
 C,Genetics:
A,Gene: glr5
A,Map position: 2
 A,Gene: At2g32400
A,Map position: 2
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 homo sapien
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 vibrio chol
 oryza sativ
 gallus gall
 chlorobium
 rickettsia
 TISSUE=Skin;
MEDLINE=94308225; PubMed=8034709;
Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A.,
Egelrud T.;
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 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 45, Last annotation update)
Kallikrain 7 precursor (EC 3.4.21.-) (Stratum corneum chymotryptic enzyme) (hSCCE).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1011_TaxID=9606;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 "Čloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase.";
J. Biol. Chem. 269:19420-19426(1994).
 092973 1098re6 v 098re6 v 0658a9 c 069yf9 b 088ak3 c 06ahd8 l 072az4 c 08nhill b 09ukj0 b 1
 Ogder4
O6zjf7
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Q8mxk6
 0; Indels
 Kishi T., Michael I.P., Diamandis B.P.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY646152; AAT66047.1; -.
SEQUENCE 66 AA; 7171 MW; 82E1C392BC822FDB CRC64;
 Length
 Last sequence update)
Last annotation update)
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 66 AA
 253 AA
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088SS33
069DER4
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062BIF
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065BA9
069YF9
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06AHD8
06AHD8
06AHD8
 PRT;
 enzyme) (hSCCE).
Name=KLK7; Synonyms=PRSS6, SCCE;
Homo sapiens (Human).
 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, Kallikrein 7 splice variant Homo sapiens (Human).
 (TrEMBLrel. 28,
 STANDARD;
 PRELIMINARY;
 809
11048
11048
11048
1126
1139
1149
1149
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 σ
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Matches 9; Conserv
 1 MARSLLLPL
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 NCBI_TaxID=9606;
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 25-OCT-2004
 HUMAN
 P49862
 Q6DTY1
 RESULT 2
KLK7_HUMAN
ID_KLK7 H
 RESULT 1
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 streptomyce
rhizobium s
oryza sativ
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 homo sapien
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arabidopsis
 synechococc
candida gla
saccharomyc
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arabidopsis
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mus musculu
 arabidopsis
 arabidopsis
 oryza sativ
 homo sapien
 oryza sativ
 symbiobacte
 saccharomyc
 chromobacte
 oryza sativ
 caulobacter
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 mus musculu
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 (without alignments)
74.069 Million cell updates/sec
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P49862 h
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Q9nzll h
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0945z0
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095z0
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001x37
001
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Q6zk46
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P53690
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Oebtx2
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 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
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 SUMMARIES
 Q6DTY1
KLK7 HUMAN
Q8NSN9
Q9NZL1
Q9NZL2
BAE2 HUMAN
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 SSL1 YEAST
Q6B237
 Q827F2
OTSA RHISN
Q9ZRH9
 MM14_RAT
Q6DFU5
Q8BTX2
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - protein search, using sw model
 QBLC74
Q9FNC4
Q8W2V5
Q7P016
Q8SAT6
 Q6ZK46
Q9SYC9
 Q9S7T0
Q7RZ54
 Q8H584
Q67P07
 Q7U4K2
Q6FTA5
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 26SSD7
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Query
Match Length DB
 1 MARSLLLPL 9
 BLOSUM62
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 Scoring table:
 Perfect score:
 Score
 Minimum DB
Maximum DB
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 Sequence:
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Result Š. 

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DISULFID
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 688889
 08N5N9
 Matches
 RESULT 3
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 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 chymotryptic enzyme.";
Biochem. Biophys. Res. Commun. 211:586-589(1995).

-!- FUNCTION: May catalyze the degradation of intercellular cohesive structures in the cornified layer of the skin in the continuous shedding of cells from the skin surface. Specific for amino acid residues with aromatic side chains in the PI position. SCCE cleaves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-Phe-|-Tyr-26, and 26-Tyr-|-Thr-27. Could play a role in the activation of precursors to inflammatory cytokines.

-!- TISSUE SPECIFICITY: Abundantly expressed in the skin and is expressed by keratinocytes in the epidermis. Very low levels are also seen in the brain and kidney.
 MIM; 604438; -.
60; GO:0008326; F:serine-type peptidase activity; TAS.
60; GO:0008326; P:serine-type peptidase activity; TAS.
60; GO:0008344; P:epidermal differentiation; TAS.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001324; Peptidase_S1.
InterPro; IPR001325; CHYMOTRYPSIN.
SMART; SM0020; Trypsin, I.
PRINTS; PS00125; TRYPSIN_DOM; I.
PROSITE; PS00134; TRYPSIN_DSF; I.
PROSITE; PS00135; TRYPSIN_SER; I.
Direct protein sequencing; Glycoprotein; Hydrolase; Serine protease;
 SEQUENCE FROM N.A.

Hansson L., Backman A., Ny A., Edlund M., Edholm E., Tornell J.,
Wallbrandt P., Egelrud T.;
"Epidermal overexpression of stratum corneum chymotryptic enzyme in
mice; a model for chronic ithchy dermatitis.";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
 MEDLINE=95314630; PubMed=7794273;
Skytt A., Stroemqvist M., Egelrud T.;
"Primary substrate specificity of recombinant human stratum corneum
 Yousef G.M., Scorilas A., Diamandis E.P.; involcoular characterization, mapping and tissue expression of the human stratum corneum chymotryptic enzyme gene."; submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
Moss P., Paeper B., Wang K.;
 Moss P., Paeper B., Wang K.; "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region."; Gene 257:119-130(2000).
 SIMILARITY: Belongs to the peptidase S1 family. Kallikrein
 Activation peptide
 EMBL; L33404; AAC37551.1; -.
EMBL; AF166330; AAD49718.1; -.
EMBL; AF243527; AAG33360.1; -.
EMBL; AF33583; AAK69624.1; -.
 Genew; HGNC:6368; KLK7.
 H-InvDB; HIX0015373; -. MIM; 604438; -.
 22
 PIR; A53968; A53968.
HSSP; P00760; 1EZX.
 MEROPS; S01.300; -
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 CHARACTERIZATION.
 Signal; Zymogen.
SIGNAL 1
PROPEP 23
 subfamily.
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A REDLINE=2218825; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Klausher R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B. Buetcow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B. Buetcow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B. Buetcow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B. Buetcow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeperg B. Buetcow K.H., Schaefer C.F., Bhat N.K., Antechnik D., Marusina K., Farmer A.A., Rubin G.M., Hong L., Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Anting M. McGan P.J., McKernan S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Halton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Shevinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E., Schmerch A., Sche
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 Gaps
 Charge relay system (By similarity).
Charge relay system (By similarity).
Charge relay system (By similarity).
By similarity.
A similarity.
 Bukaryota; Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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 100.0%; Score 41; DB 1; Length 253; 100.0%; Pred. No. 2.7;
 0; Indels
 2D68B6B15A76A668 CRC64;
 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 Stratum corneum chymotryptic enzyme, preproprotein
 0; Mismatches
 27525 MW;
 Similarity 100.
9, Conservative
 and mouse cDNA sequences.
 PRELIMINARY;
253
70
1112
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137
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71
71
239
211
190
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176
201
246
253 AA;
 1 MARSLLLPL
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 Name=KLK7;
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ACT_SITE
ACT_SITE
DISULFID
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MEDLINE-20422477; PubMed=10965118;

A med sapartyl protease on 21q22.3; BACE2, is highly similar to 21q22477; PubMed=10965118;

Solans A., Estivill X., de La Luna S.;

A new aspartyl protease on 21q22.3; BACE2, is highly similar to 21d2einer's amyloid precursor protein beta-secretase.";

Cytogenet. Cell Genet. 89:177-184 (2000).

LEMBL; AF188276; AAF35835.1; -...

REMBL; AF188276; AAF35835.1; -...

REMBL; AF188276; AAF35835.1; -...

RO; GO:0016021; C:integral to membrane; ISS.

GO; GO:0042985; P:negative regulation of amyloid precursor pr. .; ISS.

GO; GO:001486; P:peptide hormone processing; ISS.

RITERPRO; IPR00141; Peptidase Al.

RITERPRO; IPR00121; Peptidase Al.

RITERPRO; IPR00131; Peptidase Al.

RITERPRO; IPR001301; Peptidase Al.

RITERPRO; IPR00131; Peptidase Al.
 SECUENCE FROM N.A.
MEDLINE=20057170; PubMed=10591213; DOI=10.1038/990107;
Yan R., Bienkowski M.J., Shuck M.E., Miao H., Tory M.C., Pauley A.M.,
Brashier J.R., Stratman N.C., Mathews W.R., Buhl A.E., Carter D.B.,
Tomasselli A.G., Parodi L.A., Heinrikson R.L., Gurney M.E.;
"Membrane-anchored aspartyl protease with Alzheimer's disease beta-
 09Y5Z0; Q9UJT6;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Beta secretase 2 precursor (BC 3.4.23.45) (Beta-site APP-cleaving
enzyme 2) (Aspartyl protease 1) (Asp 1) (Asp1) (Membrane-associated
aspartic protease 1) (Memapsin-1) (Down region aspartic protease)
 Xin H., Stephans J.C., Duan X., Harrowe G., Kim E., Grieshammer U., Giese K.;
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Identification of a novel aspartic-like protease differentially
 85.4%; Score 35; DB 2; Length 468; 77.8%; Pred. No. 92; ive 2; Mismatches 0; Indels
 Aspartyl protease; Hydrolase; Protease.
SEQUENCE 468 AA; 50324 MW; 717E0920126A0142 CRC64;
 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 518 AA
 PRT;
 PROSITE; PS00141; ASP_PROTEASE; 2.
 PRINTS; PR01817; BACE2.
PRINTS; PR01815; BACEFAMILY.
PRINTS; PR00792; PEPSIN.
 Name=BACE2; Synonyms=ASP21;
 secretase activity.";
Nature 402:533-537(1999).
 Conservative
 STANDARD;
 :||:|||||
LARALLLPL 12
 1 MARSLLLPL 9
 Homo sapiens (Human)
 SEQUENCE FROM N.A.
 Local Similarity
les 7; Conserv
 TISSUE=Bone marrow
 Aspartyl protease
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 BAE2 HUMAN
 Query Match
 BAE2 HUMAN
 RESULT 6
 ö
 precursor pr. . .; ISS.
 Gaps
 A Schoule From M.N.

MEDLINE-20422477; PubMed=10965118;

A clama A., Estivill X., de La Luna S.;

Solans A., Estivill X., de La Luna S.;

A law aspartyl protease on 21q22.3; BACE2, is highly similar to a lazheimer's amyloid precursor protein beta-secretase.";

Cytogenet. Cell Genet. 89:177-184 (2000).

- I-SIMILARITY: Belongs to peptidase family Al.

REMBL; API88277; AAR35836.1; -.

REMBL; API88277; ARA35836.1; -.

RESP; P56817; 1FRN.

GO; GO:0006205; Finedariar to membrane; ISS.

GO; GO:0006205; P:negative requiation of amyloid precursor pr. .;

RO; GO:0016486; P:peptide hormone processing; ISS.

RO; GO:0016486; P:peptide hormone processing; ISS.

RICEPTO; IPR009109; Pept_Al_BACE.

InterPro; IPR009101; Pept_Al_BACE.

InterPro; IPR009101; Pept_Al_BACE.

InterPro; IPR009109; Pept_Al_BACE.

InterPro; IPR009109; Pept_Al_BACE.

InterPro; IPR001969; Pept_Aspartic.

PROMINGS PROMINGS PROMINGS PEPT_AL_BACE.

INTERPROSITE PROMINGS PEPT_AL_BACE.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ;
 ö
 100.0%; Score 41; DB 2; Length 253; 100.0%; Pred. No. 2.7; ive 0; Mismatches 0; Indels
 85.4%; Score 35; DB 2; Length 396; 77.8%; Pred. No. 78; ive 2; Mismatches 0; Indels
 Pfam; PF00089; Trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp_SPC; 1.

PROSITE; PS00134; TrypSIN HIS; UNKNOWN 1.

PROSITE; PS00135; TRYPSIN HIS; UNKNOWN 1.

Hydrolase; Pscrease; Serine protesse.

SEQUENCE 253 AA; 27608 MW; 2D68B6A41B22A668 CRC64;
 PROSITE; PS00141; ASP PROTEASE; 2.
Aspartyl protease; Hydrolase; Protease.
SEQUENCE 396 AA; 43013 MW; 5023A7AR391CEAC9 CRC64;
 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 Created)
Last sequence update)
 396 AA
 468 AA
InterPro; IPR009003; Pept_Ser_Cys
 PRINTS; PRO1817; BACE2. - PRINTS; PRO1815; BACEFAMILY. PRINTS; PRO0792; PEPSIN.
 (TrEMBLrel. 15, (TrEMBLrel. 15,
 9; Conservative
 7; Conservative
 PRELIMINARY;
 PRELIMINARY;
 1 MARSLLLPL 9
 1 MARSLLLPL 9
 Homo sapiens (Human)
 Best Local Similarity
Matches 7: Conser
 Local Similarity
 Aspartyl protease.
Name=BACE2;
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 09NZL2;
01-OCT-2000
01-OCT-2000
 Query Match
 Query Match
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**Q9NZL2** 

RESULT 5 Q9NZL2

O9NZL1

Best Loc Matches

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Gaps

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MEDLINE=20289799; PubMed=10830953; DOI=10.1038/35012518;
A Hattori M. Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
Park H.-S., Toyoda A., Iahli K., Totoki Y., Choi D.-K., Soeda E.,
A Ohki M., Takagi T., Sakaki Y., Taudien S., Blechechmidt K., Polley A.,
A Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
A Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
A Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
Minnoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
A Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Blocker H.,
A Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
Lehrach H., Reinhardt R., Yaspo M.-L.;
"The DNA sequence of human chromosome 21.";
 SEQUENCE FROM N.A.
MEDILINE-20144066; PubMed=10677483; DOI=10.1073/pnas.97.4.1456;
Lin X., Koelsch G., Wu S., Downs D., Dashti A., Tang J.;
"Human aspartic protease memapsin 2 cleaves the beta-secretase site of "Human aspartic protease memapsin 2 cleaves the beta-secretase site of
 Accarino M.P., Fumagalli P., Ottolenghi S., Taramelli R.; Cloning of a gene from chromosome 21 Down region encoding a potential transmembrane aspartyl procease "; Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
 Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Girmaldi C., Gu Q., Hass P.E., Heldens S., Lewis L., Ialao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Colline F.S., Wagner L. Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Maruslina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 MEDLINE=20120043; PubMed=10656250; DOI=10.1006/mcne.1999.0811; Hussain I., Powell D.J., Howlett D.R., Tew D.G., Meek T.D., Chapman C., Gloger I.S., Murphy K.E., Southan C.D., Ryan D.M., Smith T.S., Simmons D.L., Walsh F.S., Dingwall C., Christie G.; "Identification of a novel aspartic proteinase (Asp 2) as beta-
 SEQUENCE FROM N.A.
MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 expressed in human breast cancer cell lines.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
 Solans A., Estivill X., de la Luna S.; "Cloning of a novel mammalian aspartyl protease."; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
 beta-amyloid precursor protein.";
Proc. Natl. Acad. Sci. U.S.A. 97:1456-1460(2000).
 secretase.";
Mol. Cell. Neurosci. 14:419-427(1999).
 bioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
 Nature 405:311-319(2000)
 [5]
SEQUENCE FROM N.A.
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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEvan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhitim M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G., Blakeeley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
 "Specificity of memapsin 1 and its implications on the design of memapsin 2 (beta-secretase) inhibitor selectivity.";
Biochemistry 41:8742-8746(2002)
-1- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-1- CATALYTIC ACTIVITY: Broad endopeptidase specificity. Cleaves Glu-1- Ann-Leu-|-Asp.Ala-Glu-Phe in the Swedish variant of Alzheimer's amyloid precursor protein.
-1- SUBCELLUIAR LOCATION: Type I membrane protein.
-1- SIMILARITY: Belongs to the peptidase Al family.
 Pfam; PF00026; Asp; 1.
PRINTS; PR01817; BACE2.
PRINTS; PR01915; BACEFAMILY.
PRINTS; PR00792; PEPSIN.
PROSITE; PS00141; ASP PROTEASE; 2.
Aspartyl protease; Glycoprotein; Hydrolase; Signal; Transmembrane;
 CHARACTERIZATION.
MEDDLINE-22088158; PubMed=12093293; DOI=10.1021/bi025926t;
Turner R.T. III., Loy J.A., Nguyen C., Devasamudram T., Ghosh A.K.,
Koelsch G., Tang J.;
 MIM; 605689; --
GO; GO:0005624; C:membrane fraction; TAS.
GO; GO:0005644; C:membrane fraction; TAS.
GO; GO:0006449; F:aspartic-type endopeptidase activity; TAS.
GO; GO:0005644; P:protein modification; TAS.
GO; GO:000306; P:protein secretion; TAS.
InterPro; IPR009119; Pept A1 BACE.
InterPro; IPR009121; Pept A1 BACE.
InterPro; IPR00965; Pept A5P AS.
InterPro; IPR009007; Pept A5P AS.
InterPro; IPR009007; Pept A5P AS.
InterPro; IPR009007; Pept A5P AS.
 Extracellular (Potential)
 Cytoplasmic (Potential).
By similarity.
By similarity.
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 Beta secretase 2.
 Potential.
Potential.
 Potential
 EMBL, AF200342; AAF17078.1; --
EMBL, AF117892; AAD45240.1; --
EMBL, AF178532; AAD45963.1; --
EMBL, AF204944; AAF26368.1; --
EMBL, AF201943; AAF20494.1; --
EMBL, AF201925; AAF20491.1; --
EMBL, AL65284; CAB90458.1; --
EMBL, AL165284; CAB90458.1; --
EMBL, AL165285; CAB90554.1; --
EMBL, AL165285; AAH14453.1; --
HSSP, P56817; 1M4H.
 and mouse cDNA sequences.";
 Genew; HGNC:934; BACE2.
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303
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474
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 CHAIN
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A Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Eltins T., Engels R., Wand D., Balance B., Butler J., Endrizzi M., Oui D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., A. Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D., Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., A. Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D., Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., A. DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Paulsen I., Sache M.S., Lander E.S., Nubbaum C., Birren B., The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
 Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R., Nyakatura G., Mewes H.W., Mannhaupt G.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
 Gaps
 Gaps
 18
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 Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
 German Neurospora genome project;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
 85.4%; Score 35; DB 2; Length 1192; 77.8%; Pred. No. 2.3e+02; ive 2; Mismatches 0; Indels
 82.9%; Score 34; DB 2; Length 118;
87.5%; Pred. No. 40;
ive 1; Mismatches 0; Indels
 InterPro; IPR008938; ARM.
InterPro; IPR002048; EF-hand.
PROSITE; PS00018; EF-HAND; UNCHOWN 1.
SEQUENCE 1192 AA; 132863 MW; 4F67B124CBAFF154 CRC64;
 Bowman C.L., White O., Nierman W.C., Fraser C.M.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ACOLO797; AAF03433.1; -.
EMBL; ACO09325; AAF01560.1; -.
 preliminary data.

EMBL, AABX01000720; EAA28261.1; -.

EMBL, BX908808; CAF06025.1; -.

Hypothetical protein.

SEQUENCE 118 AA; 12596 MW; DIF84E47108B2145 CRC64;
 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
25-CCT-2004 (TrEMBLrel. 28, Last annotation update)
Predicted protein (Hypothetical protein G21B4.400).
Name=NCU04420.1; Synonyms=G21B4.400;
 118 AA.
 (TrEMBLrel. 26, Created)
 PRT;
 Query Match
Best Local Similarity 77.0-
 PRELIMINARY;
 237 MARSLVLPV 245
 1 MARSLLLPL 9
 2 ARSLLLPL 9
 Nature 0:0-0(2003).
 Neurospora crassa.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=5141;
 STRAIN=OR74A;
 01-MAR-2004
 Q7RZ54
Q7RZ54;
 RESULT 9
 Q7R254
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 SEQUENCE FROM N.A.

Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
Southmick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
 Gaps
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TREMBLrel. 27, Last annotation update)
F2847.11 protein (F4F13.33)
Name=F2847.11; Synonyms=F4F13.33;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 Gaps
 Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplanteė; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 SEQUENCE FROM N.A.
Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
 N-linked (GlcNAc. . .) (Potential). N-linked (GlcNAc. . .) (Potential).
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 .;
0
 Score 35; DB 2; Length 1135;
Pred. No. 2.2e+02;
2; Mismatches 0; Indels
 85.4%; Score 35; DB 1; Length 518; 77.8%; Pred. No. 1e+02; tive 2; Mismatches 0; Indels
 Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BT004227; AAO42241; -...
Interpro; IPR002939; ARM. Interpro; IPR002048; EF-hand. PROSITE; PS00018; EF-HAND; UNKNOWN_1.
 1135 AA; 126119 MW; CSFDDC178D1E2D96 CRC64;
170 170 N-linked (GlcNAC. . .) (Pc
36 36 N-linked (GlcNAC. . .) (Pc
36 36 A -> T (in Ref. 6)
518 AA; 56180 MW; 2E903150823760D3 CRC64;
 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein At3901780 (Fragment).
 PRT; 1135 AA
 PRT; 1192 AA
 85.4%;
 PRELIMINARY;
 7; Conservative
 Best Local Similarity 77.8
Matches 7; Conservative
 PRELIMINARY;
 1135
 237 MARSLVLPV 245
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4 LARALLLPL 12
 1 MARSLLLPL 9
 1 MARSLLLPL 9
 Hypothetical protein
 Local Similarity
 NCBI_TaxID=3702;
 Name=At3g01780
 Theologis A.;
 NON TER
SEQUENCE
 CARBOHYD
CARBOHYD
CONFLICT
SEQUENCE
 Query Match
 Query Match
 Q84W49
 Q9S7T0
 Matches
 RESULT 8
095770
095770
AC 09577
DT 01-M
DT 01-M
DT 01-M
DT 05-M
DE F28J
GN NAME
CO BUKA
CO BUKA
CO SPERIO

 RESULT 7
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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Lafontaine I., de Montigny J., Marck C., Newveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykaaten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Bespons L., Fabre E., Fairhead C., Ferry Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozter-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 SEQUENCE FROM N.A.

MEDILINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;

MEDILINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;

A Palenik B., Barhamsha B., Larimer F.W., Land M.L., Hauser L.,

Chain P., Lamerdin J.E., Regala W., Allen E.E., McCarren J.,

Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;

The genome of a motile marine Synechococcus.";

Nature 424:1037-1042(2003):

R BMEL; BX565694; CAE06580.1; -.

R GO; GO:0005489; F:electron transporter activity; IEA.

R GO; GO:0005489; F:electron transport; IEA.

R GO; GO:000518; P:electron transport; IEA.

R GO; GO:000518; F:electron transport; IEA.

R Pfam; PF00037; Fer4; 1.
 Eukaryotā; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
 Complete proteome, Iron, Iron-sulfur, Metal-binding
E 348 AA; 37531 MW; IE1903E684081A95 CRC64;
 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
65-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Similar to sp[(04673 Saccharomyces cerevisiae YLR005w SSLI.
ORFNames=CAGL0G040599;
 Length 348;
 Synechococcus sp. (strain WH8102).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=84588;
 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 82.9%; Score 34; DB 2; I 77.8%; Pred. No. 1.1e+02; ive 1; Mismatches 1;
 439 AA.
 PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
 Created)
 05-JUL-2004 (TrEMBLrel. 27, Created)
 PRT;
 Putative ldpA protein.
OrderedLocusNames=SYNW2065;
 Local Similarity 77.8
nes 7; Conservative
 Candida glabrata CBS138.
 PRELIMINARY;
 PRELIMINARY;
 01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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298 MARRLLMPL 306
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 1 MARSLLLPL 9
 1 MARSLLLPL
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 SEQUENCE FROM N.A.
 STRAIN=CBS138;
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 SEQUENCE
 Query Match
 Q7U4K2;
 Q6FTA5
 Q7U4K2
 Matches
 RESULT 13
 Q6FTA5
 Q7U4K2
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 STRAIN=IAM14863;
Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
Morimura K., Ikeda H., Hattori M., Beppu T.;
"Complete genome sequence of an uncultured bacterium Symbiobacterium
thermophilum.";
 Gaps
 Gaps
 Oryza sativa (japonica cultivar-group).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoldeae, Oryzeae, Oryza.
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 BAC
 Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC
clone:P0496D04.";
 Score 34; DB 2; Length 322;
Pred. No. 1e+02;
1; Mismatches 1; Indels
 82.9%; Score 34; DB 2; Length 129;
87.5%; Pred. No. 44;
tive 1; Mismatches 0; Indels
 01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein OJ1656_E11.113 (Hypothetical protein
 SEQUENCE FROM N.A.
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7,
 Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP003843; BAC24850.1; -.
EMBL; AP004670; BAD30793.1; -.
 Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AP006840; BAD40586.1; -. InterPro; IRR006522; PecD.
Pfam; PF01032; PecCD; 1.
SEQUENCE 322 A4; 34949 MW; 80157DE1532812D9 CRC64;
 Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
 Hypothetical protein.
SEQUENCE 129 AA; 13891 MW; 6334E639E1A6DEAE CRC64;
 Last sequence update)
Last annotation update)
 Ferrichrome ABC transporter permease protein.
 322 AA.
 129 AA
 Name=OJ1656_E11.113; Synonyms=P0496D04.53;
 Symbiobacterium thermophilum.
Bacteria; Actinobacteria; Symbiobacterium.
NCBI_TaxID=2734;
 Created)
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 PRT;
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Matches 7; Conservative
 (TrEMBLrel. 28, (TrEMBLrel. 28, (TrEMBLrel. 28,
 7; Conservative
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 PRELIMINARY;
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40 LARSLLLP 47
ARSLLLPM 30
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 SEQUENCE FROM N.A.
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 ORFNames=STH1601;
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 25-OCT-2004
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25-OCT-2004
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 Q8H584
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 Q67P07
 RESULT 11
067P07
AC 067P0
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DT 25-OC
DF PERTI
GN ORFNA
OX NCBI
NRN SEQUE
RRC STRAI
RR MORIN
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RR MORIN
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Gaps

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Name=SSL1;
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MEDLINE=27313267; PubMed=9169871;

MEDLINE=97313267; PubMed=9169871;

MEDLINE=97313267; PubMed=9169871;

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MEDLINE=28 (Medle M.)

MEDLINE=38 (Medle M.)

Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Mincker P., Souciet J.L.;
"Genome evolution in yeasts.";
II "Genome evolution in yeasts.";
II Nature 430:35-44(2004).

IX EMBL; CR380953; CAG59466.1; -.
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GO; GO:0005634; C:nocleus; IEA.
ROG GO:0005639; Pregulation of transcription; IEA.
InterPro; IPR007198; Sall. like.
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RINTERPRO; IPR007055; VWP Ā..
REFPRO; IRR00635; VWP Ā..
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REFPRO; IRR00635; Sall; I.
REFPRO; IRR00635; VWP; Ā..
REFRAMS; TIGR0662; Sall; I.
REFRORIE: PS00028; ZINC FINGER C2H2 1; UNKNOWN I.
 SEQUENCE FROM N.A.
MEDLINE-94040711; PubMed=1340463;
Yoon H., Miller S.P., Pabich E.K., Donahue T.F.;
"SSIL, a suppressor of a HIS4 5'-UTR stem-loop mutation, is essential for translation initiation and affects UV resistance in yeast.";
 Gaps
 SEQUENCE OF 400-461 FROM N.A.
MEDLINE-94239498; PubMed-8183345; DOI=10.1038/369242a0;
Maeda T., Wurglar-Murphy S.M., Saito H.;
"A two-component system that regulates an osmosensing MAP kinase
cascade in yeast.";
 Suppressor of stem-loop protein 1.
Name=SSL1; OrderedLocusNames=Y1R005W;
Saccharomyces cerevisiae (Bakert's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotia; Saccharomycetes;
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 01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
 Genes Dev. 6:2463-2477(1992).
 7; Conservative
 STANDARD;
 Nature 387:87-90(1997).
 194 MARGLLLPV 202
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 SSL1 YEAST
Q04673;
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GN Saccha
OC BUKALY
OC BUK
 Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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 Marsischky G., Rolfs A., Richardson A., Kane M., Baqui M., Taycher E., Hu Y., Vannberg F., Weger J., Kramer J., Moreira D., Kelley F., Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A., Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
 Gaps
Nature 369:242-245(1994).
 Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
 LaBaer J.;
"Creation of the YPLEX clone resource: cloning of Saccharomyces cerevisiae ORF9 in the Gateway recombinational cloning system."; Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AX692893; AAT92912.1;
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 Length 461;
 1; Indels
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 activity; IEA.
 25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 resistance in yeast.
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: Contains 1 C2H2-type zinc finger.
 Pfam; PF04056; Sal1; 1.
Pfam; PF04056; zf-C2H2; 1.
SWART; SW00355; ZnF C2H2; 1.
TIGRFAMS; TIGR06022; Ssl1; 1.
PROSITE; PS00028; ZINC FINGER C2H2 1; 1.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; FALSE_NEG.
Metal-binding; Nuclear protein; Zinc-finger.
 82.9%; Score 34; DB 1; L
77.8%; Pred. No. 1.5e+02;
iive 1; Mismatches 1;
 SGD; S000003995; SSLI.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:00015676; F:nucleic acid binding; IEA.
GO; GO:0003700; F:transcription factor activ
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TRANSFAC; T02191; -.
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 216 MARGLLLPV 224
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DR GO; GO: 0006281; P:DNA repair; IEA.

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DR InterPro; IRR00139; Sall.

DR SWART; SM00327; VWA; 1.

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DR PROSITE; PS50234; VWFA; 1.

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TYPE: PRT
ORGANISM: Homo sapiens
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 US-09-502-600-86
 FEATURE:
 LENGTH:
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 Sequence 2, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 7716, App
Sequence 116, App
Sequence 116, App
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
 July 13, 2005, 16:58:04; Search time 19.4444 Seconds (without alignments) 34.552 Million cell updates/sec
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 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-243-86
US-08-257-146-2
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US-09-154-344-2
US-09-210-084-3
US-09-764-762-3
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US-09-99-723-2
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 -09-794-927A-2
 ·09-795-847B-2
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Maximum Match 100%
Listing first 45 summaries
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100.0
87.8
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 Title:
Perfect score:
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 Minimum DB
Maximum DB
 Searched:
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 Database
 Run on:
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8
 Result
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 1659, Ap
10, Appl
5, Appli
4, Appli
 355, App
33977, A
49194, A
8, Appli
 APPLICANT: O'BRIGH, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: Ovarian Cancer
FILE REFERENCE: D6223CIP-C
CURRENT FILLING DATE: 2000-22-11
CURRENT APPLICATION NUMBER: 09/039,211
PRIOR APPLICATION NUMBER: 09/039,211
PRIOR PILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 86
LENGTH: 9
 Appli
Appli
 Sequence 86, Application US/09918243

Sequence 86, Application US/09918243

Sequence 86, Application US/09918243

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

APPLICANT: Santin, Alessandro

TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

FILE REFERENCE: D6223CIP/C/D/1918, 243

CURRENT APPLICATION NUMBER: US/09/918, 243

CURRENT FILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

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US-09-149-476-355
US-09-270-767-33977
US-09-869-388-8
US-09-134-000C-3659
US-09-869-388-10
US-09-869-388-6
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US-09-869-388-7
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US-09-969-969-7
US-09-969-969-7
US-09-969-969-7
US-09-969-97-794A-177
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 Sequence 86, Application US/09502600A Patent No. 6294344
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Best Local Similarity
Local 9; Conserve
 ; LIBRARY: GenB:
; CLONE: 532504
US-08-824-874-3
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 STATE: CJ
COUNTRY:
 RESULT 5
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 Gaps
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 Sequence 2, Application US/08557146
| Patent No. 5834290
| GENERAL INFORMATION:
| APPLICANT: Eqelund, Torbjorn
| APPLICANT: Hansson, Lennart
| TITLE OF INVENTION:
| TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
| TITLE OF INVENTION: Income (SCCE)
| NUMBER OF SEQUENCES: 17
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: White & Case, Patent Department
| STREET: 1155 Avenue of the Americas
| CITY: New York
 Query Match 100.0%; Score 41; DB 2; Length 253; Best Local Similarity 100.0%; Pred. No. 0.45; Matches 9; Conservative 0; Mismatches 0; Indels
 STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2787.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTION DATA:

APPLICATION NUMBER: US/08/557,146

FILING DATE: 14-DEC-1995

CLASSIFICATION: 424-1995
 Query Match 100.0%; Score 41; DB 4; Length 9; Best Local Similarity 100.0%; Pred. No. 4.1e+05; Matches 9; Conservative 0; Mismatches 0; Indels
) NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 1-9 of the SCCE protein
US-09-918-243-86
 ATTORNEY AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
 Sequence 3, Application US/08824874
; Patent No. 596230;
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 5
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 1 MARSLLLPL 9
 TYPE: amino acid
TOPOLOGY: linear
 US-08-557-146-2
 LENGTH:
 US-08-824-874-3
FEATURE:
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Gaps
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SEQUENCE 2, Application US/09154344

FACTOR NO. 5981256

GENERAL INFORMATION:

APPLICANT: Egelrud, Torbjorn

APPLICANT: Hansson, Lennart

TITLE OF INVENTION: REcombinant Stratum Corneum Chymotryptic

TITLE OF INVENTION: Enzyme (SCCE)

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: White & Case, Patent Department

STREET: 1155 Avenue of the Americas

COUNTRY: Usw York

STATE: New York

COUNTRY: Usw. York

COUNTRY: Usw. York

COMPUTER READABLE FORM:

MEDIUM TYPE: TBM PC Compatible

COMPUTER: DATE: New PC-DOS/MS-DOS

SOFTWARE: Patentin By PC-DOS/MS-DOS

SOFTWARE: Patentin By PC-DOS/MS-DOS

SOFTWARE: Patentin DATA:

FILING DATE: 16-SEP-1998

CLASSIFICATION: DATA:

FRIOR APPLICATION: DATA:

FRIOR APPLICATION: DATA:
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 100.0%; Score 41; DB 2; Length 253; 100.0%; Pred. No. 0.45;
 0; Indels
 COUNTRY: USAGE
ZIF: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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APPLICATION NUMBER: US/08/824,874
FILING DATE: Filed Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: BY 18,08/824,874
FILING DATE: FILED HEREWITH
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APPLICATION NUMBER: S,749
FILING DATE: ATONNUMBER: T,749
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FILING DATE: ATONNUMBER: T,749
FILING
 Mismatches
ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto
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Gaps

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100.0%; Score 41; DB 3; Length 253; 100.0%; Pred. No. 0.45; ive 0; Mismatches 0; Indels
 100.0%; Score 41; DB 3; Length 253; 100.0%; Pred. No. 0.45;
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,084
FILING DATE:
 APPLICANT: Hillman, Jennifer L.
Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
 Sequence 3, Application US/09210084
; Patent No. 6197511
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, In
 NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0252 US
TELECOMMINICATION:
TELEPHONE: 415-855-0555
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE:
 Sequence 3, Application US/09764762 Patent No. 6472195 GENERAL INFORMATION:
 ATTORNEY/AGENT INFORMATION:
 LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 9; Conservative
 TELEFAX: 415-845-4166
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SEQUENCE CHARACTERISTICS:
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Matches 9; Conservative
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 LIBRARY: GenB
CLONE: 532504
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 94304
 STATE: C.
 US-09-764-762-3
 US-09-210-084-3
 Query Match
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 ö
 Gaps
 Sequence 2, Application US/08930188
Patent No. 6093397
GENERAL INFORMATION:
APPLICANT: Diano, Eric P.
APPLICANT: Little, Shella P.
TITLE OF INVENTION: RELATED NUCLEIC ACIDS
 100.0%; Score 41; DB 2; Length 253; 100.0%; Pred. No. 0.45;
 0.45;
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,188
 0; Mismatches
 1103326-181
 PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/416,257
PILING DATE: 04-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTATION NUMBER: 38,082
REFERENCE/DOCKET NUMBER: X9239
TELECOMMUNICATION INFORMATION:
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
 STATE: Indiana
COUNTRY: United States of America
 NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSES: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
 CLASSIFICATION:
CLASSIFICATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
 TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
 TELEPHONE: 317-277-1090
TELEPAX: 317-276-3861
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amino acid
 LENGTH: 253 amino acids
TYPE: amino acid
 Best Local Similarity 100.
Matches 9; Conservative
 STRANDEDNESS: single
TOPOLOGY: linear
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 US-08-930-188-2
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APPLICATION NUMBER: US 08/416,257
FILING DATE: 04-APR-1995
ATTONNEY/AGENT INFORMATION:
NAME: Blalock, Donna K.
REGISTRATION NUMBER: 38,082
REFENNEK/DOCKET NUMBER: 39,082
REFENNEK/DOCKET NUMBER: X9239
TELEPHONE: 317-277-1090
TELEPHONE: 317-277-1090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
 Query Match
Best Local Similarity 100...
 STRANDEDNESS: single
 TOPOLOGY: linear MOLECULE TYPE: protein
 13 MARSLLLPL 21
 1 MARSLLLPL 9
 1 MARSLLLPL 9
 amino acid
 TYPE: PRT
ORGANISM: Human
 RESULT 10
US-09-949-016-7716
 US-09-949-016-7716
 RESULT 11
US-09-502-600-116
 PCT-US96-04294-2
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 Gaps
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 Sequence 2, Application PC/TUS9604294

Sequence 2, Application PC/TUS9604294

GENERAL INFORMATION:

APPLICANT: Dixon, Eric P.

APPLICANT: Little, Sheila P.

TITLE OF INVENTION: RELATED NUCLEIC ACIDS

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSE: Bli Lilly and Company

STREET: Lilly Corporate Center

CITY: Indianapolis
 Query Match 100.0%; Score 41; DB 4; Length 253; Best Local Similarity 100.0%; Pred. No. 0.45; Matches 9; Conservative 0; Mismatches 0; Indels
 COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
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COMPUTER: IBM Compatible
COMPUTER: IBM COMPATE:
COMPUTER: IBM COMPATE:
COMPARE: 16-13n-2001
CLASSIFICATION DATA:
APPLICATION NUMBER: 09/210,084
FILING DATE: 4UNKNOWN-
PRIOR APPLICATION NUMBER: 09/210,084
FILING DATE: CUNKNOWN-
ATTONNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REPRENCE/DOCKET NUMBER: 36,749
REPRENCE / DOCKET
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
 CLONE: 532504
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-764-762-3
 PCT/US96/0429
 STATE: Indiana
COUNTRY: United States of America
CORRESPONDENCE ADDRESS:
 LIBRARY: GenBank
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
 1 MARSLLLPL 9
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 CLASSIFICATION:
 ZIP: 46285
 PCT-US96-04294-2
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Sequence 7716, Application US/09949016

Fatent No. 6812339

GENERAL INFORMATION:
FAREAL INFORMATION:
FOUNDAMY:
TITLE OF INVENTION:
FILE OF INVENTION:
FILE OF INVENTION:
FILE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 00/241,755

FRIOR APPLICATION NUMBER: 60/241,755

FRIOR APPLICATION NUMBER: 60/241,766

FRIOR APPLICATION NUMBER: 60/241,766

FRIOR FILING DATE: 2000-10-20

FRIOR FILING DATE: 2000-10-30

FRIOR FILING DATE: 2000-10-30

FRIOR FILING DATE: 2000-10-30

FRIOR FILING DATE: 2000-10-30

FRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NOS: 207012

SEQ ID NO 7716
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 Sequence 116, Application US/09502600A
Batent No. 6294344
GENERAL INFORMATION:
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: Ovarian Cancer
FILE REFERENCE: D62231CP-C
CURRENT FILING DATE: 2000-02-11
CURRENT APPLICATION NUMBER: US/09/502,600A
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us-09-905-083a-86.rai

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Best Local Similarity 77.5
7; Conservative
 1 MARSLLLPL 9
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Best Local Similarity
Matches 7; Conserv
 US-09-548-372D-2
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 Gaps
 Gaps
 GENERAL INCORNATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro.
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer FILE REFERENCE: D6223CIP/C/D/CIP
CURRENT APPLICATION NUMBER: US/09/918,243
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 136
LENGTH: 9
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87.8%; Score 36; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels
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 RESULT 13
US-08-999-723-2
i Sequence 2, Application US/08999723A
j Patent No. 6025180
i GENERAL INFORMATION:
APPLICANT: Powell, David J.
APPLICANT: Southan, Christopher
APPLICANT: Chapman, Conrad G.
APPLICANT: Chapman, Conrad G.
APPLICANT: Evames, Joanne R.
TITLE OP INVENTION: ASP1
FILE REFERENCE: GH70262
CURRENT FILING DATE: 1997-10-06
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 518
TYPE: BRT.
 Sequence 116, Application US/09918243 Patent No. 6627403
PRIOR APPLICATION NUMBER: 09/
PRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 116
LENGTH: 9
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Matches 8; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
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US-08-999-723-2
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 2 ARSLLLPL 9
 1 ARSLLLPL 8
 FEATURE:
NAME/KEY: CHAIN
 RESULT 12
US-09-918-243-116
 Query Match
 FEATURE:
 ઠે
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GENERAL INPORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALBERER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 29915/62801
CURRENT APPLICATION NUMBER: US/09/548,372D
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-23
PRIOR FILING DATE: 1999-09-24
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PRIOR PELING DATE: 1999-09-24
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: PALENTIN VERSION 3.1
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 Score 35; DB 3; Length 518;
Pred. No. 20;
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 Score 35; DB 3;
Pred. No. 20;
2; Mismatches
 APPLICANT: POWELL, DAVID J.
APPLICANT: POWELL, DAVID J.
APPLICANT: SOUTHAN, CHRISTOPHER
APPLICANT: SOUTHAN, CHRISTOPHER
APPLICANT: EVANS, JOANNE R.
TITLE OF INVENTION: ASP1
FILE REFERENCE: GH-70262-D1
CURRENT APPLICATION NUMBER: US/09/434,427
CURRENT FILING DATE: 1999-11-04
EARLIER FILING DATE: 1997-10-06
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EARLIER FILING DATE: 1997-10-06
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EARLIER PILING DATE: 1997-10-06
SARLIER PILING DATE: 1996-12-14
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PRESEQ for Windows Version 3.0
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Patent No. 6420534
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US-09-434-427-2
 TYPE: PRT
ORGANISM: Homo sapiens
US-09-548-372D-2
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Best Local Similarity
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Matches 7; Conservative 2; Mismatches 0; Indels Search completed: July 13, 2005, 17:34:29 Job time: 20.4444 secs 1 MARSLLLPL 9 :||:||||| 4 LARALLLPL 12 ر او

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6 US-10-173-999-48 (US-10-648-755A-639 (US-10-948-518-95 7 US-10-948-518-95 7 US-10-948-518-95 8 US-10-344-394-38 10S-10-342-36-88 10S-10-312-4668-6 10S-10-918-243-116 10S-10-918-243-116 10S-10-918-243-116 10S-10-918-243-116 10S-10-918-243-116 10S-10-918-243-116 10S-10-425-114-50699 10S-10-425-114-50699 10S-10-425-114-66721 10S-10-425-114-6721 10S-10-425-113-318442 10S-10-425-114-66721 10S-10-425-114-66721 10S-10-425-114-66721 10S-10-425-114-66721 10S-10-425-114-66721 10S-10-425-114-66721 10S-10-425-114-66721 10S-10-425-114-6721 10S-10-425-114-6721 10S-10-425-114-6721 10S-10-425-114-6721 10S-10-425-148-4

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Sequence 196 Sequence 196

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Sequence 86, Appl
Sequence 86, Appl
Sequence 86, Appl
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 (without alignments)
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 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-81-075-86
US-09-888-615-98
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US-09-71-214-2
US-10-071-214-2
US-10-071-214-8
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 Listing first 45 summaries
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 1 MARSLLLPL 9
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Match Length
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 Database
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 Result
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ö
Sequence 86, Application US/09918243

Patent No. US20020142317A1

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

APPLICANT: Cannon, Martin J.

APPLICANT: Cannon, Martin J.

APPLICANT: Santin, Alesandro

TITLE REFERENCE: D6223CIP/C/D/CIP

CURRENT APPLICATION NUMBER: US/09/918,243

CURRENT PILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US

PRIOR PILING DATE: 2001-07-13

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 86
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 Length 9;
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 NAME/KEY: CHAIN; OTHER INFORMATION: Residues 1-9 of the SCCE protein US-09-918-243-86
 100.0%; Score 41; DB 9; I. larity 100.0%; Pred. No. 1.6e+06; Conservative 0; Mismatches 0;
 TYPE: PRT
ORGANISM: Homo sapiens
 Similarity
9, Conserva
 1 MARSLLLPL
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Best Local S:
Matches
 g
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~ RESULT

Sequence 96, Appl Sequence 98, Appl Sequence 3, Appli Sequence 2, Appli

100.0 100.0 100.0

26433432

Sequence 48, Appl Sequence 90, Appl Sequence 498, App

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Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
 Shimkets, Richard A. Rothenberg, Mark E. Leach, Martin D. Agee, Michele L.
 Ji, Weizhen
Miller, Charles E.
Rastelli, Luca
Stone, David J.
 Ellerman, Karen
Malyankar, Uriel M.
 Zerhusen, Bryan D.
Anderson, David W.
 Zhong, Mei
Catterton, Elina
 Pena, Carol E. A.
Shenoy, Suresh G.
 APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
 Best Local Similarity 100.
Matches 9; Conservative
 Ort, Tatiana
Gorman, Linda
 Ju, Jingfang
Li, Li
 TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
 1 MARSLLLPL 9
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 NAME/KEY: CHAIN
 US-10-262-511-96
 Query Match
 APPLICANT:
APPLICANT:
 APPLICANT:
APPLICANT:
APPLICANT:
 APPLICANT:
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 Sequence 86, Application US/09905083

Patent No. US20020146708A1

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: O'Arian Cancer

FILE REPRENCE: D623GTP/C/Div

CURRENT APPLICATION NUMBER: US/09/905,083

CURRENT FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 09/502,600

PRIOR FILING DATE: 2000-02-11

SEQ ID NO 86

LENGTH: 9
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; Sequence 86, Application US/10372521
; Publication No. US20030223973A1
; GENERAL INFORMATION
; APPLICANT: Cannon, Martin J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer; FILE REFERENCE: D6223CIP/C/D/CIP2
; CURRENT FILING NAMBER: US/10/372,521
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/918,243
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF EQ ID NOS: 136
; SEQ ID NO 86
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 US-10-831-075-86
US-10-831-075-86
Sequence 86, Application US/10831075
Publication No. US20040224891A1
GENERAL INFORMATION:
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
ITILE OF INVENTION: Methods for the early diagnosis of ovarian cancer
 ö
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Matches 9; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
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 08-69-905-083-86
US-09-905-083-86
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 Gaps
 APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462C
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 Indels
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CURRENT APPLICATION NUMBER: U5/10/831,075
CURRENT FILING DATE: 2004-04-23
PRIOR APPLICATION NUMBER: US 10/372,521
PRIOR FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 140
SEQ ID NO 86
LENGTH: 9
 CURRENT APPLICATION NUMBER: US/10/262,511 CURRENT FILING DATE: 2003-05-28
 PRIOR APPLICATION NUMBER: 60/326,483
PRIOR PELING DATE: 2003-05-28
PRIOR FILING DATE: 2001-10-02
PRIOR FILING DATE: 2001-10-03
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2001-10-09
PRIOR PELING DATE: 2001-10-09
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PRIOR FILING DATE: 2002-05-17
 Sequence 96, Application US/10262511 Publication No. US20040038223A1 GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
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 1 MARSLLLPL 9
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 US-10-071-214-2
 US-09-764-762-3
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 PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2002-04-17
PRIOR FILING DATE: 2002-04-17
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2001-10-05
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NUMBER OF SEQ ID NOS: 439
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 0; Indels
 Lal, Preeti
TITLE OF INVENTION: NOVEL KALLIKREIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
SADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
 APPLICANT: MANNING, GERARD
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: US/09/888,615
CURRENT FILING DATE: 2001-06-26
PRIOR PILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 98
LENGTH: 253
 Sequence 3, Application US/09764762
Patent No. US20020068341A1
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
 Sequence 98, Application US/0988615
Patent No. US20020064886A1
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
FILING DATE: 2002-05-16
 APPLICANT: WHYTE, DAVID
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
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Matches 9; Conserv
 US-09-764-762-3
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 TYPE: PRT
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Sequence 2, Application US/20030066099A1
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APPLICANT: HANSSON, Lennart
APPLICANT: BGELRUD, Torbjorn
TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MAMMALS AND THEIR USE AS MODELS OF HUMAN
CURRENT APPLICATION NUMBER: US/10/071,214
CURRENT FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin version 3.1
SEQ ID NO 2.
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 Gaps
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 100.0%; Score 41; DB 14; Length 253; 100.0%; Pred. No. 5.8;
 Length 253;
 Indels
 IndelB
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOPTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/764,762
FILING DATE: 16-Jan-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION NUMBER: 09/210,084
FILING DATE: cUnknown>
APPLICATION NUMBER: 09/210,084
FILING DATE: cunknown>
APPLICATION NUMBER: 36,749
REGISTATION NUMBER: 36,749
REGISTATION NUMBER: PF-0252 US
TELECOMMUNICATION INFORMATION:
TELEFRANCA/DOCKET NUMBER:
TELEPHONE: 415-845-0555
TELEFRANCA/DOCKET NUMBER:
TELEFRANCA/TERISTICS:
 Query Match 100.0%; Score 41; DB 9;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 9; Conservative 0; Mismatches 0
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JOSTICAL AS 959-48, Application US/10173999

Sequence 48, Application US/2004000553A1

GENERAL INFORMATION:
APPLICANT: Mack, David H.
APPLICANT: Bos Biotechnology, Inc.
APPLICANT: Eos Biotechnology, Inc.
TILLE OF INVENTION: and Methods of Screening for Modulators of Ovarian
TITLE OF INVENTION: Cancer;
TITLE OF INVENTION: Cancer;
FILE REFERENCE: 01861-002420US
FILE REPERENCE: 01861-002420US
CURRENT APPLICATION NUMBER: US 60/299,234
PRIOR APPLICATION NUMBER: US 60/299,234
PRIOR APPLICATION NUMBER: US 60/315,287
PRIOR APPLICATION NUMBER: US 60/315,287
PRIOR PILING DATE: 2001-06-18
PRIOR PILING DATE: 2001-06-18
PRIOR PLING DATE: 2001-06-18
PRIOR PLING DATE: 2001-08-27
PRIOR PLING DATE: 2001-01-18
PRIOR PLING DATE: 2001-01-11-13
PRIOR APPLICATION NUMBER: US 60/372,246
 APPLICANT: Glash, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: March, David H.
APPLICANT: Marchy, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Bos Biotechnology, Inc.
ITILE OF INVENTION: Methods of Diagnosis of Cancer.
ITILE OF INVENTION: Methods of Screening for Modulators of Cancer.
ITILE OF INVENTION: Methods of Screening for Modulators of Cancer.
ITILE OF INVENTION: Methods of Screening for Modulators of Cancer.
ITILE OF INVENTION: WABRE: US/10/295,027
CURRENT APPLICATION NUMBER: US 60/350,666
RRIOR APPLICATION NUMBER: US 60/350,666
RRIOR PILING DATE: 2001-11-13
PRIOR PILING DATE: 2001-11-13
PRIOR PAPLICATION NUMBER: US 60/335,394
PRIOR PILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR PELING DATE: 2001-11-21
PRIOR PELING DATE: 2001-11-21
PRIOR PELING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR PILING DATE: 2001-11-3
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-01-08
PRIOR PELING DATE: 2002-02-08
PRIOR PELING DATE: 2002-02-08
PRIOR PELING DATE: 2002-02-03
PRIOR PE
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 100.0%; Score 41; DB 15; Length 253; 100.0%; Pred. No. 5.8;
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 Ginsberg, Wendy M. Gish, Kurt C.
 Conservative
 Aziz, Natasha
 ORGANISM: Homo sapiens
 Query Match
Best Local Similarity
'-haq 9; Conserv?
 1 MARSLLLPL 9
 US-10-295-027-498
 RESULT 12
US-10-173-999-48
 qq
 GENERAL INFORMATION

APPLICANT: HANSON, Lennart

APPLICANT: HANSON, Lennart

APPLICANT: HANSON, Lennart

TITLE OF INVENTION: SCCE MODIFIED TRANSGENIC MANMALS AND THEIR USE AS MODELS OF HUMAN

FILE REPERENCE: HANSON=3A

CURRENT APPLICATION NUMBER: US/10/071,214

CURRENT FILING DATE: 2002-02-11

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin version 3.1

SEQ ID NO 48
 ; OTHER INFORMATION: Deduced amino acid sequence from the C-terminal part of SCCE from US-10-071-214-48
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 Gaps
 Gaps
 US-10-264-283-90

Sequence 90, Application US/10264283

Sequence 90, Application US/10264283

Publication No. US20030144494A1

GENERAL INFORMATION:

APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.590

CURRENT FILING DATE: 2002-10-02

CURRENT FILING DATE: 2002-10-02

NUMBER OF SEQ ID NOS: 111

SOFTWARE: Corixa Invention Disclosure Database

SEQ ID NO 90

LENGTH: 253
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 100.0%; Score 41; DB 14; Length 253; 100.0%; Pred. No. 5.8; ative 0; Mismatches 0; Indels (
 Query Match
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 9; Conservative 0; Mismatches 0; Indels
 US-10-295-027-498
Sequence 498, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
 US-10-071-214-48
; Sequence 48, Application US/10071214
; Publication No. US20030066099A1
 ORGANISM: Artificial Sequence FEATURE:
 Conservative
 ; ORGANISM: Homo sapiens
US-10-264-283-90
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1 MARSLLLPL 9
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1 MARSLLLPL 9
 Query Match
Best Local Similarity
9; Conserve
 TYPE: PRT
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Query Match
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Matches 9; Conservative 0; Mismatches 0;
 0; Mismatches
 PRIOR FILING DATE: 2002-08-21
PRIOR APPLICATION NUMBER: US 60/413,192
PRIOR PILING DATE: 2002-09-23
PRIOR PILING DATE: 2002-09-23
PRIOR FILING DATE: 2002-10-15
PRIOR FILING DATE: 2002-11-15
PRIOR PILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US 60/484,959
PRIOR PILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 158
LENGTH: 253
 Sequence 95, Application US/10948518
Publication No. US20050064492A1
 APPLICANT: FREDERIC J. DESAUVAGE
APPLICANT: GRETCHEN FRANTZ
APPLICANT: KENNETH J. HILLAN
APPLICANT: PAUL POLAKIS
APPLICANT: ANDREW POLSON
APPLICANT: VICTORIA SMITH
APPLICANT: SUSAN D. SPENCER
 Query Match
Best Local Similarity 100.
Matches 9; Conservative
 TYPE: PRT
CORGANISM: Homo sapien
US-10-643-795A-95
 1 MARSLLLPL 9
 LENGTH: 253
TYPE: PRT
ORGANISM: Homo sapien
 1 MARSLLLPL 9
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 US-10-948-518-95
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 APPLICANT: VICTORIA SMITH
APPLICANT: SUSAN D. SPENCER
APPLICANT: THOMAS D. WAS
APPLICANT: THOMAS D. WAS
APPLICANT: ZEMIN ZHANG
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF TUMOR
FILE REFERENCE: PSO26RI-US
 Sequence 639, Application US/10408765A
| Publication No. US20040101874A1
| GENERAL INFORMATION:
| APPLICANT: Ghosh, Sounitra S.
| APPLICANT: Taylor, Eoin D.
| APPLICANT: Taylor, Steven W.
| APPLICANT: Glosn, Bradford W.
| APPLICANT: Gloss, Gl
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 DB 15; Length 253;
 100.0%; Score 41; DB 16; Length 253; 100.0%; Pred. No. 5.8;
 0; Indels
 0; Indels
 Mismatches
 0; Mismatches
 100.0%; Score 41; 100.0%; Pred. No.
 CURRENT APPLICATION NUMBER: US/10/643,795A CURRENT FILING DATE: 2003-08-19 PRIOR APPLICATION NUMBER: US 60/404,809 PRIOR FILING DATE: 2002-08-19
 Sequence 95, Application US/10643795A
Publication No. US20040241703A1
GENERAL INFORMATION:
APPLICANT: FREDERIC J. DESAUVAGE
APPLICANT: GRETCHEN FRANTZ
APPLICANT: PRENETH J. HILLAN
APPLICANT: PAUL POLAKIS
APPLICANT: ANDREW POLSON
 ;
0
; PRIOR FILING DATE: 2001-04-12; NUMBER OF SEQ ID NOS: 163; SOFTWARE: PAtentIN Ver. 2.1; SEQ ID NO 48; LENGTH: 253; TYPE: PRT ORGANISM: HOMO SAPIENS
 Query Match
Best Local Similarity 100.
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Matches 9; Conservative
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-639
 1 MARSLLLPL 9
 1 MARSLLLPL 9
 RESULT 13
US-10-408-765A-639
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APPLICANT: ANDREW POLSON
APPLICANT: ANDREW POLSON
APPLICANT: ANDREW POLSON
APPLICANT: ANDREW POLSON
APPLICANT: VICTORIA SMITH
APPLICANT: SUSAN D. SPENCER
APPLICANT: THOMAS D. WU
TITLE OF INVENTION: TREATMENT OF TUMOR
TITLE OF INVENTION: WHEER: US/10/948,518
CURRENT APPLICATION NUMBER: US/04/43,795
PRIOR FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: US 60/404,809
PRIOR FILING DATE: 2002-08-19
PRIOR FILING DATE: 2002-08-19
PRIOR FILING DATE: 2002-08-21
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PRIOR FILING DATE: 2002-10-15
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PRIOR FILING DATE: 2003-07-02
NUMBER OF SEQ ID NOS: 158 Gaps Gaps ö ö 100.0%; Score 41; DB 16; Length 253; 100.0%; Pred. No. 5.8; Length 253; 0; Indels Indels

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Search completed: July 13, 2005, 18:23:42 Job time: 65.8889 secs

Amino aci Protein d Protein d

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ADL06515
ADN04182
ADR72880
AAB21326
ABB84422
ABB84422
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ADR68858
ABG68630
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(without alignments)
45.402 Million cell updates/sec
 July 13, 2005, 16:12:23 ; Search time 76.6667 Seconds
 GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
 - protein search, using sw model
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 US-09-905-083A-99
 1 QRIKASKSF 9
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Aau82740 Amino aci Abu07440 Protein d Abr58471 Protein d Abr58471 Human str Adb80484 Ovarian c Adj68833 Human hea Adj68833 Human chea Adn04182 Amtipsori Adr72880 Human ova Abb21326 Human ova Abb21326 Human str Abr68858 Human str Adr68858 Human str Abg68630 Stratum c Abb84423 Murine SC Abb84423 Murine SC Abb844128 Murine SC Abb844128 Murine SC Add40226 Human NOV Add40226 Human NOV

## ALIGNMENTS

ADE40216

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000

Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2001s:\*

A\_Geneseq\_16Dec04:\*

Database

geneseqp2003as:\* geneseqp2003bs:\*

geneseqp2004s:\*

2105692 segs, 386760381 residues

Scoring table:

Searched:

score:

Title: Perfect

Sequence:

OM protein

Run on:

Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia. Human stratum corneum chymotrypsin enzyme peptide #99 (residues 91-99). Ā AAE08334 standard; peptide; 9 11-FEB-2000; 2000US-00502600. 07-FEB-2001; 2001WO-US003977 (first entry) (UYAR-) UNIV ARKANSAS WO200159158-A1. Homo sapiens 01-NOV-2001 16-AUG-2001. O'brien TJ; AAE08334; RESULT 1 AAE08334 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

DB

Length

Query Match

Result ģ 100.0

WPI; 2001-514676/56

Human str Human str Human str Human str Human NOV

Description

Aae08334

AAE08334 AAE08304 ADR68891 ADR68860

ADA05740 ADN62904 ADI39727 ADI37151 ADA05738 ADN62902

Diagnosing cancer comprises detecting stratum corneum chymotrypsin

Disclosure; Page 124; 127pp; English.

Stratum c Stratum c Human NOV Human NOV Human NOV Human NOV Human NOV Human Str Human NOV Human NOV Human NOV Human NOV

Adec08304 Adr68891 Adr68891 Adac5740 Adi3727 Adi3727 Adi3727 Adac5738 Adac5738 Adac5738 Adac5908 Adac5

ADA05736 ADN62900 ADA05744

1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00 1000.00

ADN62908 AAB98502 ADA05742 ADN62906

ADA05732 ADN62896 ADA05734 ADN62898

> 100.0 100.0 100.0 100.0

The invention relates to diagnosing cancer especially ovarian cancer, by screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, carcinoma and malignant hyperplasia. The SCCE oligonucleotide may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide

Sequence 9 AA;

Human amy Human SCC Human SCC Human str

Aar67888 1 Aaw05383 1 Abb84421 1 Abb84406 1

DB 4; Length 9; 100.0%; Score 42;

Query Match

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20-FEB-2004; 2004WO-US005134.
 21-FEB-2003; 2003US-00372521
 (first entry)
 Conservative
 Cannon MJ,
 (UYAR-) UNIV ARKANSAS
 σ
 WPI; 2004-653294/63.
 chymotrytic enzyme)
 ORIKASKSF
 1 QRIKASKSF
 WO2004075723-A2.
 WO2004075723-A2
 Sequence 9 AA;
 Homo sapiens
 02-DEC-2004
 O'brien TJ,
 10-SEP-2004.
 10-SEP-2004
 ADR68860;
 RESULT 4
 ADR68860
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 screening for stratum corneum chymotrypsin enzyme (SCCE). Proteases are considered to be an integral part of tumour growth and metastasis, and therefore, markers indicative of their presence or absence are useful for the diagnosis of cancer. The method is useful for diagnosing cancer, to treat a cancer the presence or absoluted may be used to treat a cancer selected from ovarian, breast, lung, colon, prostate and other cancers in which SCCE is overexpressed. The present sequence is human SCCE peptide
 The invention relates to diagnosing cancer especially ovarian cancer, by
 Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:130.
 Stratum corneum chymotrypsin enzyme; SCCE; cytostatic; vaccine; tumour; cancer; ovarian; breast; lung; colon; prostate; carcinoma; human; antisense therapy; malignant hyperplasia.
 Human stratum corneum chymotrypsin enzyme peptide #69 (residues 91-99).
 Gaps
 Gaps
 Diagnosing cancer comprises detecting stratum corneum chymotrypsin
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0
 100.0%; Score 42; DB 4; Length 9; 100.0%; Pred. No. 1.8e+06; tive 0; Mismatches 0; Indels
 Indels
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 Pred. No. 1.8e+06;
 Mismatches
 Claim 25; Page 117; 127pp; English.
 AAE08304 standard; peptide; 9 AA.
 ADR68891 standard; peptide; 9 AA.
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100.08;
 07-FEB-2001; 2001WO-US003977.
 11-FEB-2000; 2000US-00502600.
 02-DEC-2004 (first entry)
 01-NOV-2001 (first entry)
 9; Conservative
 Conservative
 (UYAR-) UNIV ARKANSAS
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 QRIKASKSF 9
 WPI; 2001-514676/56.
 1 ORIKASKSF
 QRIKASKSF
 Best Local Similarity
 WO200159158-A1.
 Sequence 9 AA;
 Homo sapiens
 16-AUG-2001
 O'brien TJ;
 AAE08304;
 ADR68891;
 cancer;
 Matches
 ADR68891
ID ADR.
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 RESULT 2
 RESULT 3
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The invention relates to a novel method for vaccinating an individual against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating an individual with a SCCE peptide, which elicits an immune response in the individual with a SCCE peptide, which elicits an immune response in chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating an individual against SCCE, particularly an individual having, suspected or at risk of getting ovarian, lung, prostate, pancreatic or colon cancer. The oligomucleotide is useful for treating a neoplastic state in an individual, such as ovarian, breast, lung, colon, prostate, or pancreatic cancer, and other cancers in which SCCE is overexpressed. The peptides are also useful in the monitoring and development of immunotherapies for ovarian and other mallgnancies. The present sequence represents a peptide fragment of serine protease SCCE (stratum corneum
 Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for vaccinating an individual against SCCE, and in monitoring and developing immunotherapies for ovarian and other malignancies.
 Human stratum corneum chymotrytic enzyme peptide fragment SEQ ID NO:99.
 Gaps
 ..
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serine protease; stratum corneum chymotrytic enzyme; SCCE; immune response; ovarian cancer; lung cancer; prostate cancer; pancreatic cancer; colon cancer.
 serine protease; stratum corneum chymotrytic enzyme; SCCE; immune response; ovarian cancer; lung cancer; prostate cancer; pancreatic cancer; colon cancer.
 100.0%; Score 42; DB 8; Length 9;
100.0%; Pred. No. 1.8e+06;
 Disclosure; SEQ ID NO 130; 117pp; English.
 Santin A;
 ADR68860 standard; peptide; 9 AA.
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ö
 The invention relates to a novel method for vaccinating an individual against stratum corneum chymotrytic enzyme (SCCE), comprising inoculating in individual with a SCCE peptide, which elicits an immune response in the individual with a SCCE peptide, which elicits an immune response in the individual. A peptide of the invention acts as a stratum corneum chymotrytic enzyme inhibitor. The SCCE peptide is useful for vaccinating an individual against SCCE, particularly an individual having, suspected or at risk of getting ovarian, lung, prostate, pancreatic or colon cancer. The oligonucleotide is useful for treating a neoplastic state in an individual, such as ovarian, breast, lung, colon, prostate, or pancreatic cancer, and other cancers in which SCCE is overexpressed. The peptides are also useful in the monitoring and development of immunocherapies for ovarian and other malignancies. The present sequence represents a peptide fragment of serine protease SCCE (stratum corneum corneum
 Use of stratum corneum chymotrytic enzyme (SCCE) peptides, for vaccinating an individual against SCCE, and in monitoring and developing
 Gaps
 ö
 100.0%; Score 42; DB 8; Length 9; 100.0%; Pred. No. 1.8e+06; tive 0; Mismatches 0; Indels
 immunotherapies for ovarian and other malignancies
 Claim 5; SEQ ID NO 99; 117pp; English.
 Santin A;
 ADA05740 standard; protein; 97 AA.
 20-FEB-2004; 2004WO-US005134
 21-FEB-2003; 2003US-00372521
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 Cannon MJ,
 (UYAR-) UNIV ARKANSAS
 1 QRIKASKSF 9
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 WPI; 2004-653294/63
 chymotrytic enzyme)
 1 ORIKASKSF
 Best Local Similarity
Matches 9; Conserv
 Sequence 9 AA;
 O'brien TJ,
 ADA05740;
 Query Match
 RESULT 5
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06-NOV-2003 (first entry)

human, NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antipaemic; gene therapy; human disease; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachaxia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;

02-OCT-2002; 2002WO-US031373

05-OCT-2001; 05-OCT-2001;

Human NOV18e protein SEQ ID NO:100. Homo sapiens

immune disorder; haematopoietic disorder; dyslipidaemia 2001US-0327435P. 2001US-0327449P. 2001US-0327917P. 2001US-0328029P. 2001US-0328044P. WO2003029424-A2 09-OCT-2001; 09-OCT-2001; 09-OCT-2001; 02-OCT-2001; 10-APR-2003 

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2002US-0373815P.
2002US-0373817P.
2002US-0373826P.
2002US-0373884P.
 2001US-0349575P.
2001US-0346357P.
2002US-0373260P.
 2002US-0381042P.
 2002US-0374977P
 2002US-0381037P
 2002US-0383656P.
2002US-0383831P.
 2002US-0391335P
 2002US-00262511
18-OCT-2001; 22-OCT-2001; 24-OCT-2001; 24-OC
 29-OCT-2001;
 01-NOV-2001;
 17-APR-2002;
 19-APR-2002;
 19-APR-2002;
 19-APR-2002;
 19-APR-2002;
 16-MAY-2002;
 16-MAY-2002;
 16-MAY-2002;
 17-MAY-2002;
 28-MAY-2002;
 29-MAY-2002;
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(CURA-) CURAGEN CORP.

Dipippo VA; Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Jiw, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;

2003-381626/36. N-PSDB; ADA05739.

obesity, New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, cancer or dyslipidemia, and in chromosome mapping, tissue typing pharmacogenomics

Claim 1; Page 171; 586pp; English.

The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOV1). Also described: (1) a composition comprising a polypeptide

coestribed above and a carrier; (2) a kit comprising, in one or more

containers, the composition described above; (3) an isolated nucleic acid

molecule which encodes a NOVX protein of the invention; (4) a vector

comprising the nucleic acid molecule described above; (5) a cell

comprising the above vector; (6) an antibody that immunospecifically

binds to the polypeptide described above; (7) methods for determining the

comprising the above polypeptide or nucleic acid molecule in a

sample; (8) methods for determining the presence of or predisposition to

a disease associated with altered levels of expression of the above

co polypeptide or nucleic acid molecule in a first mammalian subject; (9) a

method of identifying an agent that binds to the polypeptide described

above; (10) a method for identifying a potential therapeutic agent for

cuse in treating a pathology that is related to an aberrant expression or

above; (10) a method for identifying a potential therapeutic agent for

cuse in treating a pathology that is related to an aberrant expression or

above; (10) a method got identifying a potential therapeutic agent for

co a pathology associated with the polypeptide; (12) a method for modulating

co perventing a pathology associated with the above polypeptide. NoVX

sequences have antidiabetic, anorectic, antibacterial, virucide,

con preventing a pathology associated with the above polypeptide in a

configuration and antilipamenic activities, and can be used in gene therapy. The

colypeptide is useful in manufacturing a medicament for treating a

colypeptide is useful in manufacturing a redicament for treating a

colypeptide is useful in manufacturing a redicament for treating a

contained to the polypeptide or an event or proverse method for and antilipament associated with a noverse or preventy maps above polypeptide. acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's

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 human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
disease, immune disorders, haematopoietic disorders and various dyslipidaemias. The nucleic acids can also be used as hybridiation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
 Gaps
 ..
 100.0%; Score 42; DB 6; Length 97; 100.0%; Pred. No. 0.24; tive 0; Mismatches 0; Indels
 ADN62904 standard; protein; 97 AA.
 2001US-0327449P.
2001US-0328021P
2001US-0328044P.
2001US-03280644P.
2001US-0328066P.
2001US-0328064P.
2001US-032844P.
2001US-0339414P.
2001US-0330309P.
 2001US-0339266P.
2001US-0343629P.
2001US-0349575P.
2001US-0346357P.
 2002US-0373815P.
2002US-0373817P.
2002US-0373826P.
 2002US-0373260P.
 2002US-0373884P.
 2002US-0374977P.
2002US-0381037P.
 2002US-0381038P.
 2002US-0381642P,
 2002US-0383656P.
 2002US-0383831P.
 25-JUN-2002; 2002US-0391335P.
 01-OCT-2002; 2002US-00262511
 01-JUL-2004 (first entry)
 Local Similarity 100.
 80
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 (SMIT/) SMITHSON G. (MILL/) MILLET I.
 1 QRIKASKSF
 72 ORIKASKSF
 present invention.
 wasting disorder.
 US2004038223-A1.
 Sequence 97 AA;
 09-007-2001;
09-007-2001;
09-007-2001;
12-007-2001;
11-007-2001;
11-007-2001;
12-007-2001;
24-007-2001;
24-007-2001;
24-007-2001;
10-007-2001;
10-007-2001;
10-007-2001;
10-007-2001;
10-007-2001;
 Human NOV18e.
 Homo sapiens.
 19-APR-2002;
22-APR-2002;
16-MAY-2002;
 19-APR-2002;
 17-APR-2002;
 19-APR-2002;
 26-FEB-2004.
 16-MAY-2002
 ADN62904;
 Query Match
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Matches
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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 EISEN A.
GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
 MILLER C B.
RASTELLI L.
STONE D J.
PENA C B A.
SHENOY S G.
SHENOY S G.
SHINGERS R A.
ROTHENBERG M B
LEACH M D.
 ELLERMAN K.
MALYANKAR U M.
 AGEE M L.
BERGHS C.
DIPIPPO V A.
 PATTURAJAN M.
 ZERHUSEN B D.
ANDERSON D W.
 SPYTEK K A.
EDINGER S R.
 CATTERTON E.
PEYMAN J A.
KEKUDA R.
 GORMAN L.
 ZHONG M.
 GUOX
 (EISE/) (GANG/) (RIEG/) (SPAD/)
 (CATT/)
(JIWW/)
(MILL/)
(RAST/)
(STON/)
(PENA/)
 (SHIM/)
(ROTH/)
(LEAC/)
(AGEE/)
(BERG/)
 (EDIN/)
(ELLE/)
(MALY/)
(ORTT/)
 (JUJJ/)
(LILL/)
(GUOX/)
(PATT/)
(SPYT/)
 (GORM/)
 (ANDE/)
(ZHON/)
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WPI; 2004-213931/20. N-PSDB; ADN62903. Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.

Claim 1; SEQ ID NO 100; 395pp; English.

The invention relates to isolated NOVX polypeptides and polynucleotides.

NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and colynucleotides may be used to treat disorders associated with decreased polynucleotides may be used to treat disorders associated with decreased conduction or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polymelectides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be in need of similar sequences in samples, and so which patients may be not need of similar sequences in samples, and so which patients may be used as anti-NOVX polypeptides and in assays to identify of NOVX. The production of antibodies and in assays to identify of NOVX.

Colypeptides. The anti-NOVX polypeptide antibodies may also be used as anti-NOVX polypeptide antibodies, agonists and antagonists and polymucleotide expression and activity of NOVX colypeptides and polymucleotides may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious disorders, alreaments, cancer, cancer associated cachexia, mencadegemerative disorders, harmadegemerative charmatopoietic disorders, and the various dysl

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The invention relates to extracellular serine protease termed tumour antigen derived gene-14 (TADG-14) and its nucleic acid. Composition comprising TADG-14 peptide is useful for treating a neoplastic state in individual. The neoplastic state is chosen from ovarian cancer, breast cancer, lung cancer, colon cancer, prostate cancer in which TADG-14 is overexpressed. The present sequence is Stratum corneum chymotryptic enzyme (scce) catalytic domain. This sequence is used in the exemplification of the invention.
 Novel isolated DNA encoding tumor antigen derived gene-14 protein, useful
 for treating neoplastic state (such as ovarian cancer, breast cancer, lung cancer, colon cancer, prostate cancer) in an individual.
 immunomodulator; cytostatic; nootropic; neuroprotective;
antiparkinsonian; antilipaemic; gene therapy; human disease;
metabolic disorder; diabetes; obesity; infection; cachexia; cancer;
 Serine protease; tumour antigen derived gene-14; TADG-14; neoplastic state; cancer; ovary; breast; lung; colon; prostate; chymotryptic enzyme; scce; enzyme.
 antidiabetic; anorectic; antibacterial; virucide;
 Stratum corneum chymotryptic enzyme (scce) catalytic domain.
 100.0%; Score 42; DB 8; Length 144; 100.0%; Pred. No. 0.37;
 0.37;
 Mismatches
 Example 1; SEQ ID NO 4; 46pp; English.
 ADI37151 standard; protein; 144 AA
 ADA05738 standard; protein; 181 AA.
 Human NOV18d protein SEQ ID NO:98.
 .
0
 97US-00915659.
98US-00137944.
2000US-00618259.
 2003US-00461787.
 3
 06-NOV-2003 (first entry)
 Conservative
 Underwood
 (UYAR-) UNIV ARKANSAS
 28 QRIKASKSF 36
 σ
 Query Match
Best Local Similarity
9; Conserve
 WPI; 2004-141550/14.
 1 ORIKASKSF
 US2003199010-A1.
 Sequence 144 AA;
 21-AUG-1997;
21-AUG-1998;
18-JUL-2000;
 Homo sapiens.
 13-JUN-2003;
 human; NOVX;
 06-MAY-2004
 O'brien TJ,
 23-OCT-2003
 ADI37151;
 ADA05738;
 ADA05738
 ADI3715
 RESULT
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 The present invention relates to novel activated immune T cells or dendritic cells directed toward extracellular serine protease termed tumour antigen derived gene-14 (TADG-14). The method of the invention involves exposing the immune cells to a TADG-14 protein fragment, where exposure to the TADG-14 protein fragment activates the immune cells. The invention is used for the production of activated immune T cells or dendritic cells. The invention allows screening to identify proteases overexpressed in carcinoma. The present sequence is stratum corneum chymotryptic enzyme (scce) catalytic domain. This sequence is used in the
 Production of activated immune cells or dendritic cells by exposing immune cells to tumor antigen derived gene protein fragment consisting of
wasting disorders associated with chronic diseases and various cancers. They may also be used as antibacterial agents. The present sequence represents the amino acid sequence of a human NOVX protein.
 Gaps
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 Immune T cell; dendritic cell; extracellular serine protease,
 Stratum corneum chymotryptic enzyme (scce) catalytic domain.
 100.0%; Score 42; DB 8; Length 144; 100.0%; Pred. No. 0.37; ive 0; Mismatches 0; Indels
 8; Length 97;
 1 Score 42; DB 8; Length 97 Similarity 100.0%; Pred. No. 0.24; 9; Conservative 0; Mismatches 0; Indels
 tumour antigen derived gene-14; TADG-14; carcinoma; stratum corneum chymotryptic enzyme; scce.
 Example 1; SEQ ID NO 4; 44pp; English.
 ADI39727 standard; protein; 144 AA
 (UYAR-) UNIV ARKANSAS MEDICAL SCI.
 18-JUL-2000; 2000US-00618259.
 98US-00137944.
 15-APR-2004 (first entry)
 Underwood LJ;
 9; Conservative
 80
 QRIKASKSF 36
 1 QRIKASKSF 9
 amino acid sequences.
 1 QRIKASKSF 9
 WPI; 2004-118109/12.
 Query Match
Best Local Similarity
 72 ORIKASKSF
 Local Similarity
 Sequence 144 AA;
 Sequence 97 AA;
 Unidentified
 21-AUG-1997;
 US6642013-B1
 21-AUG-1998;
 04-NOV-2003
 O'brien TJ,
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RESULT 7

AD139727

AD1397

ADI39727;

Matches

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Gaps

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0; Indels

invention

Query Match Matches 28

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(e.g. NOVI). Also described: (1) a composition comprising a polypeptide described above and a carrier; (2) a kit comprising, in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVY protein of the invention; (4) a vector comprising the above vector; (6) an antibody that immunospecifically binds to the polypeptide described above; (5) a cell binds to the polypeptide described above; (5) an encode or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a
 Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Offr T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shinkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo VA;
Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
 present invention describes NOVX proteins, where X can be 1 to 55
neurodegenerative disorder, Alzheimer's disease; Parkinson's disease;
immune disorder; haematopoietic disorder; dyslipidaemia.
 New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, cancer or dyslipidemia, and in chromosome mapping, tissue typing pharmacogenomics.
 Claim 1; Page 171; 586pp; English.
 2001US-0346357P.
2002US-0373260P.
2002US-0373815P.
2002US-0373817P.
2002US-0373886P.
 2001US-0328029P.
2001US-0328044P.
2001US-0328056P.
2001US-0328414P.
2001US-03303142P.
2001US-0330309P.
 2001US-0341058P.
2001US-0339266P.
2001US-0343629P.
2001US-0349575P.
 2002US-0381037P.
2002US-0381038P.
2002US-0381042P.
 2002US-0374977P.
 2002US-0381642P.
2002US-0383656P.
 01-OCT-2002; 2002US-00262511.
 2001US-0327449P
 2002US-0383831P
 02-OCT-2002; 2002WO-US031373
 2001US-0327917P
 2002US-0391335P
 (CURA-) CURAGEN CORP.
 WPI; 2003-381626/36.
 N-PSDB; ADA05737.
 WO2003029424-A2
 16-MAY-2002;
16-MAY-2002;
16-MAY-2002;
 15-OCT-2001;
17-OCT-2001;
18-OCT-2001;
 24-OCT-2001;
29-OCT-2001;
 Homo sapiens.
 01-NOV-2001;
17-APR-2002;
 22-OCT-2001;
24-OCT-2001;
 19-APR-2002;
 02-OCT-2001;
 09-OCT-2001;
 09-OCT-2001;
 9-APR-2002;
 17-MAY-2002;
 09-OCT-2001;
 09-OCT-2001;
 19-APR-2002;
 22-APR-2002;
 29-MAY-2002
 10-APR-2003
 25-JUN-2002
 05-OCT-2001
 28-MAY-
 The
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method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for above; (10) a method for identifying a potential therapeutic agent for above; (11) a method of second an aborrant expression or aberrant physiological interactions of the polypeptide; (11) a method of considerable above; (13) method of modulating the above polypeptide in a method for modulating or preventing a pathology associated with the above polypeptide. NovX considerable and (14) a method for producing the above polypeptide. NovX sequences have antidiabetic, anoredtic, antibacterial, virucide, immunomodulator, cytostatic, nootropic, neuroprotective, antiparkinsonian confilialization associated with a human disease. The polypeptide or the nucleic syndrome associated with a human disease. The polypeptide or the nucleic cid methodeore such as diabetes such as Alzheimer's disease or Parkinson's disease immune disorders such as Alzheimer's disorders and various cytobes, in chromosome mapping, tissue typing, preventive medicine and cytobes, in chromosome mapping, tissue typing, preventive medicine and cytobes, in chromosome mapping, tissue typing, preventive medicine and cytobes, in chromosome mapping, tissue typing, preventive medicine and cytobes, in chromosome mapping, tissue typing, preventive medicine and cytobes, in chromosome mapping, tissue typing, preventive medicine and cytobes. human; NOVX; metabolic disorder; diabetes; obesity; infectious disease; anorexia; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X; Gaps ö 100.0%; Score 42; DB 6; Length 181; 100.0%; Pred. No. 0.47; ive 0; Mismatches 0; Indels ADN62902 standard; protein; 181 AA 2001US-0328029P. 2001US-0328044P. 2001US-0328056P. 2001US-0330142P. 2001US-0330309P. 2001US-0339266P. 2001US-0343629P. 2001US-0349575P. 2001US-0328849P. 2001US-0329414P. 01-OCT-2002; 2002US-00262511 2001US-0326483P. 2001US-0327435P. 2001US-0327449P 2001US-0327917P 2001US-0341058P 01-JUL-2004 (first entry) 9; Conservative 72 ORIKASKSF 80 1 ORIKASKSF 9 Query Match Best Local Similarity present invention wasting disorder Sequence 181 AA; US2004038223-A1. 09-OCT-2001; 2 12-OCT-2001; 2 15-OCT-2001; 2 Homo sapiens. 09-OCT-2001; Human NOV18d 02-OCT-2001; 05-OCT-2001; 09-OCT-2001; 17-OCT-2001; 18-OCT-2001; 22-OCT-2001; 24-OCT-2001; 26-FEB-2004. ADN62902; Matches RESULT 10 ADN62902 \$\$9999999999999999 셤 ò

29-OCT-2001;

obesity,

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binding with the cells own genes and preventing their expression. NOVX
 2001US - 0327435P
2001US - 032743P
2001US - 0327917P
2001US - 0328029P
2001US - 0328044P
2001US - 0328849P
 2001US-0329414P.
2001US-0330142P.
 2001US-0330309P.
2001US-0341058P.
 02-OCT-2002; 2002WO-US031373
 06-NOV-2003 (first entry)
 Query Match
Best Local Similarity 100.
Matches 9, Conservative
 80
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 72 ORIKASKSF
 1 ORIKASKSF
 Sequence 181 AA;
 WO2003029424-A2.
 09-OCT-2001;
09-OCT-2001;
09-OCT-2001;
09-OCT-2001;
12-OCT-2001;
 05-OCT-2001;
05-OCT-2001;
 15-OCT-2001;
17-OCT-2001;
 18-OCT-2001;
22-OCT-2001;
 Homo sapiens
 02-OCT-2001;
 LO-APR-2003
 ADA05736;
 RESULT 11
 ADA05736
 8
 셤
 The invention relates to isolated NOVX polypeptides and polynucleotides. NOVX polypeptides and polynucleotides are used to prevent, diagnose or treat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides. For example, NOVX polypeptides and polynucleotides may be used to treat disorders associated with decreased polynucleotides may be used to creat disorders associated with decreased expression or activity of NOVX by supplementing the patient our production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NOVX polypeptides by
 Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X;
Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM;
Ott T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton B;
Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG;
Shimkets RA, Rothenberg ME, Leach ND, Agee ML, Berghs C, Dipippo VA;
Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 Claim 1; SEQ ID NO 98; 395pp; English.
 19-APR-2002; 200205-0373815P.
19-APR-2002; 200205-0373815P.
19-APR-2002; 200205-0373817P.
19-APR-2002; 200205-037384P.
22-APR-2002; 200205-037384P.
16-MAY-2002; 200205-0381037P.
16-MAY-2002; 200205-0381042P.
16-MAY-2002; 200205-0381042P.
17-MAY-2002; 200205-0381642P.
28-MAY-2002; 200205-0381642P.
28-MAY-2002; 200205-0383656P.
2001US-0346357P
 25-JUN-2002; 2002US-0391335P.
 MILLER C B.
RASTELLI L.
STONE D J.
PENA C B A.
SHENOY S G.
SHINKETS R A.
ROTHENBERG M E.
LEACH M D.
 SPYTEK K A.
EDINGER S R.
ELLERMAN K.
MALYANKAR U M.
 GORMAN L.
ZERHUSEN B D.
ANDERSON D W.
ZHONG M.
 AGEE M L.
BERGHS C.
DIPIPPO V A.
 EISEN A.
GANGOLLI E A.
 RIEGER D K.
SPADERNA S K.
 PATTURAJAN M.
 MILLET I.
PEYMAN J A.
KEKUDA R.
 WPI; 2004-213931/20.
 SMITHSON G.
 N-PSDB; ADN62901
 GUO X.
 35
 (EISE/)
(GANG/)
(RIEG/)
(SPAD/)
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(ORTT/)
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problem of the Certain own general proventing uncertainty which complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of restorative therapy. NOVX polypeptides may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NOVX. The anti-NOVX polypeptide antibodies, agonists and antagonists may also be used to modulate NOVX polymelectide expression and activity of NOVX polypeptide antibodies agonists and antagonists may also be used as diagnostic agents for detecting the presence of NOVX in samples. NOVX polypeptides and polymclectide may be used in this way to prevent, diagnose and treat: metabolic disorders, diabetes, obesity, infectious disorders, Alzheimer's Disease, Parkinson's Disorder; immune disorders, haematopoietic disorders, and the various dyslipidaemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases and various cancer. They may also be used as antibacterial agents. The present sequence of a human NOVX protein.
 human; NOVX; antidiabetic; anorectic; antibacterial; virucide; immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obesity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.
 Gaps
 ..
0
 100.0%; Score 42; DB 8; Length 181; 100.0%; Pred. No. 0.47; ive 0; Mismatches 0; Indels
 ADA05736 standard; protein; 198 AA
 Human NOV18c protein SEQ ID NO:96.
 2001US-0339266P.
2001US-0343629P.
2001US-0349575P.
2001US-0346357P.
 29-OCT-2001;
 24-OCT-2001;
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Gaps

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0; Indels

Mismatches

. 0

9; Conservative

Matches

2002US-0373260P

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Sequence 198 AA;
 19-APR-2002;
19-APR-2002;
22-APR-2002;
16-MAY-2002;
 19-APR-2002;
19-APR-2002;
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ADN62900;
 (SMIT/)
(MILL/)
(PEYM/)
 (JUJJ/)
(LILL/)
(GUOX/)
(PATT/)
 KEKU/)
 RESULT 12
 ADN62900
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 The present invention describes NOVX proteins, where X can be 1 to 55

(e.g. NOV1). Also described: (1) a composition comprising a polypeptide
described above and a carrier; (2) a kit comprising, in one or more
containers, the composition described above; (3) an isolated nucleic acid
molecule which encodes a NOVX protein of the invention; (4) a vector
comprising the nucleic acid molecule described above; (5) a cell
comprising the above vector; (6) an antibody that immunospecifically
binds to the polypeptide described above; (7) methods for determining the
presence or amount of the above polypeptide or nucleic acid molecule in a
sample; (8) methods for determining the presence of or predisposition to
a disease associated with altered levels of expression of the above
polypeptide or nucleic acid molecule in a first mammalian ubject; (9) a
method of identifying an agent that binds to the polypeptide described
above; (10) a method for identifying a potential therappeutic agent for
compression of the above polypeptide or nucleic agent for
aberrant physiological interactions of the polypeptide; (11) a method of
above; (10) a method for identifying a potential therappeutic agent for
compression or aberrant bypasological interactions of the polypeptide; (11) a method of
above; (10) a method for identifying a potential presence or pathology associated with the polypeptide; (12) a method of
corporating of the polypeptide described above; (13) methods of treating
cor preventing a pathology associated with the above polypeptide. NOVX
sequences have antidiabetic, anorectic, antibacterial, virucide,
corporated and and an appropriate or the nucleic
and antilipaemic activities, and can be used in gene therapy. The
colypeptide is useful in manufacturing a medicament for treating a
colypeptide is useful in manufacturing a medicament for treating a
colypeptide is useful in manufacturing a medicament for treating a
cold molecule may be used to dispose, treat or prevent metabolic
collesse, immune disorders, haemacopoletic disorders
 Peyman JA, Kekuda R, Ju C. Malyc...
Edinger SR, Ellerman K, Malyc...
Anderson DW, Zhong M, Catterto..
Pena CEA, Shenoy SG;
 New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
 mapping, tissue typing, preventive medicine and present sequence represents a human NOVX from the
 Smithson G, Millet I, Peyman, Smithson G, Millet I, Peyman, Spturajan M, Spytek KA, Edinger SR, Corturajan M, Spytek KA, Edinger SR, Cortusan L, Scrhusen BD, Anderson DW, Zhous Oft W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Ji K, Rieger DK, Spaderna SK;
 Claim 1; Page 170; 586pp; English
 16-MAY-2002; 2002US-0381042P.
17-MAY-2002; 2002US-0381642P.
28-MAY-2002; 2002US-0383656P.
29-MAY-2002; 2002US-038331P.
25-JUN-2002; 2002US-0331335P.
01-OCT-2002; 2002US-0362511.
 2002US-0373884P.
2002US-0374977P.
2002US-0381037P.
 16-MAY-2002; 2002US-0381038P.
2002US-0373815P
 2002US-0373826P
 probes, in chromosome
 present invention
 N-PSDB; ADA05735
 pharmacogenomics
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Score 42; DB 6; Length 198; Pred. No. 0.51;

100.0%; 100.0%;

Best Local Similarity

Query Match

```
anorexia; cancer; cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X; wasting disorder.
 human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
 ADN62900 standard; protein; 198 AA
 2001US-0328044P.
2001US-0328056P.
2001US-0328849P.
2001US-0329414P.
 2001US-0326483P.
2001US-0327435P.
2001US-0327449P.
2001US-0327917P.
 2001US-0341058P.
2001US-0339266P.
2001US-0343629P.
 2001US-0349575P.
2001US-0346357P.
 01-OCT-2002; 2002US-00262511
 2001US-0328029P
 2001US-0330142P
2001US-0330309P
 2002US-0373260P
2002US-0373815P
 2002US-0373817P
 002US-0373826P
 2002US-0373884P
 2002US-0374977P
 2002US-0381037P
 002US-0381038P
 2002US-0381042P
 2002US-0381642P
 2002US-0383656P
 2002US-0383831P
2002US-0391335P
 01-JUL-2004 (first entry)
 SPYTEK K A.
BDINGER S R.
ELLERMAN K.
MALYANKAR U M.
 91 QRIKASKSF 99
 PATTURAJAN M.
σ
 SMITHSON G.
MILLET I.
PEYMAN J A.
KEKUDA R.
1 QRIKASKSF
 US2004038223-A1.
 15-OCT-2001;
17-OCT-2001;
18-OCT-2001;
 GUO X
 Homo sapiens.
 Human NOV18c.
 09-OCT-2001;
 09-OCT-2001;
 09-OCT-2001;
 22-OCT-2001;
 24-OCT-2001;
 24-OCT-2001;
 01-NOV-2001;
 25-JUN-2002;
 09-OCT-2001;
 29-OCT-2001;
 17-APR-2002;
 19-APR-2002;
 19-APR-2002;
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 16-MAY-2002;
 16-MAY-2002;
 17-MAY-2002;
 26-FEB-2004
 (EDIN/)
(ELLE/)
(MALY/)
```

immunomodulator; cytostatic; nootropic; neuroprotective; antiparkinsonian; antilipaemic; gene therapy; human disease; metabolic disorder; diabetes; obseity; infection; cachexia; cancer; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia.

antidiabetic; anorectic; antibacterial; virucide;

Human NOV18g protein SEQ ID NO:104.

human; NOVX;

06-NOV-2003 (first entry)

ADA05744;

ADA05744 standard; protein; 224 AA

RESULT 13

ADA05744

91 ORIKASKSF 99

a

QRIKASKSF

-1

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Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X; Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E, Ji W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen A, Gangolli EA, Rieger DK, Spaderna SK;
 Isolated NOVX polypeptides and nucleic acids, useful for preventing, . diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 100.0%; Score 42; DB 8; Length 198;
100.0%; Pred. No. 0.51;
tive 0; Mismatches 0; Indels
 Claim 1; SEQ ID NO 96; 395pp; English.
 MILLER C E.
RASTELI L.
STONE D J.
PENA C E A.
SHENOY S G.
SHENOY S G.
STINKETS R A.
ROTHENBERG M E.
 EISEN A.
GANGOLLI E A.
RIEGER D K.
SPADERNA S K.
 AGEE M L.
BERGHS C.
DIPIPPO V A.
 ZERHUSEN B D.
ANDERSON D W.
 WPI; 2004-213931/20.
 CATTERTON E.
 N-PSDB; ADN62899.
 ZHONG M.
 Sequence 198 AA;
 (EISE/)
(GANG/)
(RIEG/)
(SPAD/)
(ORTT/)
(GORM/)
(ZERH/)
(ANDE/)
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(JIWW/)
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The invention relates to isolated NoVX polypeptides and polymucleotides. NoVX polypeptides and polymucleotides are used to prevent, diagnose or novX polypeptides and polymucleotides are used to prevent, diagnose or creat a medical condition in human related to the aberrant expression and activity of NoVX polypeptides. For example, NoVX polypeptides and controlled to the administered to down regulate expression of NoVX polypeptides by production or to rectify mutations. Conversely, antisense NA molecules may be administered to down regulate expression of NoVX polypeptides by binding with the cells own genes and preventing their expression. NoVX polypeptides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of crestorative therapy. NoVX polypeptides may also be used as intigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of NoVX. The cust of modulate NoVX polypeptide antibodies, agonists and antagonists and antagonists and the expression and activity of NoVX polypeptides. The anti-NoVX polypeptide antibodies, agonists may also be used as diagnose and treat: metabolic disorders, diabetes, obesity, infectious disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, ciscurer, cancer_associated cachexia, neurodegemerative disorders, Alzheimer's Disease, Parkinson's Disorder, immune disorders, cancer_associated with obesity, the metabolic cachexia, and the various dyslipidaemias, metabolic wasting disorders associated with obesity, the metabolic cachesian and various cancers. They may also be used as antibacterial agents. The present sequence of a human NoVX protein.
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2001US-0349575P. 2001US-0346357P. 2002US-0373260P. 2002US-0373815P.

29-OCT-2001; 01-NOV-2001;

17-APR-2002; 19-APR-2002; 19-APR-2002;

2002US-0373817P. 2002US-0373826P. 2002US-0373884P.

2002US-0374977P 2002US-0381037P 2002US-0381038P 2002US-0381042P

22-APR-2002; 16-MAY-2002;

16-MAY-2002; 16-MAY-2002; 17-MAY-2002;

2001US-0328849P. 2001US-0329414P. 2001US-0330142P.

12-OCT-2001; 2 15-OCT-2001; 2 17-OCT-2001; 2

22-OCT-2001;

18-OCT-2001; 24-OCT-2001; 24-OCT-2001;

09-OCT-2001;

02-OCT-2002; 2002WO-US031373

02-OCT-2001;

WO2003029424-A2.

10-APR-2003

Dipippo VA;

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A, Shenoy SG;
Berghs C, Dipippo VA;
 Smithson G, Millet I, Peyman JA, Kekuda R, Ju J, Li L, Guo X, Patturajan M, Spytek KA, Edinger SR, Ellerman K, Malyankar UM; Ort T, Gorman L, Zerhusen BD, Anderson DW, Zhong M, Catterton E; Ni, W, Miller CE, Rastelli L, Stone DJ, Pena CEA, Shenoy SG; Shimkets RA, Rothenberg ME, Leach MD, Agee ML, Berghs C, Dipippo Eisen AJ, Gangolli EA, Rieger DK, Spaderna SK;
 (CURA-) CURAGEN CORP.
 WPI; 2003-381626/36.
N-PSDB; ADA05743.
ö
 Gaps
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9; Conservative

Best Local Similarity Matches 9; Conserv

Query Match

26-FEB-2004

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The present line present line presents when the present line present and a carrier; (2) a kit comprising in one or more containers, the composition described above; (3) an isolated nucleic acid molecule which encodes a NOVX protein of the invention; (4) a vector comprising the nucleic acid molecule described above; (5) a cell comprising the nucleic acid molecule described above; (5) a cell comprising the polypeptide described above; (7) methods for determining the presence or amount of the above polypeptide or nucleic acid molecule in a sample; (8) methods for determining the presence of or predisposition to a disease associated with altered levels of expression of the above polypeptide or nucleic acid molecule in a first mammalian subject; (9) a method of identifying an agent that binds to the polypeptide described above; (10) a method for identifying a potential therapeutic agent for use in treating a pathology that is related to an aberrant expression or a berrant physiological interactions of the polypeptide; (11) a method of screening for a modulator of activity or of latency or predisposition to can pathology associated with the polypeptide; (12) a method for modulating the activity of the polypeptide above polypeptide. NoVX sequences have antidiabetic, anorectic, antibacterial, virucide, or mammal; and (14) a method for producing the above polypeptide. NoVX sequences have antidiabetic, anorectic, antibacterial, virucide, and antilipaemic activities, and can be used in gene therapy. The polypeptide is useful in manufacturing a medicament for treating a colypeptide is useful in manufacturing a medicament for treating a colypeptide is useful in manufacturing a medicament for treating a colypeptide.
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 anorexia; cancer, cancer-associated cachexia; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; immune disorder; haematopoietic disorder; dyslipidaemia; metabolic syndrome X;
New NOVX polypeptides and nucleic acids, useful for diagnosing, preventing or treating NOVX-associated disorders, e.g. diabetes, obesity, cancer or dyslipidemia, and in chromosome mapping, tissue typing or
 acid molecule may be used to diagnose, treat or prevent metabolic disorders such as diabetes or obesity, infections, cachexia, cancer, neurodegenerative disorders such as Alzheimer's disease or Parkinson's disease, immune disorders, haematopoietic disorders and various dyslighdeamias. The nucleic acids can also be used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. The present sequence represents a human NOVX from the
 human; NOVX; metabolic disorder; diabetes; obesity; infectious disease;
 present invention describes NOVX proteins, where X can be 1 to 55
 Gaps
 ö
 100.0%; Score 42; DB 6; Length 224; 100.0%; Pred. No. 0.58; cive 0; Mismatches 0; Indels
 ADN62908 standard; protein; 224 AA.
 Claim 1; Page 172; 586pp; English
 01-JUL-2004 (first entry)
 Local Similarity 100.
les 9; Conservative
 77 ORIKASKSF 85
 σ
 QRIKASKSF
 present invention.
 wasting disorder
 pharmacogenomics
 Sequence 224 AA;
 US2004038223-A1
 Human NOV18g.
 Homo sapiens.
 ADN62908;
 Query Match
 Matches
 RESULT 14
 ADN62908
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Catterton E;
 Kekuda R, Ju J, Li L, L., The Line of the Control o
 לאר Caure.
Zhong M, Caure.
מואל Shenoy SG;
 Pena CEA,
 Peyman JA, Kekuda k, v.v.,
KA, Edinger SR, Ellerman K,
husen BD, Anderson DW, Zhong
 2001US-03290179
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2002US-0383831P.
 25-JUN-2002; 2002US-0391335P
 EISEN A.
GANGOLLI E A.
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 ELLERMAN K.
MALYANKAR U M.
 GUO X.
PATTURAJAN M.
 SPADERNA S K.
 SPYTEK K A.
EDINGER S R.
 ZERHUSEN B D.
ANDERSON D W.
 MILLET I.
PEYMAN J A.
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 SMITHSON G.
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BERGHS C.
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 09-OCT-2001;
09-OCT-2001;
12-OCT-2001;
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18-OCT-2001;
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 22-APR-2002;
 16-MAY-2002;
 16-MAY-2002;
 16-MAY-2002;
 28-MAY-2002;
 29-MAY-2002;
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Berghs C, Dipippo VA;

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The invention relates to isolated NOVX polypeptides and polynucleotides.

NOVX polypeptides and polynucleotides are used to prevent, diagnose or creat a medical condition in human related to the aberrant expression and activity of NOVX polypeptides and activity of NOVX polypeptides and activity of NOVX by supplementing the patient our crecify mutations. Conversely, antisense NA molecules can be administered to down regulate expression of NOVX polypeptides by binding with the cells own genes and preventing their expression. NOVX polymericleotides and complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar sequences in samples, and so which patients may be in need of crestorative therapy. NOVX polypeptides may also be used as mrigens in the production of antibodies and in assays to identify modulators crestorative therapy. NOVX polypeptides may also be used as mrigens in the production of antibodies, agonists and activity of NOVX. The anti-NOVX polypeptide antibodies, agonists and antagonists of the expression and activity of NOVX polypeptides. The anti-NOVX polypeptide antibodies agonists and polymercetide may also be used as diagnose and polymucleotide expression and activity of NOVX polypeptides. The anti-NOVX polypeptide antibodies may also be used as diagnose and treat: metabolic disorders, induced cachexia, neurodegenerative disorders, anorexia, cancer, cancer-associated cachexia, neurodegenerative disorders, and the various dyslipidaemia, metabolic disorders, and the various dyslipidaemia, metabolic disorders, and the various dyslipidaemia, metabolic disorders associated with obesity, the metabolic syndrome X and entered and antibodies and the arrious disturbances associated with chronic diseases and entered and the various desarrious disturbances associated with chronic diseases and entered and the various desarrious disturbances associated with chronic diseases and entered and the various desarrious desarrious desarrious desarrious desa
 Isolated NOVX polypeptides and nucleic acids, useful for preventing, diagnosing and treating e.g. cancer, diabetes and Alzheimer's disease.
 They may also be used as antibacterial agents. The present sequence
 represents the amino acid sequence of a human NOVX protein.
W. Rothenberg ME, Leach MD, Agee ML,
Gangolli EA, Rieger DK, Spaderna SK;
 Claim 1; SEQ ID NO 104; 395pp; English
 WPI; 2004-213931/20
 N-PSDB; ADN62907
Shimkets RA,
 Eisen A,
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Sequence 224 AA;

Gaps . 0 100.0%; Score 42; DB 8; Length 224; 100.0%; Pred. No. 0.58; tive 0; Mismatches 0; Indels 9; Conservative Query Match Best Local Similarity Matches

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ORIKASKSF 85 6 1 QRIKASKSF 11 g

AAB98502 standard; protein; 225 AA. 03-AUG-2001 (first entry) AAB98502; 

Human Stratum Corneum Chymotryptic Enzyme, SCCE, catalytic domain.

Human; TADG-15; cytostatic; vaccine; ovarian tumour; cancer; tumour antigen-derived gene 15; serine protease; Stratum Corneum Chymotryptic Enzyme; SCCE.

Homo sapiens.

#0200129056-A1.

26-APR-2001.

20-OCT-2000; 2000WO-US029095.

```
The present invention relates to human tumour antigen-derived gene 15 (TADG-15) protein and coding sequence (see AAH23601 and AAB98600). TADG-15 is an extracellular serine protease. It was found that TADG-15 is over-expressed in ovarian tumours. TADG-15 protein or its fragments of 9-20 residues that lack TADG-15 protease activity are useful for vaccinating an individual against TADG-15, having, suspected of having or at risk of getting cancer. Furthermore, the TADG-15 gene can be used as a diagnostic or therapeutic target in cancer. The present sequence was used in a sequence homology alignment with the catalytic domain of TADG-15
 Novel extracellular serine protease, termed tumor antigen-derived gene : protein overexpressed in carcinomas and DNA encoding it, for diagnosis, treatment, prevention of cancer, particularly breast, ovarian cancer.
 Gaps
 ö
 100.0%; Score 42; DB 4; Length 225; 100.0%; Pred. No. 0.58; ive 0; Mismatches 0; Indels
 Example 10; Fig 1; 130pp; English
 99US-00421213.
 9; Conservative
 Tanimoto
 (UYAR-) UNIV ARKANSAS
 63 ORIKASKSF 71
 1 QRIKASKSF 9
 WPI; 2001-381031/40.
 Local Similarity
 Sequence 225 AA;
 20-OCT-1999;
 O'brien TJ,
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Search completed: July 13, 2005, 17:19:57 Job time : 77.6667 secs

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| GenCore | (c) 1993  |  |
|         | Copyright |  |
|         |           |  |

OM protein - protein search, using sw model

Run on:

July 13, 2005, 16:54:03; Search time 13.5556 Seconds (without alignments) 63.882 Million cell updates/sec

US-09-905-083A-99 42 1 QRIKASKSF 9 Title:

Perfect score: Sequence:

Scoring table:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## CITAMADIES

|           | Description    | serine proteinase | protein_T24A6.11 ( | kallistatin precur | probable DNA-direc | tetrachloro-p-hydr | beta-SNAP protein | mak16-like protein | probable phosphate | BET1 protein - yea | probable p-loop AT | probable dehydroge | hypothetical prote | hypothetical prote | ш      | lactococcal endope | endopeptidase PepO |        | pyruvate dehydroge | probable ubiquitin | dystrophin, muscle | hypothetical prote | 16K protein - toba | NADH2 dehydrogenas | hypothetical prote | thiogalactoside ac | thiogalactoside ac | quinolinate phosph | WD repeat protein | hypothetical prote |
|-----------|----------------|-------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|
| SUMMARIES | DI.            | A53968            | D89004             | A49518             | D72571             | A40625             | S32368            | T50147             | F81409             | C39610             | C71463             | H97051             | T48159             | T40129             | C86850 | A47098             | F53290             | T19678 | D82776 ·           | H84545             | S02041             | AF2269             | B46322             | H81251             | C64176             | C90678             | G85528             | E84339             | 25                | T22587             |
|           | DB             | 7                 | ~                  | ~                  | ~                  | ~                  | ~                 | ~                  | ~                  | ~                  | ~                  | N                  | N                  | ~                  | ~      | ~                  | ~                  | 7      | ~                  | ~                  | Н                  | 7                  | -                  | ~                  | 7                  | ~                  | ~                  | N                  | ~                 | 7                  |
|           | Length         | 253               | 373                | 427                | 895                | 248                | 298               | 302                | 362                | . 142              | 321                | 331                | 427                | 517                | 627    | 627                | 627                | 875    | 985                | 1102               | 3660               | 65                 | 141                | 172                | 182                | 203                | 203                | 268                | 349               | 368                |
| d         | Query<br>Match | 100.0             | 81.0               | 78.6               | 76.2               | 73.8               | 73.8              | 73.8               | 73.8               | 71.4               | 71.4               | 71.4               | 71.4               | 71.4               | 71.4   | 71.4               | 71.4               | 71.4   | 71.4               | 71.4               | 71.4               | 69.0               | 0.69               | 69.0               | φ.                 | ę,                 | 69.0               | ٩.                 | •                 | 69.0               |
|           | Score          | 42                | 34                 | 33                 | 32                 | 31                 | 31                | 31                 | 31                 | 30                 | 30                 | 30                 | 30                 | 30                 | 30     | 30                 | 30                 | 30     | 30                 | 30                 | 30                 | 29                 | 29                 | 29                 | 29                 | 29                 | 29                 | 29                 | 29                | 29                 |
|           | Result<br>No.  |                   | 8                  | m                  | 4                  | ល                  | 9                 | 7                  | æ                  | σı                 | 10                 | 11                 | 12                 | 13                 | 14     | 15                 | 16                 | 17     | 18                 | 19                 | 20                 | 21                 | 22                 | 23                 | 24                 | 25                 | 56                 | 27                 | 28                | 29                 |

Cipacesion: D89004

Rianonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www\_sanger.ac.uk/Projects/C\_elegans/ A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Notecule type: DNA
A;Restdus: preliminary
A;Residues: 1-373 <STO>

protein T24A6.11 [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004

A,Cross-references: UNIPROT: 061942; GB:chr V; PIDN:AAC17798.1; PID:g3168946; GSPDB:GN000; A;Note: contains similarity to C4-type zinc fingers C;Genetics: A;Genetics: A;Genet

| aspartyl/asparagin | phosphogluconate d | probable helicase | hypothetical prote | hypothetical prote | calicin - human (f | hypothetical prote | hypothetical prote | DNA topoisomerase | hypothetical prote | hypothetical prote | probable membrane | projectin - fruit | hypothetical prote | projectin - fruit | projectin - fruit |
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| G97300             | JC5282             | G71081            | B82883             | T48273             | 137216             | AB2028             | T46476             | AC1419            | E86294             | C86168             | S67164            | A40985            | T15297             | S24600            | T13931            |
| N                  | ~                  | н                 | ~                  | ~                  | ~                  | ~                  | ~                  | 7                 | 0                  | ~                  | N                 | ~                 | ~                  | 0                 | 7                 |
| 463                | 484                | 526               | 563                | 584                | 585                | 699                | 691                | 717               | 738                | 743                | 759               | 940               | 1018               | 1742              | 6658              |
| 69.0               | 0.69               | 0.69              | 0.69               | 0.69               | 0.69               | 0.69               | 69.0               | 0.69              | 0.69               | 0.69               | 69.0              | 0.69              | 69.0               | 69.0              | 69.0              |
| 29                 | 29                 | 29                | 29                 | 53                 | 29                 | 53                 | 53                 | 53                | 29                 | 29                 | 53                | 53                | 59                 | 53                | 29                |
| 30                 | 31                 | 32                | 33                 | 34                 | 35                 | 36                 | 37                 | 38                | 39                 | 40                 | 41                | 42                | 43                 | 44                | 45                |

## ALIGNMENTS

| A53968  A53968  Berine proteinase SCCE precursor - human NyAlternate names: stratum corneum chymotryptic enzyme C;Species: Homo sapiens (man) C;Decies: 10-Jul-1995 #texy C;Accession: A53968 R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Walbrand J. Biol. Chem. 269, 19420-19426, 1994 A;Title: Cloning, expression, and characterization of s A;Reference number: A53968; MUID: 94308225; PMID: 8034709 A;Accession: A53968 A;Accession: A53968 A;Residues: 1-253 cHAN> A;Residues: 1-253 cHAN> A;Residues: 1-253 cHAN> A;Cenetics: C;Genetics: A;Genetics: A;Genetics: A;Genetics: C;Genetics: C;Genetics: A;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: C;Genetics: A;Genes: Trypsin; trypsin; homology C;Soperfamily: trypsin; trypsin homology C;Soperfamily: trypsin; ho                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Assisted serine proteinase SCCE precursor - human NyAlternate names: stratum corneum chymotryptic enzyme CiSpecies: Homo sapiens (man) CiSpecies: Homo sapiens (man) CiAccession: A53968 R;Hansson, L.; Stroemqvist, M.; Baeckman, A.; Wallbrandt, P.; Carlstein, A.; Egelrud, T. A; Biol. Chem. 269, 1942-019426, 1994 A; Hitle: Cloning, expression, and characterization of stratum corneum chymotryptic enzyme A; Reference number: A53968; MUID: 94308225; PMID: 8034709 A; Recession: A53968 A; Recession: A53068 A; Recess |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 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| serine proteinase SCCE precursor - hu N;Alternate names: stratum corneum ch C;Species: Homo sapiens (man) C;Date: 07-Jul-1995 #sequence_revisio C;Accession: A53968 R;Hansson, L.; Stroemgvist, M.; Baeck J. Biol. Chem. 269, 19420-19426, 1994 A;Title: Cloning, expression, and cha A;Reference number: A53968; MUID:9430 A;Accession: A53968 A;Reference number: A53968; MUID:9430 A;Reference number: A53968; MUID:9430 A;Reference number: A53968 A;Residues: 1-253 < HAN> A;Residues: 1-253 < HAN> A;Residues: 1-253 < HAN> A;Gence 1-253 < HAN> A;Cross-references: UNIPROT:P49862; G C;Gentics: A30-245/Domain: trypsin; homol C;Superfamily: trypsin; trypsin homology < TR Ouery Match Best Local Similarity 100.0%; pr                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           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| N'Alternate names: stratum corneum C'Species: Homo sapiens (man) C'Sbecies: Homo sapiens (man) C'Sbecies: Homo sapiens (man) C'Date: 07-Jul-1995 #sequence_revisio C'Accession: A51968 R;Hansson, L.; Stroemqvist, M.; Baeck J. Balol. Chem. 269, 19420-19426, 1994 A;Title: Cloning, expression, and cha A;Recession: A53968 A;Retus: preliminary A;Moccule type: mRNA A;Mocule type: mRNA A;Residues: 1-253 <4HAN A;Residues: 1-253 <4HAN A;Residues: 1-253 <4HAN A;Cross-references: UNIPROT: P49862; G C;Genetics: A;Gene: GDB: PRSS6; SCCE A;Gene: GDB: PRSS6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              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chymotryptic enzyme 4308225; PMID:8034709 ; GB:L33404; NID:g521214; PIDN:AAC37551.1; PID:g532504 chypy chypy                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             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| C; Species: Homo sapiens (man) C; Dates: 07-Jul-1995 #sequence_revisio C; Dates: 07-Jul-1995 #sequence_revisio C; Accession: A53968 R; Hansson, L.; Stroemqvist, M.; Baeck J. Biol. Chem. 269, 19426, 1994 A; Title: Cloning, expression, and cha A; Reference number: A53968; MuID:9430 A; Reference number: A53968; MuID:9430 A; Residues: preliminary A; Molecule type: mRNA A; Residues: 1-253 cHAN> A; Cross-references: UNIPROT: P49862; G C; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: C; Genetics: A; Genetics: C; Genetics: C; Genetics: A; Genetics: C; Genetics: C; Genetics: A; Genetics: A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     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| C;Date: 07-Jul-1995 #sequence_revisio C;Accession: A53968 R;Hansson, L.; Stroemqvist, M.; Baeck J. Biol. Chem. 269, 19420-19426, 1994 A;Title: Cloning, expression, and cha A;Reference number: A53968; MUID:9430 A;Accession: A53968 MUID:9430 A;Accession: A53968 MUID:9430 A;Accession: A53968 MUID:9430 A;Accession: A53968 MUID:9430 A;Residues: 1-253 cHAN>A;Residues: 1-253 cHAN>A;Residues: 1-253 cHAN>A;Genetices: UNIPROT:P49862; G;Genetices: GDB:77730 A;Gene: GDB:PRSS6; SCCE A;Gene: GDB:77730 A;Map position: Trypsin; trypsin homology cTR Guery Match Cocal Similarity 100.0%; Pr                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                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Chem. 269, 19420-19426, 1994 A; Title: Cloning, expression, and cha A; Recession: A53968 A; Retue: preliminary A; Mocleule type: mRNA A; Residues: 1-253 «HANA A; Residues: 1-253 «HANA A; Gene: GDB: PRSS6; SCCE A; Cross-references: GDB: 377730 A; Map position: 7435-7435 C; Superfamily: trypsin; trypsin homology «TR Couery Match Cuery Match Est Local Similarity 100.0%; Pr                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     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| 4308225; PMID:B034709<br>; GB:L33404; NID:G521214; PIDN:AAC37551.1; PID:G532504<br>mology<br><try></try>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               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| A:Accession: A53968 A;Status: preliminary A;Wolecule type: mRNA A;Rossoures: 1-253 «HAN> A;Conetics: C;Genetics: DNIPROT:P49862; G C;Genetics: GDB:PRSS6; SCCE A;Gene: GDB:PRSS6; SCCE A;Grosreferences: GDB:377730 A;Map position: 7q35-7q35 C;Superfamily: trypsin; trypsin homol C;Superfamily: trypsin; trypsin homol C;Superfamily: trypsin; trypsin homol C;Superfamily: trypsin; trypsin homology «TR C;Uery Match Best Local Similarity 100.0%; Pr                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             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| A.Status: preliminary A.Molecule type: mRNA A.Residues: 1-233 «HANA A.Residues: 1-233 «HANA A.Cross-references: UNIPROT: P49862; G C.Genetics: A.Gene: GDB: PRSS6; SCCE A.Gene: GDB: PRSS6; SCCE A.Gross-references: GDB: 377730 A.Molecule position: 7435-7435 C.Superfamily: trypsin; trypsin homol F;30-245/Domain: trypsin; homology «TR Couery Match Best Local Similarity 100.0%; Pr                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             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| A Molecule type: mRNA A, Rolecule type: mRNA A, Rossidues: 1.253 «HAN> A, Cross = references: UNIPROT: P49862; G C, Genetics: A, Gene: GDB: PRSS6; SCCE A, Gene: GDB: PRSS6; SCCE A, Gene: GDB: 377730 A, Map position: 7435-7435 C, Superfamily: trypsin; trypsin homology «TR F; 30-245/Domain: trypsin homology «TR Query Match Best Local Similarity 100.0%; Pr                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    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Score 34; DB: Pred. No. 9.3; 1; Mismatches

81.0%; 77.8%;

Query Match Best Local Similarity 7; Conserv?

A; Map position: 5

Conservative

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A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-427 <CHA>

Molecule type: DNA Residues: 1-427 <CH2>

Gene: GDB:P14; KLST

Accession: A45093

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awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ku
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyri
A;Reference number: A72450; MUID:99310339; PMID:10382966
 tetrachloro-p-hydroquinone reductive dehalogenase (EC 1.....) - Flavobacterium sp.
NyAlternate names: glutathione S-transferase homolog; TeCH reductive dehalogenase
C;ppecies: Flavobacterium sp.
C;baces: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C;Accession: A40625
R;Orser, C.S.; Dutton, J.; Lange, C.; Jablonski, P.; Xun, L.; Hargis, M.
J. Bacteriol. 175, 2640-2644, 1993
A;Fitle: Characterization of a Flavobacterium glutathione S-transferase gene involved rec
 A;Cross-references: UNIPROT:Q9YAU1; DDBJ:AP000062; NID:g5105244; PIDN:BAA80857.1; PID:g51
A;Experimental source: strain Kl
 T.; Buhrow, S.A.; Rothn
 beta-SNAP protein - bovine
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Accession: S32268
R;Whiteheart, S.W.; Griff, I.C.; Brunner, M.; Clary, D.O.; Mayer, T.; Buhrow, S.A.
Nature 362, 353-355, 1993
A;Title: SNAP family of NSF attachment proteins includes a brain-specific isoform.
A;Reference number: S32367; MUID:93205122; PMID:8455721
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 A;Residues: 1-248 <ORS>
A;Cross-references: GB:M98559; NID:g148689; PIDN:AAA24921.1; PID:g148690
A;Experimental source: ATCC 39723
A;Note: sequence extracted from NCBI backbone (NCBIN:130432, NCBIP:130433)
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 Length 895;
 C; Superfamily: Halobacterium DNA-directed RNA polymerase chain
 2; Length 248;
 Length 298,
 Indels
 Indels
 1; Indels
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 A;Residues: 1-298 «WHI>
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C;Superfamily: alpha-soluble NSF attachment protein
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 5,
 / Match 73.8%; Score 31; DB Local Similarity 66.7%; Pred. No. 30; nes 6; Conservative 2; Mismatches
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A;Status: preliminary
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 227 QRMKARRSF 235
 ||:||||:
885 QRVKASKA 892
 C; Keywords: oxidoreductase
 1 ORIKASKS 8
 1 ORIKASKSF
 A,Accession: D72571
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-895 <KAW>
 A, Accession: S32368
A, Status: preliminary
A, Molecule type: mRNA
 A; Gene: APE1853
 Query Match
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Matches
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 C;Species: Homo sapiens (man)
C;Species: 10-Nov-1995 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: A49518; A55560; Ā45093
R;Chal, K.X.; Chen, L.M.; Chao, J.; Chao, L.
J. Biol. Chem. 268, 24498-24505, 1993
A;Title: Kallistatin: a novel human serine proteinase inhibitor. Molecular cloning, tiss A;Reference number: A49518; MUID:94043294; PMID:8227002
A;Accession: A49518
 A;Cross-references: UNIPROT:P29622; GB:L19684; NID:g425145; PIDN:AAA59454.1; PID:g425146 R;Chai, K.X.; Ward, D.C.; Chao, J.; Chao, L. Genomics 23, 370-378, 1994 A;Title: Molecular cloning, sequence analysis, and chromosomal localization of the human A;Reference number: A55560; MUID:95137583; PMID:7835886
 A)Cross-references: GB:L28101, NID:g609489; PIDN:AAC41706.1; PID:g619783
R;Zhou, G.X.; Chao, L.; Chao, J.
Biol. Chem. 267, 25873-25880, 1992
A;Title: Kallietatin: a novel human tissue kallikrein inhibitor. Purification, character A)Reference number: A45093; MUID:93100304; PMID:1334488
 A, Cross-references: GDB:266537; OMIM:147935
A; Map position: 14q31-14q32.1
A; Map position: 14q31-14q32.1
C; Superfamily: Serpin
C; Superfamily: Serpin
C; Superfamily: Serpin
C; Superfamily: Serpin
C; Serpin
C; F21-20/Domain: signal sequence #status predicted <SIG>F31-20/Domain: signal sequence #status predicted <MAT>F31-427/Product: kallistatin #status predicted <MAT>F31-427/Product: kallistatin #status predicted <MAT>F31/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted F;33,108,157,238/Binding site: carboxydrate (Asn) (covalent) #status predicted F;388/Inhibitory site: Phe (tissue kallikrein) #status experimental
 C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: D72571
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
 probable DNA-directed RNA polymerase subunit A' APE1853 - Aeropyrum pernix (strain K1)
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 kallistatin precursor – human
N.Alternate names: proteinase inhibitor 4; tissue kallikrein inhibitor
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 Status: preliminary; not compared with conceptual translation
 78.6%; Score 33; DB 2; Length 427; 66.7%; Pred. No. 18; tive 3; Mismatches 0; Indels
 Length 373;
 Indels
 Molecule type: protein

Ameldues: 389-403 «ZMO»

(Croses: 389-403 «ZMO»

(Croses: Pederonces: PIDN: PID: G261993

Note: Requence extracted from NCBI backbone (NCBIP:120847)
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Best Local Similarity 66.7 Matches 6; Conservative

Query Match

QKLEASKSF 363

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RESULT 4

1 QRIKASKSF 9

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A;Residues: 1-142 <ROW>
A;Cross-references: 0B:Z47047; EMBL:Z38113; NID:g603997; PID:g763342; MIPS:YIL004c
A;Cross-references: 0B:Z47047; EMBL:Z38113; NID:g603997; PID:g763342; MIPS:YIL004c
X-0581 11, 61-78, 1995
A;Tille: Nucleotide sequence and analysis of the centromeric region of yeast chromosome 1
A;Reference number: S50795; MUID:95282515; PMID:7762303
 A,Residues: 1-321 <ARN>
A,Cross-references: UNIPROT:084847; GB:AE001357; GB:AE001273; NID:g3329311; PIDN:AAC6843;
A,Experimental source: serotype D, strain UW-3/Cx
 probable dehydrogenase, YULF B. subtilis ortholog [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
 C;Accession: C71463
K:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia track A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Title: Identification and structure of four yeast genes (SLY) that are able to suppress A;Reference number: A39610, MUID:91117254; PMID:1990290
 A;Residues: 1-142 <VOS>
A;Cross-references: EMBL:X79743
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994
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 probable p-loop ATPase - Chlamydia trachomatis (serotype D, strain UW3/Cx) C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
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0; Mismatches 1; Indels
 Length 321;
 1; Indels
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F;126-142/Domain: transmembrane #status predicted <TMM>
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Pred. No. 65;
2; Mismatches
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A;Gross-references: SGD:S0001266; MIPS:YIL004c
A;Map position: 9L
 71.4%;
66.7%;
 y Match 71.4%;
Local Similarity 87.5%;
les 7; Conservative (
 Query Match 71.4
Best Local Similarity 66.7
Matches 6; Conservative
 ORIKALKS 74
 QRIKASKS 8
 1 QRIKASKSF
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277 ERLVASKSF
 A;Status: preliminary
 A; Accession: C71463
 Query Match
 RESULT 10
 Matches
 RESULT 11
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 C;Accession: F81409
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.w.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel A;tute. 403, 655-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyph. Reference number: A81250; MUID:20150912; PMID:10688204
 A;Residues: 1-362 <PAR>
A;Cross-references: UNIPROT:Q9PHQ2; GB:AL139075; GB:AL111168; NID:g6967817; PIDN:CAB7525
A;Experimental source: serotype O2, strain NCTC 11168
 ;Cross-references: UNIPROT:Q9UTE6; EMBL:AL112798; PIDN:CAB60698.1; GSPDB:GN00066; SPDB:
Experimental source: strain 972h(-); cosmid c222
 robable phosphate transport system permease protein Cj0615 [imported] - Campylobacter
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 R;Hamlin, N.; Churcher, C.M.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, November 1999
A;Reference number: 225043
A;Accession: T50147
 BET1 protein - yeast (Saccharomyces cerevisiae)
NiAlternate names: protein YIA4c; protein YIL004c; SLY12 protein
CiSpecies: Saccharomyces cerevisiae
CiSpecies: Saccharomyces cerevisiae
CiSpecies: 13-Sep-1991 #sequence_revision 13-Sep-1991 #text_change 09-Jul-2004
CiAccession: C35610; S48453; S58677
Mol. Cell. Biol. 11, 872-885, 1992.
 C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 12-Jul-2004
C;Accession: T50147
 process. Campylobacter jejuni
C;Species: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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 mak16-like protein [imported] - fission yeast (Schizosaccharomyces pombe)
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 73.8%; Score 31; DB 2; Length 362; 77.8%; Pred. No. 43; Live 1; Mismatches 1; Indels
 Length 302;
 Indels
 Status: preliminary; translated from GB/EMBL/DDBJ
 73.8%; Score 31; DB 2; 66.7%; Pred. No. 36;
 Superfamily: ribosomal biogenesis protein MAK16
 2; Mismatches
 Conservative
 Conservative
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 ORIKLSKAY 86
 1 QRIKASKSF 9
 1 ORIKASKSF 9
 ORIKASKSF 9
 Best Local Similarity
Matches 6; Conserv
 Best Local Similarity
Matches 7; Conserv
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Gene: SPDB:SPAC222.06
 A;Status: preliminary
A;Molecule type: DNA
 A,Gene: pstA; Cj0615
 A; Accession: F81409
 A; Map position: 1
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Job time : 15.5556 secs
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570 RMKASKEF 577
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Matches 6; Conserva
 2 RIKASKSF 9
 2 RIKASKSF 9
 Query Match
Best Local Similarity
Matches 7; Conserv
 A, Accession: C86850
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-627 <STO>
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 A; Gene: pepO
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 Rivolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4839, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900, MUID:21359325, PMID:21359325
A;Accession: H97051
A;Accession: H97051
A;Restdue: preliminary
A;Molecule type: DNA
A;Residues: 1-331 <KUR>A;Accession: GB:AE001437; PIDN:AAK79203.1; PID:g15024156; GSPDB:C C;Genetics:
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 hypothetical protein T1008.80 - Arabidopsis thaliana (c)Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48159
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Lemcke, K.; Mayer, Submitted to the Protein Sequence Database, March 2000
A;Recence number: 224486
A;Accession: T48159
A;Accession: T48159
A;Accession: T48159
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-427
A;Residues: 1-427
A;Cross-references: UNIPROT:Q9M035; EMBL:All61746
A;Experimental source: cultivar Columbia; BAC clone T1008
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 hypothetical protein SPBC2F12.12c - fission yeast (Schizosaccharomyces pombe)
 C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40129
R;Wood, V; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
A;Reference number: Z21907
A;Accession: T40129
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 Length 331;
 1; Indels
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 Score 30; DB 2;
Pred. No. 87;
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C,Superfamily: Escherichia coli ygjR protein
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 140 RRVKASVSF 148
 303 ORLKVSKS 310
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Best Local Similarity
6; Conserv?
 1 ORIKASKSF 9
 A;Gene: SPDB:SPBC2F12.12c
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C;Accession: H97051
 A; Map position: 5
A; Introns: 317/1
A; Note: T1008.80
 RESULT 12
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neutral endopeptidase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Aar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Aacession: C86650
R;Bolotin, A.; Mincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic Genome Res. 11, 731-753, 2001
A;Fitle: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssg. A;Reference number: A86625; MUID:21235186; PMID:11337471
 C,Accession: A47098
R;Mierau, I.; Tan, P.S.T.; Haandrikman, A.J.; Kok, J.; Leenhouts, K.J.; Konings, W.N.; Ve
J. Bacteriol. 175, 2087-2096, 1990
A;Fitle: Cloning and sequencing of the gene for a lactococcal endopeptidase, an enzyme wj
A;Reference number: A47098; MUID:93209954; PMID:8458851
A;Accession: A47098
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-627 <MIE>
 A;Cross-references: UNIPROT:Q07744; GB:AE005176; PID:g12724829; PIDN:AAK05901.1; GSPDB:GRA;Experimental source: strain IL1403
C;Genetics:
 lactococcal endopeptidase (EC 3.4...) - Lactococcus lactis subsp. cremoris (strain P8-2-C;Species: Lactococcus lactis subsp. cremoris
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
 A;Cross-references: UNIPROT:Q09145; GB:L04938; NID:g293013; PIDN:AAA25204.1; PID:g293015
C;Genetics:
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Score 30; DB 2; Length 517;
Pred. No. 1e+02;
 Query Match 71.4%; Score 30; DB 2; Length 627; Best Local Similarity 75.0%; Pred. No. 1.38+02; Matches 6; Conservative 1; Mismatches 1; Indels
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C;Keywords: hydrolase; oligopeptide transport
 71.48;
77.88;
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campylobact bacteroides parachlamyd acrasis ros xanthomonas

sphingobium sphingomona sulfolobus homo sapien bos taurus

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(Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 45, Last annotation update)
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QGFBIO
PCPC SPHCR
Q937X0
Q975X7
Q8N8N1
SNAB BOVIN
SNAB HUMAN
SNAB MOUSE
Q9UTE
 09PHQ2
Q64WE2
Q6MAE4
Q8TA05
 PRELIMINARY;
 STANDARD;
 ORIKASKSF 9
 Query Match
Best Local Similarity
Matches 9; Conserv
 SEQUENCE FROM N.A.
 733.8
 RESULT 2
KLK7 HUMAN
ID KLK7 HUMAN
AC P49862;
DT 01-0CT-1996
DT 25-0CT-2004 (
 3377777
 13
 Q8NFV7
 RESULT 1
 Q8NFV7
 셤
 QBnfv7 homo sapien
QBnfv7 homo sapien
QBrn9 homo sapien
QBrn9 homo sapien
QBrd14 paeteurella
QBrd14 paeteurella
QBrd14 paeteurella
QBrd16 nitrosomona
GBRD 1 ymmhocysti
P5769 thermoplasm
P5962 homo sapien
QBery 0 mycoplasma
QBrd16 acinetobact
QBury 1 plasmodium
Q7rkq8 plasmodium
Q7rkq8 plasmodium
Q8ibn4 plasmodium
Q8wy1 glardia lam
Q8wy1 giardia lam
Q6wy1 giardia lam
Q6wy1 giardia lam
Q6wy1 giardia lam
Q6dy1 rattus norv
 Q6p3b2 mus musculu
Q8tb05 homo sapien
Q71mf6 homo sapien
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 July 13, 2005, 16:15:23 ; Search time 62.2222 Seconds (without alignments) 74.069 Million cell updates/sec
 Description
 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 Total number of hits satisfying chosen parameters:
 1612378 seqs, 512079187 residues
 SUMMARIES
 Q8NFV7
KLK7 HUMAN
Q8NSN9
Q9R048
Q91VE3
Y197 PASMU
Q88Q37
Q678H2
 RLAO THEAC
KAIN HUMAN
Q86TR9
Q8EUP9
 RL10 MYCPE
Q6FDR5
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 OM protein - protein search, using sw model
 Q7RKQ8
Q81BN4
Q7VRX5
Q8SAQ6
Q816K2
 Q62HP6
Q63W23
 070XY1
09YAU1
06DGM1
06AXN0
 Gapop 10.0 , Gapext 0.5
 1: uniprot_sprot:*
2: uniprot_trembl:*
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 US-09-905-083A-99
 Query
Match Length DB
 42
1 QRIKASKSF 9
 UniProt 03:*
 458
467
474
490
684
684
772
 BLOSUM62
 73.8
73.8
73.8
 Title:
Perfect score:
 Scoring table:
 Score
 Sequence:
 Searched:
 Database
 Run on:
 .
8
 Result
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ö
 CTISSUE=Ovarian carcinoma;

WEDLINE=22623266; PubMed=12738725;

WEDLINE=27624; Pelloing of KLKS and KLK7 in epithelial ovarian cancer rese. 9:1710-1720(2003).

CI. Cancer Res. 9:1710-1720(2003).

CI. Cancer Res. 9:1710-1720(2003).

CI. Cancer Res. 9:1710-1720(2003).

EMBL; AF411215; AAN03663.1; -...

CO GO:0004203; F:chymotrypsin activity; IEA.

GO; GO:0006508; P:proteclysis and peptidolysis; IEA.

InterPro; IPR001314; Peptidase S1A.

InterPro; IPR001324; Peptidase S1A.

InterPro; IPR001325; CHYMOTRYPSIN.

PROSITE; PS00135; TRYPSIN DSP: 1.

PROSITE; PS00135; TRYPSIN SEC: 1.

RYACOLABE; PROTECESE; SETINE PROTECESE.

WHydrolabe; Protecese; Serine protecese.
 Gapa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 ö
 Length 181;
 0; Indels
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 26, Last annotation update)
Kallikrein 7 short variant protein.
Homo sapiens (Human).
 100.0%; Score 42; DB 2;
ilarity 100.0%; Pred. No. 0.29;
Conservative 0; Mismatchee
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a

(hscce)

Egelrud T.;

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Genew; HGNC:6368; KLK7.
 Name=KLK7;
 ACT_SITE
ACT_SITE
 DISULFID
 SITE
 DISÜLFID
 DISULFID
 DISULFID
 DISULFID
 CARBOHYD
 SEQUENCE
 SITE
 GNSN80
 08N5N9
 Matches
 ACT
 RESULT 3
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 MEDLINE=94308225; PubMed=8034709;
Hansson L., Stroemqvist M., Baeckman A., Wallbrandt P., Carlstein A.,
 Blochcem. Blophys. Res. Commun. 211:586-589(1995).

-!- FUNCTION: May catalyze the degradation of intercellular cohesive structures in the cornified layer of the skin in the continuous structures in the cornified layer of the skin in the continuous shedding of cells from the skin surface. Specific for amino acid residues with aromatic side chains in the Pl position. SCCE claves insulin B chain at 6-Leu-|-Cys-7, 16-Tyr-|-Leu-17, 25-Phe-|-Tyr-26, and 26-Tyr-|-Thr-27. Could play a role in the activation of precursors to inflammatory cytokines.

-!- TISSUE SPECIFICITY: Abundantly expressed in the skin and is expressed by keratinocytes in the epidermis. Very low levels are also seen in the brain and kidney.

-!- SIMILARITY: Belongs to the peptidase SI family. Kallikrein
 Hansson L., Backman A., Ny A., Edlund M., Edholm E., Tornell J., Wallbrandt P., Egelrud T., "Epidermal overexpression of stratum corneum chymotryptic enzyme in mice; a model for chronic ithchy dermatitis "; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
 MEDLINE-95314630; PubMed=7794273; Skytt A., Stroemqvist M., Egelrud T.; "Primary substrate specificity of recombinant human stratum corneum chymotrypic enzyme.";
Kallikrein 7 precursor (EC 3.4.21.-) (Stratum corneum chymotryptic
 Yousef G.M., Scorilas A., Diamandis E.P.; Molcoular characterization, mapping and tissue expression of the human stratum corneum chymotryptic enzyme gene."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 PubMed=11054574; DOI=10.1016/S0378-1119(00)00382-6;
Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,
Moss P., Paeper B., Wang K.;
 Moss P., Paeper B., Wang K.; "Sequencing and expression analysis of the serine protease gene cluster located in chromosome 19q13 region.";
 "Cloning, expression, and characterization of stratum corneum chymotryptic enzyme. A skin-specific human serine proteinase."; J. Biol. Chem. 269:19420-19426(1994).
 SEQUENCE FROM N.A., AND SEQUENCE OF 23-53
 Name=KLK7; Synonyms=PRSS6, SCCE;
Homo sapiens (Human),
 EMBL; AF166330; AAD49718.1; -. EMBL; AF24557; AAG33360.1; -. EMBL; AF332583; AAK69624.1; -. PIR; A53968; A53968.
 EMBL; L33404; AAC37551.1; -.
 Gene 257:119-130(2000).
 IISSUE=Keratinocytes;
 MEROPS; S01.300; -
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A
 CHARACTERIZATION.
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subfamily.

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Attaubberg R.L., Feingold E.A., Grouse L.H., Ospurantarian Straubberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D., Altachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bahat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Araba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Willalon D.K., Muzny D.M., Sodersen B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., A Rziywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 Pfam; PF00089; Trypsin; 1
Pfam; PF00089; Trypsin; 1
PRINTS, PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp SPc; 1
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00114; TRYPSIN_HIS; 1.
PROSITE; PS00114; TRYPSIN_SER; 1.
Direct protein sequencing; Glycoprotein; Hydrolase; Serine protease; Signal; Zymogen. 2
Signal; Zymogen. 2
SIGNAL 2
PROPEP 23 Activation peptide.
CHAIN 30 253 Kallikrein 7
 Gaps
 (By similarity).
(By similarity).
(By similarity).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 .) (Potential)
 ö
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 DB 1; Length 253;
 0; Indels
 GO: GO: 0008236; F:serine-type peptidase activity; TAS. GO: GO: 0008544; P:epidermal differentiation; TAS. InterPro; IPR009003; Pept_Ser_Cys. InterPro; IPR001254; Peptidase_Si.
 .linked (GlCNAC. . .) (Po
2D68B6B15A76A668 CRC64;
 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 Stratum corneum chymotryptic enzyme, preproprotein
 Charge relay system
Charge relay system
Charge relay system
 Score 42; DB 1;
Pred. No. 0.41;
 N-linked (GlcNAc
 By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
 0; Mismatches
 PRT;
 27525 MW;
 100.0%;
 9; Conservative
 PRELIMINARY;
H-InvDB; HIX0015373; -. MIM; 604438; -.
 91 QRIKASKSF 99
 σ
 Homo sapiens (Human)
 144
176
201
246
253 AA;
 1 QRIKASKSF
 Query Match
Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
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us-09-905-083a-99.rup

Serine protease.

Hydrolase; Protease;

```
ö
 MEDLINE-99399282; PubMed=10469296;
Backman A., Stranden P., Brattsand M., Hansson L., Egelrud T.;
"Molecular cloning and tissue expression of the murine analog to human
Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
 Gaps
 Mus musculus (moube).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
 ö
 100.0%; Score 42; DB 2; Length 253; 100.0%; Pred. No. 0.41;
 Indels
 Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to peptidase family S1.
EMBL; BC032005; AAH32005.1; -.
 GG; GO:0004263; F:chymotrypsin activity; IEA.
GG; GO:0004285; F:chymotrypsin activity; IEA.
GG; GO:0004285; F:trypsin activity; IEA.
GG; GO:0004289; F:trypsin activity; IEA.
GG; GO:0006208; P:trypsin activity; IEA.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR00003; Pept_Ser_Gys.
Ffam; PP00089; Trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SW00022; Tryp_SFC; 1.
PROSITE; PS00134; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 Hydrolase; Protease; Serine protease.
SEQUENCE 253 AA; 27608 MW; 2D68B6A41B22A668 CRC64;
 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Stratum crneum chymotryptic enzyme (Fragment).
 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
 ö
 J. Invest. Dermatol. 113:152-155 (1999).
-!- SIMILARITY: Belongs to peptidase family S1
EMBL; AF124299; AAF01139.1; -.
HSSP; P00760; 1EZX.
 0; Mismatches
 MED: MGI:1346336; Klk7.
MGD; MGI:1346336; Klk7.
GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR009003; Pept_Ser_Cys.
 PRINTS; PRO0722; CHYMOTRYPSIN.
SMART; SM00020; TYP SPC; 1.
SMOSTE; PSS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; UNKNOWN_1.
PROSITE; PS00135; TRYPSIN HIS; UNKNOWN_1.
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
 stratum corneum chymotryptic enzyme.
 Pfam; PF00089; Trypsin; 1
 Conservative
 PRELIMINARY;
 91 QRIKASKSF 99
 Query Match
Best Local Similarity
9; Conserva
 QRIKASKSF 9
 Mus musculus (Mouse)
 SEQUENCE FROM N.A.
 MEROPS; S01.300; -
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 Name=K1k7
 Q9R048;
 09R048
 RESULT 4
 PAT DAY REPARENT OF THE PAT OF TH
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RX STANDERS N.A.

STRAINEFURNIN, TISSUE-Mammary tumor. C3;

RX STRAINEFURNI, TISSUE-Mammary tumor. C3;

RA STRAINEFURNI, TISSUE-Mammary tumor. C3;

RA STRAINEFURNI, TISSUE-Mammary tumor. C3;

RA MIDDINE-C2188257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA STRAINEFURNIN, Calling F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max. S.I., Wang J., Haieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Boaks S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

RA Norley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterffield Y.S.,

RA Maryinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.,

Ra Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences...
 ö
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2004 (TrEMBLrel. 28, Last sequence update)
05-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Thymopsin (Kallikrein 7) (Stratum corneum chymotryptic enzyme) (Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833444E03 product:kallikrein 7 (chymotryptic, stratum corneum)
full insert sequence) (Mus musculus 10 days neonate head cDNA, RIKEN full-length enriched library, clone:5530400609 product:kallikrein 7 (chymotryptic, stratum corneum), full insert sequence).
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
 Hansson L., Backman A., Ny A., Edlund M., Edholm E., Tornell J., Wallbrandt P., Egelrud T.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 ö
 Score 36; DB 2; Length 234;
Pred. No. 9.1;
2; Mismatches 0; Indels
 Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
 Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
 234 AA; 25220 MW; BEBE57D6C325B85F CRC64;
 roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 249 AA.
 SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 85.78;
 Query Match
Best Local Similarity 77.00.,
7; Conservative
 PRELIMINARY;
 234
 |:|||:|||
87 QKIKATKSF 95
 Mus musculus (Mouse).
 1 ORIKASKSF 9
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A
 NCBI_TaxID=10090;
 STRAIN=129/SvJ;
 rissue=Thymus;
 Yamaguchi N.
 NON TER
SEQUENCE
 Q91VE3
 RESULT 5
091083
10091083
10091083
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 SEQUENCE FROM N.A.

C STRAIN-CSTBL/G0; TISSUE=Head;
A Adachi J., Alzawa K., Akahira S., Akimura T., Aono H., Arai A.,
Adachi J., Alzawa K., Akahira S., Akimura T., Aono H., Puruno M.,
A Arakawa T., Bono H., Carninol P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Rato H.,
A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,
A Sano H., Sasaki D., Shibata K., Shibata Y., Shinaqawa A., Shiraki T.,
A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Tojima Y., Toya T., Yamanaka I., Yamanaka T.,
A Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
 STRAIN=C57BL/6J; Harbada;
A fadachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
A fadachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
A Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
I Tomaru A., Toya T., Yasunishi A., Muramateu M., Hayashizaki Y.;
L Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
 the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
 STRAIN=C57BL/6J; TISSUE=Head; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazadi Y., Muramatsu M., Hayashizaki Y., Inch M., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
 MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
 STRAIN-CSTBL/61; TISSUE-Head;
MEDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunnoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watshika M., Ohaca Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rikik integrated sequence M., Inoue Y., Kira A., Hayashizaki Y.; Rikik integrated sequence analysis (RISA) system-384-format genome Res. 10:1757-1771(2000).
 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
 SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Head;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Head;
The FANTOM Consortium,
STRAIN=C57BL/6J; TISSUE=Head;
 RIKEN FANTOM Consortium;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
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 ö
 ö
 Gaps
 Gaps
 Hypothetical protein PM1897.
N-palmitoyl cysteine (Potential).
S-diacylglycerol cysteine (Potential).
920c6iEl4A10F405 CRC64;
 ö
 Complete proteome; Hypothetical protein; Lipoprotein; Membrane;
 ö
 Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
 MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;
 Score 34; DB 1; Length 107;
Pred. No. 11;
1; Mismatches 1; Indels
 Score 36; DB 2; Length 249;
Pred. No. 9.8;
2; Mismatches 0; Indels
 0D4E380F12D14F87 CRC64;
 10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
 MGD; MGI:1346336; KIK7.

MGD; MGI:1346336; KIK7.

GO; GO:0005615; C:extracellular space; TAS.

PROMOS; Trypsin; 1.

PROMITS; PRO0022; CHYMOTRYPSIN.

SMART; SM00020; Tryp SPC; 1.

PROSITE; PS00134; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; UNKNOWN 1.
peptidase family
 107 AA
 Hypothetical lipoprotein PM1897 precursor.
OrderedLocusNames=PM1897;
 InterPro; IPR000437; Prok_lipoprot_S.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 Potential
 Hydrolase; Protease; Serine protease.
SEQUENCE 249 AA; 27257 MW; 0D4E38
 EMBL, AB008371; BAB55604.1; --
EMBL, APC278823, AAH27823.1; --
EMBL, AF33930; AAK6965.1; --
EMBL, AK029477; BAC26467.1; --
EMBL, AK077460; BAC36787.1; --
HSSP; P07076.1; --
HSSP; P07076.1; --
MEROPS; S01.300; --
 1 17 PO
18 107 HY
18 18 N-1
18 18 S-1
107 AA; 12214 MW;
 EMBL; AE006227; AAK03981.1; -.
 85.7%;
77.8%;
 Query Match
Best Local Similarity 77.8%;
Matches 7; Conservative
 Belongs to
 Local Similarity 77.8
nes 7; Conservative
 STANDARD;
 95
 Pasteurella multocida
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87 QKIKATKSF
 1 ORIKASKSF
 SEQUENCE FROM N.A.
 Palmitate; Signal
 (Potential).
 NCBI_TaxID=747;
 STRAIN=Pm70;
 YI97 PASMU
ID YI97 PASMU
 SEQUENCE
 SEQUENCE
 Query Match
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PubMed=15194775; DOI=10.1128/JVI.78.13.6982-6994.2004;
Zhang Q.Y., Xiao F., Xie J., Li Z.Q., Gui J.F.;
"Complete Genome Sequence of Lymphocystis Disease Virus Isolated from
 Hypothetical protein.
Lymphocystis disease virus - isolate China.
Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Lymphocystivirus.
NCBI_TaxID=256729;
SEQUENCE FROM N.A.

STRAIN=ATCC 19718 / IFO 14298;

MEDLINE=22586410; PubMed=12700255;

MEDLINE=22586410; PubMed=12700255;

DOI=10.1128/JB.185.9.2793.2003;

Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,

Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,

Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.,

"Complete genome sequence of the ammonia-oxidizing bacterium and
obligate chemolithoautotroph Nitrosomonas europaea.";

J. Bacteriol. 185.2759-2773(2003).

-!- SIMILARITY: Contains 1 histidine kinase domain.

HSSP: Q56310; 115D.
 R GO; GO:0016020; C:membrane; IEA.
R GO; GO:0016020; F:ATP binding; IEA.
R GO; GO:0016301; F:Kinase activity; IEA.
R GO; GO:0016301; F:Kinase activity; IEA.
R GO; GO:0016740; F:transferase activity; IEA.
R GO; GO:0007165; F:two-component sensor molecule activity; IEA.
R GO; GO:0007165; P:signal transduction; IEA.
R GO; GO:0007165; P:signal transduction; IEA.
R InterPro; IPR003594; ATPbind ATPase.
R InterPro; IPR003594; ATPbind ATPase.
R InterPro; IPR003504; His kinase.
R InterPro; IPR00561; His kinase.
 PROSITE, PS50109, HIS KIN; 1.
Complete proteome; Kinase; Phosphorylation; Sensory transduction;
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 78.6%; Score 33; DB 2; Length 310; 66.7%; Pred. No. 61; ive 3; Mismatches 0; Indels
 Length 683
 1; Indels
 683 AA; 77013 MW; 6989E95EB6543ED4 CRC64;
 Hypothetical protein. - - - - - - SEQUENCE 310 AA; 34349 MW; 714DAC2A33E42C11 CRC64;
 25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 EMBL; AY380826; AAU10885.1; -.
InterPro, IPR001545; Gly hormoneB.
PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 Score 34; DB 2;
Pred. No. 83;
0; Mismatches
 310 AA
 PRT;
 J. Virol: 78:6982-6994 (2004).
 SMART; SM00065; GAF; 1.
SMART; SM00387; HATPase c; 1.
SMART; SM00388; HisKA; 1.
 BCTRLSENSOR.
 81.0%;
88.9%;
 Query Match
Best Local Similarity 88.9
Matches 8; Conservative
 6; Conservative
 PRELIMINARY;
 Pfam; PF02518; HATPase Pfam; PF00512; HisKA; TPRINTS; PR00344; BCTRLS
 548 ORITASKSF 556
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 1 QRIKASKSF
 Best Local Similarity
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 SEQUENCE
 Query Match
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 0678H2;
 Q678H2
 Matches
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 Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H., Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M., Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F., Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M., Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K., Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S., Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
 Gaps
 GO; GO:0003700; P:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro: IPR000847; HTH Ly8R.
InterPro: IPR000847; HTH Ly8R.
InterPro: IPR001958; Wing_hlx_DNA_bnd.
Pfam; PF00126; HTH 1; 1.
Pfam; PF00126; HTH 1; 1.
PR00126; HTH 2; 1.
PR00139; HTH 2; 1.
PROSITE; PS50931; HTH_LYSR.
 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 24, Last annotation update)
8-mar-2004 (TrEMBLrel. 26, Last annotation update)
8-maroty transduction histidine kinases.
0rderedLocusNames=NE0377;
Nitrosomonas europase.
Nitrosomonas europase.
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
 Pseudomonas putida (strain KT2440).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
 ;
 "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440.";
Environ. Microbiol. 4:799-808(2002).
-!- SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.
EMBL; AE016776; AAN66286.1; -
 Length 294;
 0; Indels
 294 AA; 32995 MW; 33695F24D26560EF CRC64;
 01-UNN-2003 (TrEMBLrel. 24, Created)
01-UNN-2003 (TrEMBLrel. 24, Last sequence update)
01-UNA-2004 (TrEMBLrel. 26, Last annotation update)
Transcriptional regulator AmpR, putative.
OrderedLocusNames=Pp0661;
 Complete proteome; DNA-binding; Transcription; Transcription regulation. SEQUENCE 294 AA.
 5;
 294 AA
 683 AA
 81.0%; Score 34; DB 77.8%; Pred. No. 34;
 2; Mismatches
 SEQUENCE FROM N.A.
MEDLINE=22423060; PubMed=12534463;
 Nitrosomonadaceae; Nitrosomonas
 PRELIMINARY;
 7; Conservative
 PRELIMINARY;
 259 QRIEASESF 267
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27 QRIEAGKSF 35
 1 QRIKASKSF 9
 ORIKASKSF 9
 Query Match
Best Local Similarity
 NCBI_TaxID=160488;
 NCBI_TaxID=915;
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Q82XB0; Q82XB0

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082XB0
1D 082XE
AC 082XE
DT 01-JT
DT 01-JT
DT 01-DT
DT 01-MT
DT 01

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EMBL; L19684; AAA59454.1; -. EMBL; L28101; AAC41706.1; -.
 kallikrein's activity.
 SEQUENCE OF 388-403.
 kallikrein.
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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 Gaps
 Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma
 PS9622, 096825, 006825, 006826, 001-007-1096 (Rel. 25, Created) 01-007-1996 (Rel. 34, Last sequence update) 01-007-1996 (Rel. 34, Last sequence update) 05-001.007-1996 (Rel. 34, Last annotation update) Rallistatin precursor (Kallikrein inhibitor) (Protease inhibitor 4). Name-SERPINA4; Synonyma=KST, PI4; Homo sapiene (Human).
 SEQUENCE FROM N.A.
BEDILNES-84043234, PubMed-8227002,
Chai K.X., Chen L.-M., Chao J., Chao L.;
"Kallistatin: a novel human serine proteinase inhibitor. Molecular
 -1- FUNCTION: Ribosomal protein P0 is the functional equivalent of
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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 E.coli protein L10.
 78.6%; Score 33; DB 1; Length 314; 87.5%; Pred. No. 61; ive 1; Mismatches 0; Indels
 Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
 STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001; DOI=10.1038/35035069;
 F40D048680E0B6EB CRC64;
 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2004 (Rel. 45, Last annotation update)
Acidic ribosomal protein P0 homolog (LIOE).
 427 AA.
 or send an email to license@isb-sib.ch).
 HAMAP; MF_00280; -; 1. InterPro; IPR01790; Ribosomal L10. Pfam; PF00466; Ribosomal_L10, \overline{1}. Complete protecome; Ribosomal protein. SEQUENCE 314 AA; 34583 MW; P40D04.
 Name=rplP0; OrderedLocusNames=Ta0359;
 Thermoplasmataceae; Thermoplasma.
 EMBL; AL445064; CAC11503.1; -.
 Nature 407:508-513(2000).
 Thermoplasma acidophilum.
 Conservative
 STANDARD;
 STANDARD;
 183 ÓKÍKSSKNF 191
1 QRIKASKSF 9
 17 ORIKASRS 24
 1 ORIKASKS 8
 FROM N.A.
 Best Local Similarity
 NCBI_TaxID=2303;
 NCBI_TaxID=9606;
 acidophilum.
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 KAIN HUMAN
 SEQUENCE
 Query Match
 KAIN HUMAN

ID KAIN H

AC 02-671

DT 01-APR.

DT 01-APR.

DT 05-701

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The Columny, tissue distribution, and expression in Escherichia coll.";

30. Biol. Chem. 268:24499-24555(1993).

80. BIOLNES-5513793 pubMed-7832886;

80. MEDLINES-5513793 pubMed-7832886;

80. MEDLINES-513793 pubMed-1832886;

80. Missue processa minitaria analysis, and chromosomal localization of firm from a processa minitaria.

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10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-CCT-2004 (Rel. 45, Last annotation update)
50S ribosomal protein L10.
 161 AA.
 671 AA
 TIGREAMS; TIGRO1525; ATPASSE-IB hvy; 1.
TIGREAMS; TIGRO1494; ATPASSE_P-Cype; 2.
PROSITE; PSO0154; ATPASSE_E1_E2; UNKNOWN_1.
 Heavy-metal transporting P-type ATPase
 PRT;
 PRT;
 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26,
 OrderedLocusNames=MYPE8710;
 PRINTS; PR00119; CATATPASE.
 Local Similarity 77.8
 STANDARD;
 PRELIMINARY;
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373 QKLEASKSF 381
 551 KEİKASKSF 559
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 1 QRIKASKSF
 1 QRIKASKSF
 NCBI_TaxID=28227;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A
 NCBI_TaxID=28227;
 RL10 MYCPE
Q8EVJ0;
 01-MAR-2003
01-MAR-2003
 SEQUENCE
 Query Match
 Q8EUP9
 RESULT 14
RL10 MYCPE
 RESULT 13
Q8EUP9
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 Gaps
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 M-IMPUDS; MINULUSOU; -.

GO; GO:0005515; F:protein binding; TAS.

GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; TAS.
InterPro: IPR000215; Prot_inh_serpin.
PROMOTY: Serpin; 1.
SMART; SM00093; SERPIN; 1.
Direct protein sequencing; Glycoprotein; Plasma;
Serine protease inhibitor; Serpin; Signal.
SIGNAL.

SIGNAL.

Proteintal.
 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JURR-2004 (TrEMBLrel. 26, Last annotation update)
Full-length cDNA 5-PRIME end of clone CSODM009YCl3 of Fetal liver of
 GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
InterPro; IPR002086; Aldehyd dehydrog.
InterPro; IPR00215; Prot_inf_serpin.
 Homo sapiens (human) (Fragment).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 Nationary (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .).
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 78.6%; Score 33; DB 2; Length 445; 66.7%; Pred. No. 89; ive 3; Mismatches 0; Indels
 Score 33; DB 1; Length 427;
Pred. No. 85;
 0; Indels
 Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
 Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the serpin family.
EMBL; BX248760; CAD66567.1; -.
 -> S (in Ref. 3).
3DBBE7AF956D4DAC CRC64;
 Protease inhibitor; Serine protease inhibitor; Serpin. NON TER 1 1 SEQUENCE 445 AA; 50612 MW; B1021CE4EC606079 CRC64;
 PROSITE; PS00070; ALDEHYDE DEHYDR_CYS; UNKNOWN_1.
PROSITE; PS00284; SERPIN; 1.
 445 AA
 3; Mismatches
 Kallistatin.
 48556 MW;
 78.6%;
66.7%;
EMBL; BC014992; AAH14992.1;
 Genew; HGNC:8948; SERPINA4
 Pfam; PF00079; Serpin; 1.
SMART; SM00093; SERPIN; 1
 Best Local Similarity 66.7
Matches 6; Conservative
 Conservative
 PRELIMINARY;
 H-InvDB; HIX0011930; -.
 355 QKLEASKSF 363
 1 QRIKASKSF 9
 ; A49518; A49518.
 TISSUE=Fetal liver;
 SEQUENCE FROM N.A.
TISSUE=Fetal liver;
 Best Local Similarity
Matches 6; Conserv
 SEQUENCE FROM N.A.
 NCBI_TaxiD=9606;
 Genoscope;
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STEAIN-BE-2;

MEDLINE=2344719; PubMed=12466555; DOI=10.1093/nar/gkf667;

MEDLINE=234719; PubMed=12466555; DOI=10.1093/nar/gkf667;

A Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Menri T., Puruya K.,

Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;

"The complete genomic sequence of Mycoplasma penetrans, an intracallular bacterial pathogen in humans.";

Nucleic Acids Res. 30:5293-5300(2002).

Rubi, AP004173; BAC44663.1; -.

BR GO, GO:0015662; F:ATP binding; IEA.

GO; GO:0015662; F:ATP binding; IEA.

GO; GO:0015662; F:ATPase activity, coupled to transmembrane m. .; IEA.

GO; GO:0016877; F:Hydrolase activity, acting on acid anhydrid. .; IEA.

GO; GO:0016820; F:Hydrolase activity, acting on acid anhydrid. .; IEA.

GO; GO:0016820; F:Hydrolase activity, acting on acid anhydrid. .; IEA.

GO; GO:00101; P:metabolism; IEA.

RO; GO:00101577; ATPase = II-NY.

InterPro; IPR001777; ATPase = II-NY.

InterPro; IPR001777; ATPase = II-NY.

InterPro; IPR001279; B-12-ATPase = reg.

Pfam; PF00122; HJLE2-ATPase = reg.

Pfam; PF00122; HJLE2-ATPase = reg.
 Gaps
 Mycoplasma penetrans.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 Name=rplJ; OrderedLocusNames=MYPE5740;
Mycoplasma penetrans.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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 78.6%; Score 33; DB 2; Length 671; 77.8%; Pred. No. 1.4e+02; ive 1; Mismatches 1; Indels
 MEDLINE=22354719; PubMed=12466555; DOI=10.1093/nar/gkf667;
 671 AA; 75854 MW; 8EEE005CA3E60671 CRC64;
(TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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 Darke V., Vallence D., Fonknechten N., Kreimeyer A., Oztas S., Labarre L., Cruveiller S., Robert C., Duprat S., Wincker P., Ornaton L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.; Ornaton L.N., Weissenbach by the genome sequence of Acinetobacter sp. ADP1, a versatile and naturally transformation competent bacterium."; Nucleic Acids Res. 0:0-0(2004).

BMBL, CR543861; CAG677931; -.

GO: 0000074; P:regulation of cell cycle; IEA.

Interpro; IPR065525; MinC.

IIGREMS; TIGR01222; minC; 1.
Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
 Gaps
 Gaps
 05-JUL.2004 (TrEMBLrel. 27, Created)
05-JUL.2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cell division inhibitor, inhibits fts2 ring formation.
Namemin() OrderediocusNames-ACIAD0895;
Acinetobacter sp. (strain ADP1).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceas; Acinetobacter.
11 TaxID=62977;
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 Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
"The complete genomic sequence of Mycoplasma penetrans, an
intracellular bacterial pathogen in humans.";
Nucleic Acids Res. 30:5293-5300(2002).
 76.2%; Score 32; DB 2; Length 240; 100.0%; Pred. No. 78; Ative 0; Mismatches 0; Indels
 76.2%; Score 32; DB 1; Length 161; 66.7%; Pred. No. 51;
 0; Indels
 Pfam; PF00466; Ribosomal_L10; I. PRISE NEG.
PROSITE; PS01109; RIBOSOMAL_L10; FALSE NEG.
Complete proteome; Ribosomal protein.
SEQUENCE 161 AA; 17949 MW; 1D95D1C29B5E87D3 CRC64;
 240 AA; 26116 MW; F110BF30D94DFD90 CRC64;
 240 AA
 3; Mismatches
 HAMAP; MF 00362; -; 1.
InterPro; IPR001790; Ribosomal L10.
InterPro; IPR002363; Ribosomal L10eub.
 EMBL; AP004172; BAC44364.1; ALT_INIT.
 PRT;
 Query Match 76.2
Best Local Similarity 100.
Matches 7; Conservative
 Local Similarity 66.7
les 6, Conservative
 PRELIMINARY;
 17 EQIKSSKSF 25
 1 QRIKASKSF 9
 [1] SEQUENCE FROM N.A.
 Complete proteome.
SEQUENCE 240 AA;
 Query Match
 Q6FDR5
 RESULT 15
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Search completed: July 13, 2005, 17:29:31 Job time : 64.2222 secs

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TYPE: PRT
ORGANISM: Homo sapiens
 TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
 1 QRIKASKSF 9
 1 ORIKASKSF
RESULT 2
US-09-502-600-130
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 Sequence 130, Appl Sequence 130, Appl Sequence 130, Appl Sequence 14, Appli Sequence 12, Appl Sequence 12, Appl Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 15, Appli Sequence 2, Appli Sequence 1716, Appli Sequence 1712, Appli Sequence 1712, Appli Sequence 1712, Appli Sequence 1713, Appli Sequence 1712, Appli Sequence 1712, Appli Sequence 1712, Appli Sequence 1713, Appli Sequence 1712, Appli Sequence 1712, Appli Sequence 1713, Appli Sequence 1712, Appli Manuella M
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 (without alignments)
34.552 Million cell updates/sec
 Description
 Sequence (
 July 13, 2005, 16:58:04; Search time 19.4444 Seconds
 Sequence
 Issued Patents AA:*

1 / GgDZ 6/ptodata/1/iaa/5A_COMB.pep:*

2 / GgDZ 6/ptodata/1/iaa/6B_COMB.pep:*

3: / CgDZ 6/ptodata/1/iaa/6A_COMB.pep:*

1: / CgDZ 6/ptodata/1/iaa/6B_COMB.pep:*

2: / CgDZ 6/ptodata/1/iaa/BCTUS_COMB.pep:*

3: / CgDZ 6/ptodata/1/iaa/PCTUS_COMB.pep:*

3: / CgDZ 6/ptodata/1/iaa/PCTUS_COMB.pep:*
 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 US-09-502-600-99
US-09-502-600-130
US-09-918-243-99
US-09-918-243-130
US-09-618-259-4
US-09-618-259-4
US-09-261-416-7
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 Total number of hits satisfying chosen parameters:
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 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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 US-09-905-083A-99
42
1 QRIKASKSF 9
 Minimum DB seq length: 0
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1000.00
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 Title:
Perfect score:
 Scoring table:
 Database :
 Searched:
 Sequence:
 Run on:
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No.
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RESULT 1

US-09-502-600-99

Squence 99, Application US/09502600A

Patent No. 6294344

GENERAL INFORMATION:

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of

TITLE OF INVENTION: Ovarian Cancer

TITLE OF INVENTION: D6233GTP-C

CURRENT FILING DATE: 2000-02-11

CURRENT PAPLICATION NUMBER: US/09/502,600A

PRIOR APPLICATION NUMBER: 09/039,211

WINMER OF SEQ ID NOS: 136

SEQ ID NO 99

LENGTH: 9
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12, Appli
11, Appli
11, Appl
1160, Ap
1160, Ap
26710, A
26710, A
3400, Ap
3400, Ap
3400, Ap
357, Appli
357, Appli
10090, A
4565, Ap
 Sequence 130 Application US/09502600A

Sequence 130 Application US/09502600A

GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer
FILE REPERBENCE: D6223CIP-C
CURRENT FILING DATE: 2000-02-11
CURRENT APPLICATION NUMBER: US/09/502,600A
FRIOR APPLICATION NUMBER: US/09/502,600A
FRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 130
LENGTH: 9
 Gaps
 Sequence
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 Query Match 100.0%; Score 42; .DB 3; Length 9; Best Local Similarity 100.0%; Pred. No. 4.1e+05; Matches 9; Conservative 0; Mismatches 0; Indels
 Length 9;
 ; OTHER INFORMATION: Residues 91-99 of the SCCE protein US-09-502-600-99
ALIGNMENTS
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Sequence 7, Application US/09261416A

Patent No. 6291663
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: TANG-12: A No. 6291663el Transmembrane Serine Protease
TITLE OF INVENTION: Overexpressed in Ovarian Carcinoma
FILE REPRENCE: D6192
CURRENT APPLICATION NUMBER: US/09/261,416A
CURRENT PILING DATE: 1999-03-03
SEQ ID NO?
 NAME/KEY: DOMAIN
CTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
CTHER INFORMATION: enzyme (scce) catalytic domain
US-09-618-259-4
 FEATURE: OTHER INFORMATION: Serine protease catalytic domain of stratum corneum OTHER INFORMATION: chymotryptic enzyme (Scce) homologous to similar OTHER INFORMATION: domain in TADG-12
 Gaps
 Gaps
 US-09-618-259-4

i Sequence 4, Application US/09618259

i Sequence 4, Application US/09618259

j Patent No. 6642013

i GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

APPLICANT: Underwood, Lowell J.

TITLE OF INVENTION: NO. 6642013e1 Extracellular Serine Protease

FILE REPERENCE: D6020C1P2

CURRENT APPLICATION NUMBER: US/09/618,259

CURRENT FILING DATE: 1998-08-21

NUMBER OF SEQ ID NOS: 72

SEQ ID NO S: 72

LENGTH: 144
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 100.0%; Score 42; DB 3; Length 154; 100.0%; Pred. No. 0.23; cive 0; Mismatches 0; Indels
 100.0%; Score 42; DB 4; Length 144; 100.0%; Pred. No. 0.22; tive 0; Mismatches 0; Indels
 ; Sequence 33, Application US/08944483
 Best Local Similarity 100.
Matches 9; Conservative
 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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28 QRIKASKSF 36
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 TYPE: PRT
ORGANISM: Unknown
 TYPE: PRT
ORGANISM: unknown
 RESULT 7
US-08-944-483-33
 RESULT 6
US-09-261-416-7
 US-09-261-416-7
 Query Match
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 | Sequence 130, Application US/09918243
| Sequence 130, Application US/09918243
| Patent No. 6677403
| GENERAL INFORMATION:
| APPLICANT: Cannon, Martin J.
| APPLICANT: Santin, Alessandro
| TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer:
| FILE REFERENCE: D6223CIP/C/D/CIP
| FILE REFERENCE: D6223CIP/C/D/CIP
| CURRENT APPLICATION NUMBER: US/09/918,243
| CURRENT FILING DATE: 2001-07-30
| PRIOR FILING DATE: 2001-07-13
| NUMBER OF SEQ ID NOS: 136
 US-09-918-243-99
; Sequence 99, Application US/09918243
; Patent No. 6627401
; Patent No. 6627401
; Patent No. 1 6627401
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Marthin J.
; APPLICANT: Santin, Alessandro
; TITLE REFERENCE: D6223CIP/C/D/CIP
; FILE REFERENCE: D6223CIP/C/D/CIP
; CURRENT APPLICATION NUMBER: US/09/918,243
; CURRENT APPLICATION NUMBER: US
; PRIOR FILING DATE: 2001-07-30
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 136
; SEQ ID NO 99
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 Query Match 100.0%; Score 42; DB 4; Length 9; Best Local Similarity 100.0%; Pred. No. 4.1e+05; Matches 9; Conservative 0; Mismatches 0; Indels
 100.0%; Score 42; DB 4; Length 9; 100.0%; Pred. No. 4.1e+05; Live 0; Mismatches 0; Indels
 Length 9;
 100.0%; Score 42; DB 3; Length 9; 100.0%; Pred. No. 4.1e+05; ative 0; Mismatches 0; Indels
 FEATURE:

"NAME/KEY: CHAIN

OTHER INFORMATION: Residues 91-99 of the SCCE protein US-09-918-243-99
 ; OTHER INFORMATION: Residues 91-99 of the SCCE protein US-09-918-243-130
OTHER INFORMATION: Residues 91-99 of the SCCE protein
 Ouery Match
Best Local Similarity 100.
 9; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
 ORGANISM: Homo sapiens
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1 ORIKASKSF 9
 1 ORIKASKSF 9
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1 QRIKASKSF 9
 Query Match
Best Local Similarity
Matches 9; Conserv
 1 QRIKASKSF
 NAME/KEY: CHAIN
 RESULT 4
US-09-918-243-130
 i Olnen 1130
US-09-502-600-130
 LENGTH: 9
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225 amino acids
 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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 63 QRIKASKSF 71
 63 QRIKASKSF 71
 1 QRIKASKSF 9
 1 QRIKASKSF 9
 TYPE: amino acids STRANDEDNESS: sin
New York
 INFORMATION
 TYPE: PRT
ORGANISM: Unknown
 RESULT 10
US-09-154-344-12
 US-08-557-146-12
 US-09-027-337-4
 FEATURE
 Patent No
GENERAL
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 USEFUL FOR DETECTING AND TREATING DISEASES
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 Gaps
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 Sequence 12, Application US/08557146
Patent No. 5834290
GENERAL INFORMATION:
APPLICANT: Bgelrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Brzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
 DB 3; Length 224;
 0; Indels
 APPLICANT: CCHEN, MAURICE
APPLICANT: CCHEN, TRACEY L.
APPLICANT: FRLEDMAN, PAULA N.
APPLICANT: GRANADOS, EDMARD N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
APPLICANT: STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: OF THE PROSTATE
NUMBER OF SEQUENCES: 76
 SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,483
 Mismatches
 Query Match

100.0%; Score 42;

Best Local Similarity 100.0%; Pred. No. '
Matches 9; Conservative 0; Mismatch
 : 1155 Avenue of the Americas
New York
 6183.US.01
 SEE: Abbott Laboratories
: 100 Abbott Park Road
Abbott Park
 NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 61.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
 FILING DATE: 424
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTONNEY/AGENT INFORMATION:
 INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
TYPE: amino acid
 , MOLECULE TYPE: No. 6232456e
US-08-944-483-33
 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
 ZIP: 60064-3500
COMPUTER REDABLE FORM:
MEDIUM TYPE: Distriction
 Diskette
 single
 CORRESPONDENCE ADDRESS
 62 ORIKASKSF 70
 1 QRIKASKSF 9
 linear
 STRANDEDNESS:
 ADDRESSEE:
 US-08-557-146-12
 STREET:
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US-09-027-337-4
; Sequence 4, Application US/09027337B
; Sequence 4, Application US/09027337B
; Patent No. 5972616
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotoshi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
; TITLE OF INVENTION: Breast and Ovarian Carcinomas
; TITLE OF INVENTION: Breast und Ovarian Carcinomas
; CURRENT APPLICATION NUMBER: US/09/027,337B
; CURRENT FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 13
SEQ ID NO 4
SEQ ID NO 4
SEQ ID NO 4
SEQ ID NO 4
SEQ ID NO 4
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 OTHER INFORMATION: Serine protease catalytic domain of Scce homologous to OTHER INFORMATION: similar domain in TADG-15
 Gaps
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 Length 225;
 DB 2; Length 225;
 0; Indels
 0; Indels
 Patentin Release #1.0, Version #1.25 (EPO)
 Query Match
100.0%; Score 42; DB 2;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches
 100.0%; Score 42; DB
100.0%; Pred. No. 0.3
:ive 0; Mismatches
ZUP: 1003 6-2787.
ZUP: 1003 6-2787.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIPICATION: 424
 Sequence 12, Application US/09154344
Patent No. 5981256
 REGISTRATION NUMBER: 35,372
REGISTRATION NUMBER: 31,372
RELECOMMUNICATION INFORMATION:
TELEPONE: (212) 354-8113
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
 ATTORNEY/AGENT INFORMATION:
 TOPOLOGY: linear
MOLECULE TYPE: polypeptide
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 US-U9-b34-b0UM-4
; Sequence 4, Application US/09654600A
; Patent No. 6649741
; GENERAL INFORMATION:
; APPLICANT: O'BIGEN, HIROCOSH;
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
; TITLE OF INVENTION: O'VEREXPRESSED in Carcinomas
; FILE REFERENCE: D60641P/D
; CURRENT APPLICATION NUMBER: US/09/654,600A
; CURRENT APPLICATION NUMBER: 09/421,213
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 4
; LBNGTH: 225
; TYPE: DPT
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 Sequence 2, Application US/08557146
Patent No. 5834290
GENERAL INFORMATION:
APPLICANT: Egalrud, Torbjorn
APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Enzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCES. 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
 Lucry Match
Best Local Similarity 100.0%; Score 42; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches n. Trall
 100.0%; Score 42; DB 4; Length 225; 100.0%; Pred. No. 0.34;
 COMPUTER: New LOTK
COUNTRY: U.S.A.
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION: 424
 0; Indels
 0; Mismatches
 ATTORNEY/AGENT INFORMATION: NAME: Sterner, Richard J.
 Query Match
Best Local Similarity 100.
Matches 9; Conservative
 ; OTHER INFORMATION: SCCE US-09-654-600A-4
 TYPE: PRT
ORGANISM: Homo sapiens
 63 ORIKASKSF 71
 63 ORIKASKSF 71
 σ
 1 ORIKASKSF 9
 CITY: New York
STATE: New York
COUNTRY: U.S.A.
 1 ORIKASKSF
 US-09-654-600A-4
 US-08-557-146-2
US-09-644-600-4
 FEATURE:
 RESULT 13
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 Sequence 4, Application US/09644600

| Sequence 4, Application US/09644600
| Patent No. 6451500
| GENERAL INFORMATION:
| APPLICANT: O'Brien, Timothy J. APPLICANT: O'Brien, Timothy J. TITLE OF INVENTION: TAGG-15: An Extracellular Serine Protease:
| TITLE OF INVENTION: Overexpressed in Carcinomas |
| TITLE OF INVENTION: Overexpressed in Carcinomas |
| FILE REFERENCE: D6064C1P/D;
| CURRENT APPLICATION NUMBER: US/09/644,600 |
| CURRENT FILING DATE: 1999-10-20 |
| PRIOR FILING DATE: 1999-10-20 |
| PRIOR APPLICATION NUMBER: 09/027,337 |
| PRIOR APPLICATION NUMBER: 09/027,337 |
| PRIOR SEQ ID NOS: 98 |
| SEQ ID NO 4 |
| LENGTH: 225 |
| LENGTH: 225
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0
 APPLICANT: Hansson, Lennart
TITLE OF INVENTION: Recombinant Stratum Corneum Chymotryptic
TITLE OF INVENTION: Brzyme (SCCE)
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: White & Case, Patent Department
STREET: 1155 Avenue of the Americas
CITY: New York
CITY: New York
COUNTRY: U.S.A.
ZIP: 10036-2787
 Query Match 100.0%; Score 42; DB 2; Length 225; Best Local Similarity 100.0%; Pred. No. 0.34; Matches 9; Conservative 0; Mismatches 0; Indels
 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATE:
FILING DATE: 16-SEP-1998
 CLASSIFICATION:
ATTORNEY/AGENTINE:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783:
TELEPHONE: (212) 819-8783:
TELEPHONE: (212) 854-8113
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acids
STRANDEDNESS: alingle
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/557,146
FILING DATE: 14-DEC-1995
CLASSIFICATION:
 APPLICANT: Egelrud, Torbjorn
 TOPOLOGY: linear
MOLECULE TYPE: polypeptide
 TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: SCCE
 CLASSIFICATION:
 US-09-154-344-12
 US-09-644-600-4
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91 QRIKASKSF 99
 TOPOLOGY:
 US-09-154-344-2
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 Gaps
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 DB 2; Length 253;
 DB 2; Length 253
 0; Indels
 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/824,874
FILING DATE: Filed Herewith
CLASSIFICATION NUMBER: Biled Herewith
CLASSIFICATION DATA:
APPLICATION NUMBER: Filed Herewith
FILING DATE: Filed Herewith
APPLICATION NUMBER: 5744
ATOMNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
 100.0%; Score 42; DB 2;
100.0%; Pred. No. 0.38;
tive 0; Mismatches
 RESULT 14
US-08-824-874-3
; Sequence 3, Application US/08824874
; Patent No. 5962300
; GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Hillman, Jennif
 Mismatches
 Score 42;
Pred. No.
 REFERENCE/DOCKET NUMBER: 1103326-181
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
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0
REGISTRATION NUMBER: 35,372
 Query Match
Best Local Similarity 100.0%;
Matches 9; Conservative 0
 LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
 Query Match
Best Local Similarity 100.(
Matches 9; Conservative
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-557-146-2
 91 ORIKASKSF 99
 1 ORIKASKSF 9
 linear
 MEDLAL.
LIBRARY: General
 IMMEDIATE SOURCE
 USA
 94304
 COUNTRY:
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Sequence 33, Appl Sequence 104, Appl Sequence 4, Appli Sequence 102, Appl Sequence 92, Appl Sequence 94, Appl

Sequence

Sequence 94, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 48, Appl Sequence 48, Appl Sequence 639, Appl Sequence 95, Appl Sequence 95, Appl Sequence 38, Appl Sequence 97, Appl Sequence 12,  Appl Sequen

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Sequence 99, Application US/09918243

Fatent No. US20020142317A1

GENERAL INFORMATION

APPLICANT: O'Brien, Timothy J.

APPLICANT: Cannon, Martin J.

APPLICANT: Santin, Alessandro

ITILE OF INVENTION: Methods for the early diagnosis of ovarian cancer;

FILE REFERENCE: D6223GIP/C/D/CIP

CURRENT APPLICATION NUMBER: US/09/918,243

CURRENT FILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-07-31

NUMBER OF SEQ ID NOS: 136

SEQ ID NO 99
 ; OTHER INFORMATION: Residues 91-99 of the SCCE protein US-09-918-243-99
 US-09-888-615-98

US-09-764-762-3

US-10-71-214-48

US-10-71-214-49

US-10-264-283-90

US-10-264-283-90

US-10-29-48

US-10-13-99-48

US-10-13-99-48

US-10-49-518-95

US-10-48-518-95

US-10-868-490A-1

US-10-918-243-97

US-10-918-243-97

US-10-918-243-97

US-10-918-243-97

US-10-918-243-97

US-10-918-243-97

US-10-918-243-97

US-10-918-243-97

US-10-11-214-46

US-10-11-214-46

US-10-210-172-126

US-10-210-172-126

US-10-210-172-128

US-10-210-172-128

US-10-210-172-128
US-10-262-511-98
US-10-262-511-96
US-09-789-210-33
US-10-262-511-104
US-10-600-187-4
US-10-262-511-102
US-10-262-511-92
US-10-262-511-92
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 TYPE: PRT
ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: CHAIN
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 US-09-918-243-99
 Sequence 99, Appl
Sequence 130, App
Sequence 130, Appl
Sequence 130, Appl
Sequence 130, Appl
Sequence 130, Appl
Sequence 130, Appl
Sequence 100, Appl
Sequence 4, Appli
Sequence 4, Appli
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
 (without alignments) 53.584 Million cell updates/sec
 Description
 July 13, 2005, 17:29:45 ; Search time 64.8889 Seconds
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| Cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 US-09-918-243-99
US-09-918-243-130
US-09-905-083-99
US-09-905-083-130
US-10-372-521-99
US-10-372-521-130
US-10-811-075-99
US-10-811-075-130
US-10-811-075-130
 Total number of hits satisfying chosen parameters:
 1726220 segs, 386332138 residues
 SUMMARIES
 Published Applications AA:*
 OM protein - protein search, using sw model
 Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
 Post-processing: Minimum Match 0%
Maximum Match 100%
 US-09-905-083A-99
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 1 QRIKASKSF 9
 Length
 Query
 Perfect score:
 Scoring table:
 Score
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Database :

Sequence:

Run on:

Searched:

Sequence 130, Sequence 132, Sequence 134,

Sequence 126, Sequence 128,

ö Length 9; Indels Query Match 100.0%; Score 42; DB 9; L Best Local Similarity 100.0%; Pred. No. 1.6e+06; Matches 9; Conservative 0; Mismatches 0; ORIKASKSF н

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Gaps

RESULT

US-09-796-294-4 US-10-461-787-4

100.

100.0

Result No.

QRIKASKSF

8 g

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Query Match
Best Local Similarity 100.
Matches 9; Conservative
 9; Conservative
 NUMBER OF SEQ ID NOS: 136
SEQ ID NO 130
LENGTH: 9
 TYPE: PRT
ORGANISM: Homo sapiens
 σ
 1 QRIKASKSF 9
 1 ORIKASKSF
 1 ORIKASKSF
 1 ORIKASKSF
 Best_Local Similarity
Matches 9; Conserv
 NAME/KEY: CHAIN
 US-10-372-521-130
 RESULT 5
US-10-372-521-99
 Query Match
 LENGIH: 9
 FEATURE
 RESULT 6
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 Sequence 130, Application US/09918243
Sequence 130, Application US/09918243
Sequence 130, Application US/09918243
GENERAL INFORMATION:
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Methods for the early diagnosis of ovarian cancer;
ITILE OF INVENTION: Methods for the early diagnosis of ovarian cancer;
FILE REFRENCE: D622421PC/D/CIP
CURRENT APPLICATION NUMBER: US/09/918,243
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 130
LENGTH: 9
 Sequence 130, Application US/09905083
Patent No. US20020146708A1
GRNERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
TITLE OF INVENTION: Ovarian Cancer
FILE REFERENCE: D6223CIP/C/Div
 Gaps
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0
 100.0%; Score 42; DB 9; Length 9; 100.0%; Pred. No. 1.6e+06; tive 0; Mismatches 0; Indels
 Length 9;
 Indels
) NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-09-905-083-99
 FEATURE:

NAME/KEY: CHAIN

OTHER INFORMATION: Residues 91-99 of the SCCE protein US-09-918-243-130
 100.0%; Score 42; DB 9; L
100.0%; Pred. No. 1.6e+06;
ative 0; Mismatches 0;
 Query Match
Best Local Similarity 10v...
9; Conservative
 Query Match
Best Local Similarity 100.
Matches 9; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
 ORGANISM: Homo sapiens
 QRIKASKSF 9
 QRIKASKSF 9
 1 ORIKASKSF 9
 RESULT 4
US-09-905-083-130
US-09-918-243-130
 SEQ ID NO 99
 TYPE: PRT
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 | Sequence 99, Application US/10372521
| Publication No. US20030223973A1
| GENERAL INFORMATION:
| APPLICANT: O'Brien, Timothy J.
| APPLICANT: Cannon, Mattin J.
| APPLICANT: Santin, Alessandro
| TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer:
| FILE REFERENCE: D623GIP/C/D/CIP2.
| CURRENT APPLICATION NUMBER: US/10/372,521
| PRIOR PILIGATION NUMBER: US 09/918,243
| PRIOR FILING DATE: 2003-02-21
| PRIOR FILING DATE: 2001-07-30
| NUMBER OF SEQ ID NOS: 136
| SEQ ID NO 99
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 Sequence 130, Application US/10372521
Publication No. US20030223973A1
Publication No. US20030223973A1
GENERAL INFORMATION:
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;
FILE REFERENCE: D6223CIP/C/D/CIP2
CURRENT APPLICATION NUMBER: US/10/372,521
CURRENT FILING DATE: 2003-02-21
PRIOR FILING DATE: 2001-07-30
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 Length 9;
 Length 9;
 Indels
 Indels
 ; OTHER INFORMATION: Residues 91-99 of the SCCE protein US-09-905-083-130
 ; OTHER INFORMATION: Residues 91-99 of the SCCE protein US-10-372-521-99
 100.0%; Score 42; DB 9; I
100.0%; Pred. No. 1.6e+06;
 100.0%; Score 42; DB 15; 100.0%; Pred. No. 1.6e+06;
 0; Mismatches
 0; Mismatches
CURRENT APPLICATION NUMBER: US/09/905,083
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 09/502,600
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 130
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
PRTURE: NAME/KEY: CHAIN
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Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
 Shimkets, Richard A.
Rothenberg, Mark E.
Leach, Martin D.
 Catterton
Ji, Weizhen
Miller, Charles E.
Rastelli, Luca
erone, David J.
 Smithson, Glennda
Millet, Isabelle
Peyman, John A.
Kekuda, Ramesh
Ju, Jingfang
 Ellerman, Karen
Malyankar, Uriel M
 Zerhusen, Bryan D.
Anderson, David W.
 Pena, Carol B. A.
Shenoy, Suresh G.
 Catterton, Elina
 Agee, Michele L.
Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
 Gorman, Linda
 Ort, Tatiana
 1 ORIKASKSF
 ORIKASKSF
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 US-10-831-075-99

| Sequence 99, Application US/10831075
| Publication No. US20040224891A1
| GENERAL INFORMATION:
| APPLICANT: O'Brien, Timethy J.
| APPLICANT: Cannon, Martin J.
| APPLICANT: Santin, Alessandro
| TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;
| FILE REFERENCE: D6223CIP/C/D/CIP3|
| CURRENT APPLICATION NUMBER: US/10/831,075
| CURRENT PILING DATE: 2004-04-23
| PRIOR PILING DATE: 2003-02-21
| NUMBER OF SEQ ID NOS: 140
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 Sequence 130, Application US/10831075
Publication No. US20040224891A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cannon, Martin J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
TILE REPERENCE: D6223GIP/C/P/CIP3
CURRENT APPLICATION: Methods for the early diagnosis of ovarian cancer FILE REFERENCE: D6223GIP/C/P/CIP3
CURRENT APPLICATION NUMBER: US/10/831,075
CURRENT FILING DATE: 2004-04-23
PRIOR PILING DATE: 2003-02-21
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 100.0%; Score 42; DB 16; Length 9; 100.0%; Pred. No. 1.6e+06;
 0; Indels
 0; Indels
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 , NAME/KEY: CHAIN
; OTHER INFORMATION: Residues 91-99 of the SCCE protein
US-10-831-075-99
 CTHER INFORMATION: Residues 91-99 of the SCCE protein US-10-831-075-130
 Query Match 100.0%; Score 42; DB 15; Best Local Similarity 100.0%; Pred. No. 1.6e+06; Matches 9; Conservative 0; Mismatches 0;
 0; Mismatches
 9; Conservative
 NUMBER OF SEQ ID NOS: 140
SEQ ID NO 130
LENGTH: 9
 TYPE: PRT
ORGANISM: Homo sapiens
TYPE: PRT
ORGANISM: Homo sapiens
 ORGANISM: Homo sapiens
 1 QRIKASKSF 9
 1 QRIKASKSF 9
 ORIKASKSF 9
 1 ORIKASKSF 9
 Query Match
Best Local Similarity
Matches 9; Conserv
 FEATURE:
NAME/KEY: CHAIN
 US-10-831-075-130
 SEQ ID NO 99
LENGTH: 9
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 Gaps
 Remaining Prior Application data removed - See File Wrapper or PALM
 APPLICANT: Berghs, Constance
IITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 Indels
100.0%; Score 42; DB 16; 100.0%; Pred. No. 1.6e+06;
 Mismatches
 FILE REFERENCE: 21402-462C
CURRENT APPLICATION NUMBER: US/10/262,511
CURRENT FILING DATE: 2003-05-28
 PRIOR APPLICATION NUMBER: 60/373,815
PRIOR PLING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2002-05-19
PRIOR PILING DATE: 2002-05-19
PRIOR PRIOR DATE: 2002-05-10-09
PRIOR PILING DATE: 2002-05-16
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PRIOR PELING DATE: 2001-10-09
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PRIOR PELING DATE: 2002-04-17
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PRIOR PELING DATE: 2001-05-05-18
 Sequence 100, Application US/10262511
Publication No. US20040038223A1
GENERAL INFORMATION:
 NT FILING DATE: 2003-05-28
APPLICATION UNDBER: 60/326,483
FILING DATE: 2001-10-02
APPLICATION NUMBER: 60/373,815
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Gaps ö

0; Indels

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0; Mismatches
 Zerhusen, Bryan D.
Anderson, David W.
Zhong, Mei
Catterton, Elina
 Shimkets, Richard A
 Rothenberg, Mark E.
Leach, Martin D.
Agee, Michele L.
 Malyankar, Uriel M.
 Ji, Weizhen
Miller, Charles E.
Rastelli, Luca
 Pena, Carol E. A. Shenoy, Suresh G.
 APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
 Ellerman, Karen
 Stone, David J.
 9; Conservative
 Gorman, Linda
 Ju, Jingfang
Li, Li
 Ort, Tatiana
 TYPE: PRT
ORGANISM: Homo sapiens
US-10-262-511-98
 28 QRIKASKSF 36
 1 ORIKASKSF
 APPLICANT
 Matches
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 Sequence 4, Application US/10461787; Sequence 4, Application US/10461787; Publication Wo. US20030199010A1; Publication Wo. US20030199010A1; Publication Wo. US20030199010A1; Publicant: O'Brien, Timothy J. APPLICANT: Underwood, Lowell J. TITLE OF INVENTION: NO. US20030199010A1e1 Extracellular Serine Protease; FILE REPERENCE: D602001P2; CURRENT FILING DATE: 2003-06-13; PRIOR PILING DATE: 2000-07-18; PRIOR APPLICATION NUMBER: US/09/618,259; PRIOR FILING DATE: 2000-07-18; PRIOR APPLICATION NUMBER: US 09/127,444; PRIOR FILING DATE: 1998-08-21; NUMBER OF SEQ ID NOS: 72
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 NAMENTER: DOMAIN
OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic
OTHER INFORMATION: enzyme (scce) catalytic domain
 OTHER INFORMATION: Amino acid sequence of stratum corneum chymotryptic OTHER INFORMATION: enzyme (scce) catalytic domain
 Gaps
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 100.0%; Score 42; DB 14; Length 144; 100.0%; Pred. No. 1;
 DB 15; Length 97;
 100.0%; Score 42; DB 9; Length 144; 100.0%; Pred. No. 1; 0. Mismatches 0; Indels
 0; Indels
 Sequence 4, Application US/09796294; Patent No. US20020037581A1; GENERAL INFORMATION:
APPLICANT: O'Berien, Timothy J.
APPLICANT: Underwood, Lowell J.
FILE OF INVENTION: Extracellular Serine Protease; FILE REFERENCE: D602001P3; CURRENT APPLICATION NUMBER: US/09/796,294; CURRENT APPLICATION NUMBER: US/09/796,294; CURRENT FILING DATE: 2001-02-28; PRIOR FILING DATE: 2000-07-18; NUMBER OF SEQ ID NOS: 72; SEQ ID NO SEQ ID NOS: 72; LENGTH: 144
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9; Conservative
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Matches 9; Conservative
; ORGANISM: Homo sapiens
US-10-262-511-100
 72 ORIKASKSF 80
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 1 ORIKASKSF 9
 1 QRIKASKSF 9
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Best Local Similarity
 TYPE: PRT
ORGANISM: unknown
 TYPE: PRT
ORGANISM: unknown
 FEATURE:
NAME/KEY: DOMAIN
 LENGTH: 144
 ; OTHER INFORM
US-09-796-294-4
 US-10-461-787-4
 Query Match
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APPLICANT: Berghs, COURSTANCE
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERBERGE: 21402-462C
CURRENT APPLICATION NUMBER: 05/326,483
PRIOR PILING DATE: 2001-10-28
PRIOR FILING DATE: 2001-10-09
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PRIOR FILING DATE: 2002-05-17
PRIOR FILING DATE: 2002-06-17
PRIOR FILING DATE: 2002-06-17
PRIOR FILING DATE: 2002-06-17
PRIOR FILING DATE: 2002-04-17
PRIOR PLICATION NUMBER: 60/333, 260
PRIOR FILING DATE: 2002-04-17
PRIOR FILING DATE: 2002-04-17
PRIOR PRIOR APPLICATION NUMBER: 60/337, 435
PRIOR FILING DATE: 2001-10-05
PRIOR FILING DATE: 2001-10-05
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PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/327, 435
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PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/327, 435
PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/327, 435
PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/3000 DATE: 2002-04-17
PRIOR PRIOR APPLICATION NUMBER: 60/300 DATE: 2002-04-17
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PRIOR PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/300 DATE: 2002-04-17
PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/300 DATE: 2002-04-17
Sequence 98, Application US/10262511 Publication No. US20040038223A1 GENERAL INFORMATION:
 Guo, Xiaojia (Sasha)
Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
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Gaps

;; 0

0; Indels

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100.0%; Score 42; DB 15; Length 198; 100.0%; Pred. No. 1.4;
 ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
 0; Mismatches
 TOPOLOGY: linear MOLECULE TYPE: None SEQUENCE DESCRIPTION: SEQ ID NO: 33:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
 AND METHODS USE
 RESULT 14
US-09-789-210-33
; Sequence 33, Application US/09789210
; Publication No. US20040241646A1
; GENERAL INFORMATION:
APPLICANT: COHEN, MAURICE
: COLPITTS, TRACEY L.
 INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 amino acids
 FELEPHONE: 847/935-1729
 FILING DATE: <Unknown>
 TELEFAX: 847/938-2623
 TYPE: amino acid
STRANDEDNESS: single
 CITY: Abbott Park
STATE: IL
 9; Conservative
 NUMBER OF SEQUENCES:
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-511-96
 1 QRIKASKSF 9
 Best Local Similarity
Matches 9; Conserv
 us-09-789-210-33
 Query Match
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 APPLICANT: AGGE, MICREE L.
APPLICANT: AGGE, MICREE L.
APPLICANT: AGGE, MICREE L.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REPERBNES: 21402-462C
CURRENT APPLICATION NUMBER: 60/326,483
PRIOR APPLICATION NUMBER: 60/373,815
PRIOR APPLICATION NUMBER: 60/373,915
PRIOR APPLICATION NUMBER: 60/373,917
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR PILING DATE: 2002-05-16
PRIOR PILING DATE: 2002-05-16
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR APPLICATION NUMBER: 60/381,038
PRIOR PILING DATE: 2002-05-16
PRIOR PILING DATE: 2002-05-16
PRIOR PLING DATE: 2002-05-16
PRIOR PILING DATE: 2002-05-16
PRIOR PLING DATE: 2002-05-16
PRIOR PLING DATE: 2002-05-16
PRIOR PLING DATE: 2002-05-17
PRIOR PLING DATE: 2001-10-09
PRIOR PLING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,260
PRIOR PLING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,405
PRIOR PLING DATE: 2002-05-16
PRIOR PLING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,435
PRIOR PLING DATE: 2002-05-16
PRIOR PLING DATE: 2001-10-05
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 0; Indels
 0; Mismatches
 Sequence 96, Application US/10262511
Publication No. US20040038223A1
GENERAL INFORMATION:
 CuraSeqList version 0.1
 Xiaojia (Sasha)
 Shimkets, Richard A
 Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
 Malyankar, Uriel M.
Ort, Tatiana
 APPLICANT: Smithson, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
APPLICANT: Ju, Jingfang
APPLICANT: Li, Li
 Rothenberg, Mark E.
Leach, Martin D.
Agee, Michele L.
 Miller, Charles E. Rastelli, Luca Stone, David J.
 Zerhusen, Bryan D.
Anderson, David W.
 Carol E. A. y, Suresh G.
 Zhong, Mei
Catterton, Elina
 Ellerman, Karen
 Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
 Gorman, Linda
 Weizhen
 72 QRIKASKSF 80
 1 ORIKASKSF 9
 Pena,
 SOFTWARE: Cur
SEQ ID NO 96
LENGTH: 198
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USEFUL FOR DETECTING AND TREATING DISEASES
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 Gaps
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 Query Match
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GRANADOS, EDWARD N.
KLASS, MICHABL R.
RUSSELL, JOHN C.
STEWART, KBYT D.
STROWDE, STEWARD.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
 COMPTRY: USA
ZIP: 60064-3500
COMPUTER READABLE PORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEM; DOS
SOFTWARE: FASTEM; DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/789,210
FILING DATE: Z0-Feb-2001
CLASSIFTCATION: «UNKNOWN»
PRIOR APPLICATION DATA:
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62 QRIKASKSF 70

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APPLICANT: Garceron, Ellna
APPLICANT: Ji, Weizhen
APPLICANT: Miller, Charles E.
APPLICANT: Barelli, Luca
APPLICANT: Beney, Carol E. A.
APPLICANT: Shimket S. Richard A.
APPLICANT: Shimket S. Richard A.
APPLICANT: Shimket S. Richard A.
APPLICANT: Age, Martin D.
APPLICANT: Age, Martin D.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462
CURRENT APPLICANT: MACHAEL E.
APPLICANT: Berghs, Constance
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-462
CURRENT FILING DATE: 2001-10-02
PRIOR PELLICATION NUMBER: 60/326,483
PRIOR PELLICATION NUMBER: 60/326,917
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR PELLING DATE: 2001-10-09
PRIOR FILING DATE: 2002-10-09
PRIOR FILING DATE: 2002-00-09
PRIOR PELLING DATE: 2002-00-09
PRIOR FILING DATE: 2002-00-09
PRIOR PELLING DATE: 2002-00-09
PRIOR PELLING DATE: 2002-00-00-09
PRIOR PELLING DATE: 2002-00-09
PRIOR PELLING DATE: 2002-00-09
PRIOR PELLING DATE: 2002-00-09
PRIOR PELLING DATE: 2002-00-00-
 h Similarity 100.0%; Score 42; DB 15; Length 224; Similarity 100.0%; Pred. No. 1.6; 9; Conservative 0; Mismatches 0; Indels
US-10-262-511-104
; Sequence 104, Application US/10262511
; Publication No. US20040038223A1
 Patturajan, Meera
Spytek, Kimberly A.
Edinger, Shlomit R.
Ellerman, Karen
Malyankar, Uriel M.
Ort, Tatiana
Gorman, Linda
 Ju, Jingfang
Li, Li
Guo, Xiaojia (Sasha)
 Zerhusen, Bryan D.
Anderson, David W.
 GENERAL INFORMATION:
APPLICANT: Smithson, Glenda
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A.
APPLICANT: Kekuda, Ramesh
 Zhong, Mei
Catterton, Elina
 TYPE: PRT
CORGANISM: Homo sapiens
US-10-262-511-104
 Query Match
Best Local Similarity
Matches 9; Conserv
 SEQ ID NO 104
LENGTH: 224
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0; Gaps

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77 QRIKASKSF 85
1 QRIKASKSF 9
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Search completed: July 13, 2005, 18:23:42 Job time : 64.8889 secs